

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 07:18:59 ; Search time 140.018 Seconds

(without alignments)
273,421 Million cell updates/sec

Title: US-10-080-959A-1

Perfect score: 17

Sequence: 1 gtcgctcgcgcggaac 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 1698378

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: /SID2/gcgdata/geneseq/geneseq-nbml/NA1980.DAT.*
2: /SID2/gcgdata/geneseq/geneseq-nbml/NA1981.DAT.*
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20: /SID2/gcgdata/geneseq/geneseq-nbml/NA1999.DAT.*
21: /SID2/gcgdata/geneseq/geneseq-nbml/NA2000.DAT.*
22: /SID2/gcgdata/geneseq/geneseq-nbml/NA2001A.DAT.*
23: /SID2/gcgdata/geneseq/geneseq-nbml/NA2001B.DAT.*
24: /SID2/gcgdata/geneseq/geneseq-nbml/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	14	82.4	22	ABK29246 Aspergillus aurico
2	14	82.4	22	ABK29280 Aspergillus sclero
3	14	82.4	22	ABK29289 Aspergillus wentii
4	13	76.5	16	ABK29262 Aspergillus flavip
5	13	76.5	16	ABK29265 Aspergillus nives
6	12.8	75.3	23	ABK29249 Aspergillus caesp
7	12.8	75.3	23	ABK29286 Aspergillus unguis
8	12.4	72.9	15	ABN99623 Fungi PCR primer S
9	12.4	72.9	15	ABK29220 Trichoderma harzia

C	10	12.4	72.9	16	24	ABK29366 Penicillium expans
C	11	12.4	72.9	21	24	ABN99619 Fungi probe SEQ ID
C	12	12.4	72.9	21	24	ABN99622 Fungi probe SEQ ID
C	13	12.4	72.9	21	24	ABN99631 Fungi probe SEQ ID
C	14	12.4	72.9	21	24	Trichoderma aspre
C	15	12.4	72.9	21	24	Trichoderma aspre
C	16	12.4	72.9	21	24	Trichoderma viride
C	17	12.4	72.9	22	24	ABN99459 Fungi probe SEQ ID
C	18	12.4	72.9	22	24	ABK29056 Aspergillus ochrac
C	19	12.4	72.9	22	24	ABK29268 Aspergillus ochrac
C	20	12.4	72.9	22	24	ABK29271 Aspergillus oclian
C	21	12.2	71.8	20	16	AAQ94376 Mycosphaerella filj
C	22	12.2	71.8	20	19	AAV62554 M. fijiensis speci
C	23	12.2	70.6	24	24	AA168755 Human gp66 antibod
C	24	12	70.6	17	24	ABN99548 Fungi PCR primer S
C	25	12	70.6	17	24	ABK29145 Penicillium brevic
C	26	12	70.6	20	20	AAQ202872 PCR primer used to
C	27	11.8	69.4	19	22	AAK61866 Soybean lectin PCR
C	28	11.8	69.4	20	22	AAK69341 Integrin-linked K1
C	29	11.8	69.4	20	24	ABK29459 Capture oligonucle
C	30	11.8	69.4	24	24	ABK29459 Capture oligonucle
C	31	11.8	69.4	24	24	ABK29459 Capture oligonucle
C	32	11.8	69.4	25	22	ABK29459 Capture oligonucle
C	33	11.8	69.4	25	24	ABK29459 Capture oligonucle
C	34	11.4	67.1	15	22	AAK51334 IGF-1 oligonucleot
C	35	11.4	67.1	15	22	AAK51335 IGF-1 oligonucleot
C	36	11.4	67.1	15	22	AAK51336 IGF-1 oligonucleot
C	37	11.4	67.1	16	16	AAK51336 IGF-1 oligonucleot
C	38	11.4	67.1	16	16	Fusarium spp. ITS
C	39	11.4	67.1	16	16	Fusarium spp. ITS
C	40	11.4	67.1	16	16	Mouse rDNA hairpin
C	41	11.4	67.1	16	16	Fusarium species 8
C	42	11.4	67.1	16	16	Fusarium species 8
C	43	11.4	67.1	16	24	Fungi PCR primer S
C	44	11.4	67.1	18	14	AAQ47860 Trichoderma longib
C	45	11.4	67.1	20	19	AAK61697 Flavonoid-3',5'-hy
C	46	11.4	67.1	21	19	Hepatitis B virus
C	47	11.4	67.1	21	19	Cylindrocapsa des
C	48	11.4	67.1	21	22	ABK29419 PCR primer used to
C	49	11.2	65.9	18	16	AAQ84564 Penicillium variab
C	50	11.2	65.9	18	16	AAQ84564 Herpes simplex vir
C	51	11.2	65.9	20	17	AAK73111 RNA-binding oligon
C	52	11.2	65.9	20	20	AAK73111 PCR primer used to
C	53	11.2	65.9	20	22	AAK73299 Human B7-1 antiben
C	54	11.2	65.9	20	24	ABK29289 Capture oligonucle
C	55	11.2	65.9	24	21	AAK27216 Forward PCR primer
C	56	11.2	65.9	24	21	AAK27216 Forward PCR primer
C	57	11.2	65.9	24	21	AAK27216 Forward PCR primer
C	58	11.2	65.9	24	21	AAK27216 Forward PCR primer
C	59	11.2	65.9	24	24	ABK29024 Capture oligonucle
C	60	11.2	65.9	24	24	ABK29024 Capture oligonucle
C	61	11.2	65.9	25	21	AAK37166 Human DNA4549 rev
C	62	11.2	65.9	25	22	AAK37166 Human DNA4549 rev
C	63	11.2	65.9	15	24	AAK37166 Human F12 gene all
C	64	11.2	65.9	18	24	ABN99476 Fungi PCR primer S
C	65	11.2	65.9	18	24	ABK29073 Aspergillus versu
C	66	11.2	65.9	20	18	AAK57732 Wheat germ aggluti
C	67	11.2	65.9	23	15	AAQ56214 env amplification
C	68	11.2	65.9	23	15	AAQ56214 C-terminal gp46 pr
C	69	11.2	65.9	24	24	ABO00812 Oligonucleotide ad
C	70	11.2	65.9	24	24	ABO00812 Oligonucleotide ad
C	71	11.2	65.9	24	24	ABO00812 Oligonucleotide ad
C	72	11.2	65.9	24	24	ABO00812 Oligonucleotide ad
C	73	11.2	65.9	24	24	ABO00812 Oligonucleotide ad
C	74	11.2	65.9	24	24	ABO00812 Oligonucleotide ad
C	75	11.2	65.9	24	24	ABO00812 Oligonucleotide ad
C	76	11.2	65.9	24	24	ABO00812 Oligonucleotide ad
C	77	11.2	65.9	24	24	ABO00812 Oligonucleotide ad
C	78	11.2	65.9	24	24	ABO00812 Oligonucleotide ad
C	79	11.2	65.9	24	24	ABO00812 Oligonucleotide ad
C	80	11.2	65.9	24	24	ABO00812 Oligonucleotide ad
C	81	11.2	65.9	24	24	ABO00812 Oligonucleotide ad
C	82	11.2	65.9	24	24	ABO00812 Oligonucleotide ad

C 83	10.8	63.5	24	22	AAA89163	Canine dystrophin
C 84	10.6	62.4	20	20	AAK29338	JNK2-specific prob
C 85	10.6	62.4	20	21	AAK52881	JNK antisense olig
C 86	10.6	62.4	20	22	AAD14816	Human glycogen syn
C 87	10.6	62.4	20	24	ABL45103	Human chromosome 1
C 88	10.6	62.4	22	17	AAI27173	PLTIS exon 2 sense
C 89	10.6	62.4	22	17	AAI27173	PLTIS gene exon 2
C 90	10.6	62.4	24	19	AAV07067	Primer P3 for A. f
C 91	10.6	62.4	24	19	AB189774	Capture oligonucle
C 92	10.6	62.4	24	20	AB189775	Capture oligonucle
C 93	10.6	62.4	25	20	AAK0487	Fragment #9 of Chl
C 94	10.4	61.2	15	22	AAK51333	Igf-1 oligonucleot
C 95	10.4	61.2	18	21	AAK51337	Igf-1 oligonucleot
C 96	10.4	61.2	18	21	ABN81193	Pennaeus monodon m
C 97	10.4	61.2	18	22	AAK61752	B. napus KCS assoc
C 98	10.4	61.2	19	22	AAK52722	Human DNA polymera
C 99	10.4	61.2	20	18	AAK96810	Human IgG-gamma1 c
C 100	10.4	61.2	20	19	AAV48007	Human B7-1 target
C 101	10.4	61.2	20	19	AAK94145	Primer ZG10315 for
C 102	10.4	61.2	20	21	AAZ93619	Antisense oligonuc
C 103	10.4	61.2	20	22	AAK45617	Human PAMP-1 antis
C 104	10.4	61.2	20	22	AAH75353	Human uridine kina
C 105	10.4	61.2	20	22	AAH27664	Human bcl-x antis
C 106	10.4	61.2	20	22	AAK95123	hba gene PCR prim
C 107	10.4	61.2	20	22	AAK32849	Human B7-1 mRNA an
C 108	10.4	61.2	20	22	AAK32950	Human B7-1 antis
C 109	10.4	61.2	20	22	AAK31168	Human B7-1 antis
C 110	10.4	61.2	20	24	ABN93590	Fungi PCR primer S
C 111	10.4	61.2	20	24	AAK96601	Telomerase reverse
C 112	10.4	61.2	20	24	ABK21187	Penicillium specie
C 113	10.4	61.2	21	19	AAK26277	Human polymorphic
C 114	10.4	61.2	21	24	ABK11331	Arabidopsis Acyl c
C 115	10.4	61.2	21	24	AAK28090	Bovine fertility a
C 116	10.4	61.2	22	18	AAK65512	Oligonucleotide 8L
C 117	10.4	61.2	22	21	AAK33989	PCR primer 7 for s
C 118	10.4	61.2	24	22	AAK85898	Primer AD173. Syn
C 119	10.4	61.2	24	24	ABK89038	RT-PCR primer, #4,
C 120	10.2	60.0	18	15	AAK66783	L6 mRNA function s
C 121	10.2	60.0	18	24	ABK51920	Mouse Caenq2, PCR
C 122	10.2	60.0	19	14	AAK05090	Human prohibitin g
C 123	10.2	60.0	20	16	AAK075159	RAR-alpha-1 primer
C 124	10.2	60.0	20	17	AAI14241	Activital phosphor
C 125	10.2	60.0	20	17	AAI12435	Activital phosphor
C 126	10.2	60.0	20	18	AAV01149	Homeobox 7 PCR pri
C 127	10.2	60.0	20	19	AAV70936	PCR primer used to
C 128	10.2	60.0	20	20	AAK03809	PCR primer used to
C 129	10.2	60.0	20	20	AAK03285	PCR primer used to
C 130	10.2	60.0	20	21	AAK292608	Primer 6, a murine
C 131	10.2	60.0	20	22	AAK95204	Human cDNA clone-s
C 132	10.2	60.0	20	22	AAK25292	Antisense oligonuc
C 133	10.2	60.0	20	22	AAK92836	Human P13 Kinase P
C 134	10.2	60.0	20	24	AAK27995	Escherichia coli c
C 135	10.2	60.0	20	24	ABL52396	Mouse FLIP-c chime
C 136	10.2	60.0	21	19	AAV70926	PCR primer used to
C 137	10.2	60.0	21	19	AAV65913	Regulatory element
C 138	10.2	60.0	21	19	AAV65914	Regulatory element
C 139	10.2	60.0	21	21	AAK5389	Rat c-Rel coding s
C 140	10.2	60.0	21	22	AAK24663	Nucleotide sequenc
C 141	10.2	60.0	21	24	ABK65616	Human single nucle
C 142	10.2	60.0	22	20	AAZ07591	Primer for detecti
C 143	10.2	60.0	22	24	ABA94946	Soybean KAS II DNA
C 144	10.2	60.0	22	14	AAK05526	5'-3' primer seque
C 145	10.2	60.0	24	22	AAK13057	Probe #3 used in g
C 146	10.2	60.0	24	24	ABQ61253	Human aquaporin 5
C 147	10.2	60.0	24	24	ABQ01004	Oligonucleotide ad
C 148	10.2	60.0	24	24	ABQ05964	Oligonucleotide ad
C 149	10.2	60.0	24	24	ABQ06005	Oligonucleotide ad
C 150	10.2	60.0	24	24	AAK19005	Oligonucleotide ad
C 151	10.2	60.0	24	24	AAK19018	Wheat library acet
C 152	10.2	60.0	25	15	AAQ45170	Factor IX gene pti
C 153	10.2	60.0	25	17	AAI14243	Activital phosphor
C 154	10.2	60.0	25	20	AAK57102	Human mutant KCMQ2
C 155	10.2	60.0	25	24	ABQ61862	Human aquaporin 5
C 156	10.2	60.0	25	24	ABQ61864	Human aquaporin 5
C 157	10.2	60.0	25	24	ABQ61866	Human aquaporin 5
C 158	10.2	60.0	25	24	ABQ61868	Human aquaporin 5
C 159	10.2	60.0	25	24	ABQ61870	Human aquaporin 5
C 160	10.2	60.0	25	24	ABQ61872	Human aquaporin 5
C 161	10.2	60.0	25	24	ABQ61874	Human aquaporin 5
C 162	10.2	60.0	25	24	ABQ61876	Human aquaporin 5
C 163	10.2	60.0	25	24	ABQ61878	Human aquaporin 5
C 164	10.2	60.0	25	24	ABQ61880	Human aquaporin 5
C 165	10.2	60.0	25	24	ABQ61882	Human aquaporin 5
C 166	10.2	60.0	25	24	ABQ61915	Human aquaporin 5
C 167	10.2	60.0	25	24	ABQ61917	Human aquaporin 5
C 168	10.2	60.0	25	24	ABQ61919	Human aquaporin 5
C 169	10.2	60.0	25	24	ABQ61921	Human aquaporin 5
C 170	10.2	60.0	25	24	ABQ61923	Human aquaporin 5
C 171	10.2	60.0	25	24	ABQ61925	Human aquaporin 5
C 172	10.2	60.0	25	24	ABQ61927	Human aquaporin 5
C 173	10.2	60.0	25	24	ABQ61929	Human aquaporin 5
C 174	10.2	60.0	25	24	ABQ61931	Human aquaporin 5
C 175	10.2	60.0	15	24	AAK139510	CCBP2 detecting AS
C 176	10.2	60.0	15	24	ABK99544	Fungi probe SEQ ID
C 177	10.2	60.0	17	24	ABN99554	Fungi probe SEQ ID
C 178	10.2	60.0	17	24	ABN99556	Fungi probe SEQ ID
C 179	10.2	60.0	17	24	ABN99557	Fungi probe SEQ ID
C 180	10.2	60.0	17	24	ABN99558	Fungi probe SEQ ID
C 181	10.2	60.0	17	24	ABK26259	Increased starch p
C 182	10.2	60.0	17	24	ABK26260	Increased starch p
C 183	10.2	60.0	17	24	ABK26261	Increased starch p
C 184	10.2	60.0	17	24	ABK26292	Increased starch p
C 185	10.2	60.0	17	24	ABK29141	Penicillium specie
C 186	10.2	60.0	17	24	ABK29151	Penicillium specie
C 187	10.2	60.0	17	24	ABK29163	Penicillium specie
C 188	10.2	60.0	17	24	ABK29176	Penicillium madric
C 189	10.2	60.0	17	24	ABK29182	Penicillium roquet
C 190	10.2	60.0	17	24	ABK29274	Aspergillus parado
C 191	10.2	60.0	17	24	ABK29346	Penicillium aurant
C 192	10.2	60.0	17	24	ABK29351	Penicillium aurant
C 193	10.2	60.0	17	24	ABK29364	Penicillium digit
C 194	10.2	60.0	17	24	ABK29373	Penicillium digit
C 195	10.2	60.0	17	24	ABK29376	Penicillium glandi
C 196	10.2	60.0	17	24	ABK29382	Penicillium hirsut
C 197	10.2	60.0	17	24	ABK29422	Penicillium verruc
C 198	10.2	60.0	18	21	AAK58353	Human PRO1710 hybr
C 199	10.2	60.0	18	21	AAK58353	Human PRO1710 hybr
C 200	10.2	60.0	19	21	AAK491798	Granulocyte Ehrli
C 201	10.2	60.0	19	21	AAK49021	PCR primer #2 targ
C 202	10.2	60.0	20	20	AAK95765	PCR primer used to
C 203	10.2	60.0	20	20	AAK95765	PCR primer used to
C 204	10.2	60.0	20	24	ABK197505	Capture oligonucle
C 205	10.2	60.0	21	24	ABN99450	Fungi probe SEQ ID
C 206	10.2	60.0	21	24	ABK29047	Aspergillus fumiga
C 207	10.2	60.0	22	19	AAV20928	Aspergillus clavac
C 208	10.2	60.0	22	19	AAV20933	PCR primer used to
C 209	10.2	60.0	24	24	ABO03775	Oligonucleotide ad
C 210	10.2	60.0	24	24	ABK191002	Capture oligonucle
C 211	10.2	60.0	24	24	ABK191003	Capture oligonucle
C 212	10.2	60.0	24	24	ABK191580	Capture oligonucle
C 213	10.2	60.0	24	24	ABK191581	Capture oligonucle
C 214	10.2	60.0	24	24	ABK191582	Capture oligonucle
C 215	10.2	60.0	24	24	ABK191583	Capture oligonucle
C 216	10.2	60.0	24	24	ABK191584	Capture oligonucle
C 217	10.2	60.0	24	24	ABK191585	Capture oligonucle
C 218	10.2	60.0	24	24	ABK191586	Capture oligonucle
C 219	10.2	60.0	24	24	ABK191587	Capture oligonucle
C 220	10.2	60.0	24	24	ABK191588	Capture oligonucle
C 221	10.2	60.0	24	24	ABK191589	Capture oligonucle
C 222	10.2	60.0	24	24	ABK191590	Capture oligonucle
C 223	10.2	60.0	24	24	ABK191591	Capture oligonucle
C 224	10.2	60.0	24	24	ABK191592	Capture oligonucle
C 225	10.2	60.0	24	24	ABK191593	Capture oligonucle
C 226	10.2	60.0	24	24	ABK191594	Capture oligonucle
C 227	10.2	60.0	24	24	ABK191595	Capture oligonucle
C 228	10.2	60.0	24	24	ABK191596	Capture oligonucle

C 229	9.8	57.6	16	22	AAH42495	PCR primer used to
C 230	9.8	57.6	17	20	AAH91368	Primer for RT-PCR
C 231	9.8	57.6	17	21	AAH36448	Human genomic SNP
C 232	9.8	57.6	17	21	AAH44768	Oestrogen receptor
C 233	9.8	57.6	17	22	ABAT77290	Adenosine deaminas
C 234	9.8	57.6	17	22	ABAT77290	Adenosine deaminas
C 235	9.8	57.6	17	22	ABAT77290	Adenosine deaminas
C 236	9.8	57.6	17	22	AAH42691	T. gondii immunoge
C 237	9.8	57.6	18	14	AAH47859	Flavonoid-3',5'-hy
C 238	9.8	57.6	18	14	AAH47864	Flavonoid-3',5'-hy
C 239	9.8	57.6	18	14	AAH47866	Flavonoid-3',5'-hy
C 240	9.8	57.6	18	14	AAH47866	Flavonoid-3',5'-hy
C 241	9.8	57.6	18	15	AAH97316	Primer amplifying
C 242	9.8	57.6	18	15	AAH97316	Delta-9 desaturase
C 243	9.8	57.6	18	18	AAH63294	Paracoccus denitri
C 244	9.8	57.6	18	20	AAH90150	Human biallelic ma
C 245	9.8	57.6	18	21	AAH75332	TRAD antiserum ol
C 246	9.8	57.6	18	21	AAH93500	Human herpesviru
C 247	9.8	57.6	19	16	AAH01526	Cytomegalovirus de
C 248	9.8	57.6	19	16	AAH08028	Oligonucleotide pr
C 249	9.8	57.6	19	16	AAH08298	Epoetin-Barr virus
C 250	9.8	57.6	19	16	AAH09090	Primer 196-pri for
C 251	9.8	57.6	19	18	AAH81261	Primer P51-3.2 for
C 252	9.8	57.6	19	18	AAH81261	Primer P51-3.2 for
C 253	9.8	57.6	19	18	AAH81261	Primer P51-3.2 for
C 254	9.8	57.6	19	19	AAH51598	Zea mays genome fo
C 255	9.8	57.6	19	21	AAH84977	Cyclin G1 ribozyme
C 256	9.8	57.6	19	22	AAH60139	Cyclin G1 ribozyme
C 257	9.8	57.6	20	13	AAH026636	Primer B1. Synth
C 258	9.8	57.6	20	13	AAH048140	Staphylococcus aur
C 259	9.8	57.6	20	14	AAH068450	Primer used to det
C 260	9.8	57.6	20	15	AAH89502	Primer for porcine
C 261	9.8	57.6	20	19	AAH48026	Murine B7-1 target
C 262	9.8	57.6	20	20	AAH05791	PCR primer used to
C 263	9.8	57.6	20	20	AAH97976	EF-Tu gene region
C 264	9.8	57.6	20	20	AAH93437	PCR primer used to
C 265	9.8	57.6	20	20	AAH93437	PCR primer used to
C 266	9.8	57.6	20	20	AAH92088	Human FUT3 antigen
C 267	9.8	57.6	20	21	AAH63684	PCR primer U20 us
C 268	9.8	57.6	20	21	AAH63684	PB322 5' primer.
C 269	9.8	57.6	20	21	AAH09021	Human E-cadherin r
C 270	9.8	57.6	20	22	AAH05678	Transcription fact
C 271	9.8	57.6	20	22	AAH87576	S aureus detection
C 272	9.8	57.6	20	22	AAH89314	S aureus detection
C 273	9.8	57.6	20	22	AAH89314	S aureus detection
C 274	9.8	57.6	20	22	AAH79928	Integrin-linked ki
C 275	9.8	57.6	20	22	AAH69314	Human hmrp Al pho
C 276	9.8	57.6	20	22	AAH69314	Murine B7-1 mRNA a
C 277	9.8	57.6	20	22	AAH69314	Mouse C/EBP beta p
C 278	9.8	57.6	20	24	AAH35809	Probe for Candida
C 279	9.8	57.6	20	24	AAH35809	Probe for Candida
C 280	9.8	57.6	21	20	AAH34288	Primer TERC1 for m
C 281	9.8	57.6	21	21	AAH53672	Oligonucleotide us
C 282	9.8	57.6	21	21	AAH53671	Thid-generation p
C 283	9.8	57.6	21	23	AAH68959	Human gene single
C 284	9.8	57.6	21	23	AAH68959	Human polymorphic
C 285	9.8	57.6	22	17	AAH41401	MAGE-1 PCR primer
C 286	9.8	57.6	22	18	AAH92083	Salmonella typhimu
C 287	9.8	57.6	22	20	AAH28055	MAGE-1 gene specif
C 288	9.8	57.6	22	20	AAH28055	Probe for Candida
C 289	9.8	57.6	22	21	AAH64620	Probe for Candida
C 290	9.8	57.6	22	21	AAH39235	MAGE-1 PCR primer
C 291	9.8	57.6	22	21	AAH49184	PCR primer for MAGE
C 292	9.8	57.6	22	21	AAH35532	Sense PCR primer f
C 293	9.8	57.6	22	21	AAH35532	Forward PCR primer
C 294	9.8	57.6	22	22	AAH81414	MAGE-A1 sense PCR
C 295	9.8	57.6	22	22	AAH84232	MAGE tumour reject
C 296	9.8	57.6	22	22	AAH84232	MAGE tumour reject
C 297	9.8	57.6	23	16	AAH087643	Mouse tirka gene am
C 298	9.8	57.6	23	20	AAH80650	Primer2 for amplif
C 299	9.8	57.6	23	20	AAH81965	E. coli FMS patia
C 300	9.8	57.6	24	19	AAH63997	Mycobacterium tube
C 301	9.8	57.6	24	20	AAH81053	PCR primer for clo
					AAH15831	Oligonucleotide TNG

C 375	9.6	56.5	24	24	ABO02005	Oligonucleotide ad	448	9.4	55.3	20	19	AAV61121	L. brevis 16S ribo
C 376	9.6	56.5	24	24	ABO02970	Oligonucleotide ad	449	9.4	55.3	20	20	AA205032	PCR primer used to
C 377	9.6	56.5	24	24	ABO03189	Oligonucleotide ad	450	9.4	55.3	20	20	AA296475	PCR primer used to
C 378	9.6	56.5	24	24	ABO03719	Oligonucleotide ad	451	9.4	55.3	20	21	AA273652	Human Biallelic ma
C 379	9.6	56.5	24	24	ABO03723	Oligonucleotide ad	452	9.4	55.3	20	21	AA292055	Mammalian Lhx3 PCR
C 380	9.6	56.5	24	24	ABO04010	Oligonucleotide ad	453	9.4	55.3	20	21	AA248067	Human IGF-II antis
C 381	9.6	56.5	24	24	ABO04047	Oligonucleotide ad	454	9.4	55.3	20	22	AA293994	Immunostimulatory
C 382	9.6	56.5	24	24	ABO04684	Oligonucleotide ad	455	9.4	55.3	20	22	AA296652	Immunostimulatory
C 383	9.6	56.5	24	24	ABO06925	Oligonucleotide ad	456	9.4	55.3	20	24	AA248176	Human HLA DPB1 10c
C 384	9.6	56.5	24	24	ABO07862	Oligonucleotide ad	457	9.4	55.3	20	24	AA248192	Human HLA DPB1 10c
C 385	9.6	56.5	24	24	ABO07903	Oligonucleotide ad	458	9.4	55.3	20	24	AA2443361	Bacillus sp novel
C 386	9.6	56.5	24	24	ABO07980	Oligonucleotide ad	459	9.4	55.3	20	24	AB2494361	Mouse C/EBP beta P
C 387	9.6	56.5	24	24	ABO09822	Oligonucleotide ad	460	9.4	55.3	20	24	ABK69252	Chimeric phosphoro
C 388	9.6	56.5	24	24	ABO09863	Oligonucleotide ad	461	9.4	55.3	20	24	AB216506	Marmoset Type II G
C 389	9.6	56.5	24	24	ABO09863	Oligonucleotide ad	462	9.4	55.3	20	24	AB2193588	Capture oligonucle
C 390	9.6	56.5	24	24	ABO10241	Oligonucleotide ad	463	9.4	55.3	20	24	ABK29403	Pericillium putrup
C 391	9.6	56.5	24	24	ABO10282	Oligonucleotide ad	464	9.4	55.3	20	24	AB239021	Immunostimulatory
C 392	9.6	56.5	24	24	AB184764	Capture oligonucle	465	9.4	55.3	20	24	AB239022	Immunostimulatory
C 393	9.6	56.5	24	24	AB184765	Capture oligonucle	466	9.4	55.3	21	15	AA063806	Human megakaryocy
C 394	9.6	56.5	25	18	AA175988	Chimeric Ig gamma	467	9.4	55.3	21	15	AA056652	Human megakaryocy
C 395	9.6	56.5	25	19	AAV29824	Chimeric Ig gamma	468	9.4	55.3	21	15	AA072457	Glutathione peroxi
C 396	9.6	56.5	25	19	AAV29831	Chimeric Ig gamma	469	9.4	55.3	21	16	AA099347	Hepatitis C virus
C 397	9.6	56.5	25	19	AAV21359	Chimeric Ig gamma	470	9.4	55.3	21	19	AA226304	Human polymorphic
C 398	9.6	56.5	25	19	AAV04090	Composite CRP-CAAT	471	9.4	55.3	21	19	AA226305	Human polymorphic
C 399	9.6	56.5	25	21	AAV63439	HLA DPB1 gene PCR	472	9.4	55.3	21	19	AA256903	Regulatory element
C 400	9.6	56.5	25	21	AAV57768	Antisense oligonuc	473	9.4	55.3	21	19	AAV56504	Regulatory element
C 401	9.6	56.5	25	22	AAH49550	Primer #2 used to	474	9.4	55.3	21	20	AAV55712	PCR primer for glu
C 402	9.6	56.5	25	24	ABT03543	Human Ash-1 gene p	475	9.4	55.3	21	20	AAV83825	PCR primer used to
C 403	9.6	56.5	25	24	AA141672	Human colon cancer	476	9.4	55.3	21	21	AA269271	Human ABC1 gene ex
C 404	9.4	55.3	12	23	ABH98514	Oligonucleotide pr	477	9.4	55.3	21	21	AA259195	5' PCR primer used
C 405	9.4	55.3	13	18	AA25510	Oligonucleotide SL	478	9.4	55.3	21	21	AA249938	Human tumour suppr
C 406	9.4	55.3	13	18	ABCS2580	Oligonucleotide SE	479	9.4	55.3	21	22	AA295373	Human gene single
C 407	9.4	55.3	13	23	ABCS2581	Oligonucleotide SE	480	9.4	55.3	21	22	AA295644	Human gene single
C 408	9.4	55.3	13	23	ABCS2581	Oligonucleotide SE	481	9.4	55.3	21	22	AA295644	Partial exon 7 pub
C 409	9.4	55.3	13	23	ABCS2581	Oligonucleotide SE	482	9.4	55.3	21	22	AA24690	PCR primer used to
C 410	9.4	55.3	13	23	ABCS2581	Oligonucleotide SE	483	9.4	55.3	21	22	AA24690	PCR primer used to
C 411	9.4	55.3	13	23	ABCS2581	Oligonucleotide SE	484	9.4	55.3	21	22	AA24690	Sequence of PCR pr
C 412	9.4	55.3	14	20	AAV92826	Oligonucleotide SE	485	9.4	55.3	22	15	AA054952	meo-lacZ fusion c
C 413	9.4	55.3	14	20	AAV92826	Oligonucleotide SE	486	9.4	55.3	22	15	AA062295	Primer to amplify
C 414	9.4	55.3	14	21	AA264817	Human A-raf target	487	9.4	55.3	22	18	AA288220	Primer 3-S1 for ta
C 415	9.4	55.3	15	21	AA264817	Substrate for hair	488	9.4	55.3	22	19	AAV21077	Arabidopsis RAP2.7
C 416	9.4	55.3	15	21	AA264817	Substrate for hair	489	9.4	55.3	22	20	AA207680	RAP2.7 gene specif
C 417	9.4	55.3	15	21	AA264817	Substrate for hair	490	9.4	55.3	22	21	AA207680	RAP2.7 Ap2 domain
C 418	9.4	55.3	15	22	AA264817	Substrate for hair	491	9.4	55.3	22	21	AA207680	aac(6)-Ic resist
C 419	9.4	55.3	15	22	AA264817	Substrate for hair	492	9.4	55.3	23	22	AAH01382	aac(6)-Ic resist
C 420	9.4	55.3	15	22	AA264817	Substrate for hair	493	9.4	55.3	23	22	AAH01382	Sequence of probe
C 421	9.4	55.3	15	22	AA264817	Substrate for hair	494	9.4	55.3	24	14	AA052199	Neuroblastoma spec
C 422	9.4	55.3	15	22	AA264817	Substrate for hair	495	9.4	55.3	24	22	AA264817	Human tumour necro
C 423	9.4	55.3	15	22	AA264817	Substrate for hair	496	9.4	55.3	24	24	ABA99037	PCR primer corresp
C 424	9.4	55.3	15	24	ABK95956	Human LIPF gene po	497	9.4	55.3	24	24	ABO02919	Oligonucleotide ad
C 425	9.4	55.3	15	24	ABK95956	Human LIPF gene po	498	9.4	55.3	24	24	ABO09732	Oligonucleotide ad
C 426	9.4	55.3	15	24	ABK95956	Human LIPF gene po	499	9.4	55.3	24	24	ABO09732	Oligonucleotide ad
C 427	9.4	55.3	15	24	ABK95956	Human LIPF gene po	500	9.4	55.3	24	24	ABA95524	Human basophil gra
C 428	9.4	55.3	16	21	AA257831	HSV-2 ICP27 gene r	501	9.4	55.3	24	24	AB183746	Capture oligonucle
C 429	9.4	55.3	17	19	AAV43302	Primer JB627 for a	502	9.4	55.3	24	24	AB183747	Capture oligonucle
C 430	9.4	55.3	17	19	AAV43302	Primer JB627 for a	503	9.4	55.3	24	24	AB183747	Capture oligonucle
C 431	9.4	55.3	18	14	AA052919	Human BRCA1 gene p	504	9.4	55.3	24	24	AB188430	Capture oligonucle
C 432	9.4	55.3	18	14	AA052919	Human BRCA1 gene p	505	9.4	55.3	25	16	AA033009	Pre-invasive human
C 433	9.4	55.3	18	14	AA052919	Human BRCA1 gene p	506	9.4	55.3	25	16	AA033009	hCMV primer set 12
C 434	9.4	55.3	18	20	AA219477	Human G-alpha-11 p	507	9.4	55.3	25	18	AA209067	PCR primer 2 used
C 435	9.4	55.3	18	20	AA219477	Human G-alpha-11 p	508	9.4	55.3	25	18	AA209067	Novel method of de
C 436	9.4	55.3	18	21	AA273526	Human G-alpha-11 p	509	9.4	55.3	25	18	AA209067	Primer C3E2 for CM
C 437	9.4	55.3	18	22	AA273526	Human G-alpha-11 p	510	9.4	55.3	25	21	AA209067	PCR primer LB42M w
C 438	9.4	55.3	18	22	AA273526	Human G-alpha-11 p	511	9.4	55.3	25	21	AA209067	Cytomegalovirus et
C 439	9.4	55.3	18	22	AA273526	Human G-alpha-11 p	512	9.4	55.3	25	22	AA209067	SNP specific SNP
C 440	9.4	55.3	19	9	AA209067	Synthetic oligo LB	513	9.2	54.1	15	16	AA255044	Mouse rela hamme
C 441	9.4	55.3	19	21	AA209067	Synthetic oligo LB	514	9.2	54.1	15	16	AA255044	Mouse rela hamme
C 442	9.4	55.3	19	21	AA209067	Synthetic oligo LB	515	9.2	54.1	15	22	AA255044	IGF-I oligonucleot
C 443	9.4	55.3	19	22	AA209067	Synthetic oligo LB	516	9.2	54.1	15	22	AA255044	IGF-I oligonucleot
C 444	9.4	55.3	19	22	AA209067	Synthetic oligo LB	517	9.2	54.1	15	22	AA255044	IGF-I oligonucleot
C 445	9.4	55.3	20	15	AA071662	IGF-I oligonucleot	518	9.2	54.1	16	14	AA048283	Vibrio cholerae 16
C 446	9.4	55.3	20	15	AA071662	IGF-I oligonucleot	519	9.2	54.1	16	14	AA048283	Vibrio cholerae 16
C 447	9.4	55.3	20	19	AAV57074	Human Notch3 mutan	520	9.2	54.1	16	16	AA255594	Human rela halprin

C 521	9.2	54.1	16	16	AAT55608	Mouse relA hairpin	594	9.2	54.1	20	24	ABN74928	Mouse caspase 2 an
C 522	9.2	54.1	16	16	ABK96855	Preynl di phosphat	595	9.2	54.1	20	24	AA514411	Reverse PCR primer
C 523	9.2	54.1	16	24	ABA89572	Acidobacterium Tag	596	9.2	54.1	20	24	AA597424	Murine SMC1 gene-8
C 524	9.2	54.1	16	24	ABA89658	Serial analysis of	597	9.2	54.1	20	24	AA516653	Human Inhibitor of
C 525	9.2	54.1	16	24	ABA89768	Reverse PCR primer	598	9.2	54.1	20	24	AB182301	p53 mutation detec
C 526	9.2	54.1	17	14	AAQ37997	Reverse PCR primer	599	9.2	54.1	20	24	AB193470	Capture oligonucle
C 527	9.2	54.1	17	14	AAQ38490	Reverse PCR primer	600	9.2	54.1	20	24	AB194404	Capture oligonucle
C 528	9.2	54.1	17	18	AAK68973	Human fil1 VEGF re	601	9.2	54.1	20	24	AB194601	Capture oligonucle
C 529	9.2	54.1	17	18	AAK68973	Rat Ha-ras targete	602	9.2	54.1	20	24	AB194662	Capture oligonucle
C 530	9.2	54.1	17	19	AAK68973	Integrin alpha 6 s	603	9.2	54.1	20	24	AB194677	Capture oligonucle
C 531	9.2	54.1	17	20	AAA21342	Integrin alpha 6 s	604	9.2	54.1	20	24	AB195236	Capture oligonucle
C 532	9.2	54.1	17	20	AAA21343	Integrin alpha 6 s	605	9.2	54.1	20	24	AB196060	Capture oligonucle
C 533	9.2	54.1	17	20	AAA21343	Integrin subunit b	606	9.2	54.1	20	24	AB196602	Capture oligonucle
C 534	9.2	54.1	17	21	AAAF0799	Hammerhead ribozym	607	9.2	54.1	20	24	AB196635	Capture oligonucle
C 535	9.2	54.1	17	21	AAAF0799	Hammerhead ribozym	608	9.2	54.1	20	24	AB197345	Capture oligonucle
C 536	9.2	54.1	17	22	ABA79980	HBAl mutation corr	609	9.2	54.1	20	24	AB197345	Human chromosome 1
C 537	9.2	54.1	17	22	ABA79981	HBAl mutation corr	610	9.2	54.1	21	13	AAQ25066	DNA for modulating
C 538	9.2	54.1	17	24	ABK26555	Waxy starch produc	611	9.2	54.1	21	16	AAQ40205	Sequence of primer
C 539	9.2	54.1	17	24	ABK26556	Waxy starch produc	612	9.2	54.1	21	16	AAQ40205	Chv DNA polymerase
C 540	9.2	54.1	17	24	ABK26559	Waxy starch produc	613	9.2	54.1	21	17	AAQ40205	Bovine leukaemia v
C 541	9.2	54.1	17	24	ABK26592	Waxy starch produc	614	9.2	54.1	21	18	AAQ40205	Humicola lanuginos
C 542	9.2	54.1	17	24	ABK26615	Waxy starch produc	615	9.2	54.1	21	18	AAQ40205	Humicola lanuginos
C 543	9.2	54.1	17	24	ABK26616	Waxy starch produc	616	9.2	54.1	21	19	AAQ40205	Humicola lanuginos
C 544	9.2	54.1	18	16	AAQ93389	Mycosphaerella mus	617	9.2	54.1	21	19	AAQ40205	Humicola lanuginos
C 545	9.2	54.1	18	18	AAQ93389	Mouse fil-1 VEGF r	618	9.2	54.1	21	19	AAQ40205	Humicola lanuginos
C 546	9.2	54.1	18	18	AAQ93389	Mouse fil-1 VEGF r	619	9.2	54.1	21	19	AAQ40205	Humicola lanuginos
C 547	9.2	54.1	18	19	AAQ93389	Mouse Aop2 gene ex	620	9.2	54.1	21	21	AAQ40205	Humicola lanuginos
C 548	9.2	54.1	18	19	AAQ93389	M. musicola specie	621	9.2	54.1	21	21	AAQ40205	Humicola lanuginos
C 549	9.2	54.1	18	19	AAQ93389	Human SCA2 gene SC	622	9.2	54.1	21	21	AAQ40205	Humicola lanuginos
C 550	9.2	54.1	18	21	AAQ93389	Antisense oligonuc	623	9.2	54.1	21	21	AAQ40205	Humicola lanuginos
C 551	9.2	54.1	18	21	AAQ93389	Rat ribosomal prot	624	9.2	54.1	21	22	AAQ40205	Humicola lanuginos
C 552	9.2	54.1	18	22	ABK23208	Zmxi gene region	625	9.2	54.1	21	22	AAQ40205	Humicola lanuginos
C 553	9.2	54.1	18	24	ABK23208	Human Zmxi cDNA r	626	9.2	54.1	21	22	AAQ40205	Humicola lanuginos
C 554	9.2	54.1	18	24	ABK23208	Human HLA genotypi	627	9.2	54.1	21	22	AAQ40205	Humicola lanuginos
C 555	9.2	54.1	18	24	AAQ43123	RT-PCR reverse pri	628	9.2	54.1	21	22	AAQ40205	Humicola lanuginos
C 556	9.2	54.1	19	14	AAQ43123	HCV NS-4 antisense	629	9.2	54.1	21	22	AAQ40205	Humicola lanuginos
C 557	9.2	54.1	19	14	AAQ43123	C. trichomatis det	630	9.2	54.1	21	23	AAQ40205	Humicola lanuginos
C 558	9.2	54.1	19	19	AAQ43123	PCR primer specifi	631	9.2	54.1	21	23	AAQ40205	Humicola lanuginos
C 559	9.2	54.1	19	20	AAQ43123	PCR primer L2027 F	632	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 560	9.2	54.1	19	20	AAQ43123	Retroviral tagged	633	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 561	9.2	54.1	19	21	AAQ43123	Primer used to amp	634	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 562	9.2	54.1	19	21	AAQ43123	HIV-1 related bind	635	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 563	9.2	54.1	19	24	ABK1616	Linked linear ampl	636	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 564	9.2	54.1	20	13	AAQ20250	Hepatitis C primer	637	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 565	9.2	54.1	20	13	AAQ20250	Primer DNA 3. Syn	638	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 566	9.2	54.1	20	13	AAQ20250	Primer DNA 3. Syn	639	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 567	9.2	54.1	20	14	AAQ20250	HCV NS-4 type 3 de	640	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 568	9.2	54.1	20	14	AAQ20250	C. trichomatis det	641	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 569	9.2	54.1	20	16	AAQ20250	Murine m26 struct	642	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 570	9.2	54.1	20	16	AAQ20250	Primer OTG5024 to	643	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 571	9.2	54.1	20	18	AAQ20250	Phytophthora palmi	644	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 572	9.2	54.1	20	18	AAQ20250	Chymase antisense	645	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 573	9.2	54.1	20	20	AAQ20250	PCR primer used to	646	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 574	9.2	54.1	20	20	AAQ20250	PCR primer used to	647	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 575	9.2	54.1	20	20	AAQ20250	PCR primer used to	648	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 576	9.2	54.1	20	20	AAQ20250	PCR primer used to	649	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 577	9.2	54.1	20	20	AAQ20250	PCR primer used to	650	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 578	9.2	54.1	20	20	AAQ20250	PCR primer used to	651	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 579	9.2	54.1	20	20	AAQ20250	PCR primer used to	652	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 580	9.2	54.1	20	20	AAQ20250	PCR primer used to	653	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 581	9.2	54.1	20	20	AAQ20250	Chymase antisense	654	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 582	9.2	54.1	20	21	AAQ20250	Human chymase poly	655	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 583	9.2	54.1	20	21	AAQ20250	Human KLR-L1 PCR p	656	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 584	9.2	54.1	20	21	AAQ20250	Dog genomic marker	657	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 585	9.2	54.1	20	21	AAQ20250	BanHI adapter. SEQ	658	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 586	9.2	54.1	20	21	AAQ20250	BclII PCR primer. S	659	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 587	9.2	54.1	20	21	AAQ20250	Low adenosine anti	660	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 588	9.2	54.1	20	21	AAQ20250	PCR primer used to	661	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 589	9.2	54.1	20	21	AAQ20250	probe for mouse mc	662	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 590	9.2	54.1	20	21	AAQ20250	Human TRAP100 PCR	663	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 591	9.2	54.1	20	21	AAQ20250	Trypanosoma detect	664	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 592	9.2	54.1	20	22	AAQ20250	Antisense IGFBP-5	665	9.2	54.1	21	24	AAQ40205	Humicola lanuginos
C 593	9.2	54.1	20	22	AAQ20250	Human PERK-cytoso	666	9.2	54.1	21	24	AAQ40205	Humicola lanuginos

667	9.2	54.1	24	15	AA045043	Oligomer comprisin	C 740	9.2	54.1	25	21	AA095878	H1A H1A-A gene PCR
668	9.2	54.1	24	15	AA071900	Lo-CD2a VH leader	C 741	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
669	9.2	54.1	24	16	AA067942	Sense oligonucleot	C 742	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
670	9.2	54.1	24	18	AAV01095	Human insulin PCR	C 743	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
671	9.2	54.1	24	18	AAV6106	Primer for light c	C 744	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
672	9.2	54.1	24	19	AAV67034	Mouse Ikars Oligo	C 745	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
673	9.2	54.1	24	19	AAV42170	Mouse Ikars isofo	C 746	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
674	9.2	54.1	24	19	AAV62519	Lo-CD2a chimeric a	C 747	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
675	9.2	54.1	24	19	AAV53719	Nucleotide sequenc	C 748	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
676	9.2	54.1	24	19	AAV28475	Lo-CD2a primer VH	C 749	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
677	9.2	54.1	24	19	AAV18681	Human immunoglobul	C 750	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
678	9.2	54.1	24	20	AAV10144	PCR primer used to	C 751	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
679	9.2	54.1	24	20	AAV22476	Receptor specific	C 752	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
680	9.2	54.1	24	20	AAV80529	DBS module 1 engi	C 753	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
681	9.2	54.1	24	21	AAV75347	PCR primer COLTPCR	C 754	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
682	9.2	54.1	24	21	AAV59566	Hepatitis C virus	C 755	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
683	9.2	54.1	24	22	AAV44499	SPIK5 5' splice d	C 756	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
684	9.2	54.1	24	22	AAV5890	Human split comple	C 757	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
685	9.2	54.1	24	22	AAH01373	aac(3')-Vira resist	C 758	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
686	9.2	54.1	24	22	AAV30587	Human Factor IX ge	C 759	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
687	9.2	54.1	24	22	AAV29722	Human alpha1,2-man	C 760	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
688	9.2	54.1	24	22	AAV8462	Degenerate PCR pri	C 761	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
689	9.2	54.1	24	24	AAV98425	Human V gene libra	C 762	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
690	9.2	54.1	24	24	AAV56804	Replication start	C 763	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
691	9.2	54.1	24	24	AAV00011	Oligonucleotide ad	C 764	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
692	9.2	54.1	24	24	AAV00842	Oligonucleotide ad	C 765	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
693	9.2	54.1	24	24	AAV00900	Oligonucleotide ad	C 766	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
694	9.2	54.1	24	24	AAV01746	Oligonucleotide ad	C 767	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
695	9.2	54.1	24	24	AAV02102	Oligonucleotide ad	C 768	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
696	9.2	54.1	24	24	AAV04011	Oligonucleotide ad	C 769	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
697	9.2	54.1	24	24	AAV04048	Oligonucleotide ad	C 770	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
698	9.2	54.1	24	24	AAV0538	Oligonucleotide ad	C 771	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
699	9.2	54.1	24	24	AAV05579	Oligonucleotide ad	C 772	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
700	9.2	54.1	24	24	AAV05737	Oligonucleotide ad	C 773	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
701	9.2	54.1	24	24	AAV05778	Oligonucleotide ad	C 774	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
702	9.2	54.1	24	24	AAV07435	Oligonucleotide ad	C 775	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
703	9.2	54.1	24	24	AAV07476	Oligonucleotide ad	C 776	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
704	9.2	54.1	24	24	AAV08116	Oligonucleotide ad	C 777	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
705	9.2	54.1	24	24	AAV08157	Oligonucleotide ad	C 778	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
706	9.2	54.1	24	24	AAV10376	Oligonucleotide ad	C 779	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
707	9.2	54.1	24	24	AAV10376	Oligonucleotide ad	C 780	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
708	9.2	54.1	24	24	AAV183510	Capture oligonucle	C 781	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
709	9.2	54.1	24	24	AAV183511	Capture oligonucle	C 782	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
710	9.2	54.1	24	24	AAV184254	Capture oligonucle	C 783	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
711	9.2	54.1	24	24	AAV184255	Capture oligonucle	C 784	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
712	9.2	54.1	24	24	AAV184258	Capture oligonucle	C 785	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
713	9.2	54.1	24	24	AAV184659	Capture oligonucle	C 786	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
714	9.2	54.1	24	24	AAV184872	Capture oligonucle	C 787	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
715	9.2	54.1	24	24	AAV184873	Capture oligonucle	C 788	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
716	9.2	54.1	24	24	AAV185772	Capture oligonucle	C 789	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
717	9.2	54.1	24	24	AAV185773	Capture oligonucle	C 790	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
718	9.2	54.1	24	24	AAV185894	Capture oligonucle	C 791	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
719	9.2	54.1	24	24	AAV185895	Capture oligonucle	C 792	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
720	9.2	54.1	24	24	AAV185924	Capture oligonucle	C 793	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
721	9.2	54.1	24	24	AAV185925	Capture oligonucle	C 794	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
722	9.2	54.1	24	24	AAV186210	Capture oligonucle	C 795	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
723	9.2	54.1	24	24	AAV186211	Capture oligonucle	C 796	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
724	9.2	54.1	24	24	AAV187042	Capture oligonucle	C 797	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
725	9.2	54.1	24	24	AAV187043	Capture oligonucle	C 798	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
726	9.2	54.1	24	24	AAV186890	Capture oligonucle	C 799	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
727	9.2	54.1	24	24	AAV186891	Capture oligonucle	C 800	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
728	9.2	54.1	24	24	AAV189840	Capture oligonucle	C 801	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
729	9.2	54.1	24	24	AAV189841	Capture oligonucle	C 802	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
730	9.2	54.1	24	24	AAV191260	Capture oligonucle	C 803	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
731	9.2	54.1	24	24	AAV191261	Capture oligonucle	C 804	9.2	54.1	25	21	AA095878	H1A H1A-B gene PCR
732	9.2	54.1	25	13	AAQ21402	PCR primer GH46' f	C 805	9.2	54.1	25	13	AAQ21402	H1A H1A-B gene PCR
733	9.2	54.1	25	14	AAQ42242	Primer FPL1 to amp	C 806	9.2	54.1	25	14	AAQ42242	H1A H1A-B gene PCR
734	9.2	54.1	25	15	AAQ64546	Chromosome 11 (loc	C 807	9.2	54.1	25	15	AAQ64546	H1A H1A-B gene PCR
735	9.2	54.1	25	16	AAQ82566	Nucleotide sequenc	C 808	9.2	54.1	25	16	AAQ82566	H1A H1A-B gene PCR
736	9.2	54.1	25	19	AAV41659	Nucleotide sequenc	C 809	9.2	54.1	25	19	AAV41659	H1A H1A-B gene PCR
737	9.2	54.1	25	19	AAV41670	SNRPB gene flankin	C 810	9.2	54.1	25	19	AAV41670	H1A H1A-B gene PCR
738	9.2	54.1	25	20	AAV41670	Primer 6A4_Rc4. U	C 811	9.2	54.1	25	20	AAV41670	H1A H1A-B gene PCR
739	9.2	54.1	25	21	AAV41670	Primer 6A4_Rc4. U	C 812	9.2	54.1	25	21	AAV41670	H1A H1A-B gene PCR

C 813	52.9	20	18	AA92784	Primer #1 for c-kit	C 886	52.9	22	14	AA051893	PML mRNA ribozyme
C 814	52.9	20	18	AA78883	Primer 788NUT for	C 887	52.9	22	19	AAV60619	PCR primer used to
C 815	52.9	20	18	AA751084	Primer #1 for env	C 888	52.9	22	19	AAV20905	PCR primer used to
C 816	52.9	20	19	AAV52781	c-kit PCR primer K	C 889	52.9	22	21	AA62617	Agrobacterium Ti-p
C 817	52.9	20	19	AAV40367	Maize oligonucleot	C 890	52.9	22	21	ABT04234	Human G-protein co
C 818	52.9	20	19	AAV37070	PCR primer for ant	C 891	52.9	22	24	ABQ08630	Human GPCR reverse
C 819	52.9	20	20	AA402304	PCR primer used to	C 892	52.9	22	24	ABK14927	Bovine poly(ADP-ri
C 820	52.9	20	20	AAV93684	PCR primer used to	C 893	52.9	22	24	ABK14945	Bovine poly(ADP-ri
C 821	52.9	20	20	AAV93302	PCR primer used to	C 894	52.9	22	24	ABR01751	Oryza sativa promo
C 822	52.9	20	20	AAV29405	Control oligonucle	C 895	52.9	23	15	AAQ45021	Oligomer compresin
C 823	52.9	20	20	AAV84236	Human STAT3 phosph	C 896	52.9	23	17	AAV42148	Primer P4 for apol
C 824	52.9	20	21	AAV93176	Human STAT3 phosph	C 897	52.9	23	19	AAV36836	Mouse Ikars isofo
C 825	52.9	20	21	AAV62948	JNK antisense olig	C 898	52.9	23	21	AAV63556	Oligonucleotide sp
C 826	52.9	20	21	AAV63844	Streptomyces albul	C 899	52.9	23	22	AAV65525	Primer ZC21, 076
C 827	52.9	20	21	AAV63844	PCR primer used to	C 900	52.9	23	22	ABK66773	Human gene specif
C 828	52.9	20	21	AAV63848	PCR primer used to	C 901	52.9	23	22	AAQ05781	pol primer of HTV
C 829	52.9	20	21	AAV72550	PCR primer CB3-TM	C 902	52.9	24	11	AAQ05781	1.1ASML CKOR olig
C 830	52.9	20	21	AAV72550	PCR primer CB3-TM	C 903	52.9	24	18	AAV62575	Telomerase reverse
C 831	52.9	20	21	AAV71144	PCR primer CB3-TM	C 904	52.9	24	19	AAV30696	Human calcium chan
C 832	52.9	20	21	AAV71144	PCR primer DHRD.91	C 905	52.9	24	20	AAV09149	Primer STS sy243 1
C 833	52.9	20	21	AAV9256	Primer 1 for human	C 906	52.9	24	21	AAV96930	PCR primer used to
C 834	52.9	20	21	AAV9256	Human neurofilin m	C 907	52.9	24	21	AAV96930	Herpesvirus expres
C 835	52.9	20	21	AAV9256	Human neurofilin m	C 908	52.9	24	21	AAV96930	Murine VH 1B fro
C 836	52.9	20	22	AAK95007	Human CDNA clone-s	C 909	52.9	24	21	AAV96930	Human Y-specific S
C 837	52.9	20	22	AAK95007	Human CDNA clone-s	C 910	52.9	24	21	AAV96930	DNA fragment used
C 838	52.9	20	22	AAH45318	PCR primer for an	C 911	52.9	24	22	AAV25992	Rat fibroblast
C 839	52.9	20	22	AAH45318	Human MHC S DNA PC	C 912	52.9	24	22	AAV25992	Primer #2 used to
C 840	52.9	20	22	AAH45318	Human MHC S DNA PC	C 913	52.9	24	22	AAV25992	Human gene specif
C 841	52.9	20	22	AAH45318	Human MHC S DNA PC	C 914	52.9	24	22	AAV25992	Oligonucleotide ad
C 842	52.9	20	22	AAH45318	Human MHC S DNA PC	C 915	52.9	24	22	AAV25992	Oligonucleotide ad
C 843	52.9	20	22	AAH45318	Human MHC S DNA PC	C 916	52.9	24	22	AAV25992	Oligonucleotide ad
C 844	52.9	20	22	AAH45318	Human MHC S DNA PC	C 917	52.9	24	22	AAV25992	Oligonucleotide ad
C 845	52.9	20	22	AAH45318	Human MHC S DNA PC	C 918	52.9	24	22	AAV25992	Oligonucleotide ad
C 846	52.9	20	22	AAH45318	Human MHC S DNA PC	C 919	52.9	24	22	AAV25992	Oligonucleotide ad
C 847	52.9	20	22	AAH45318	Human MHC S DNA PC	C 920	52.9	24	22	AAV25992	Oligonucleotide ad
C 848	52.9	20	22	AAH45318	Human MHC S DNA PC	C 921	52.9	24	22	AAV25992	Oligonucleotide ad
C 849	52.9	20	22	AAH45318	Human MHC S DNA PC	C 922	52.9	24	22	AAV25992	Oligonucleotide ad
C 850	52.9	20	22	AAH45318	Human MHC S DNA PC	C 923	52.9	24	22	AAV25992	Oligonucleotide ad
C 851	52.9	20	22	AAH45318	Human MHC S DNA PC	C 924	52.9	24	22	AAV25992	Oligonucleotide ad
C 852	52.9	20	22	AAH45318	Human MHC S DNA PC	C 925	52.9	24	22	AAV25992	Oligonucleotide ad
C 853	52.9	20	22	AAH45318	Human MHC S DNA PC	C 926	52.9	24	22	AAV25992	Oligonucleotide ad
C 854	52.9	20	22	AAH45318	Human MHC S DNA PC	C 927	52.9	24	22	AAV25992	Oligonucleotide ad
C 855	52.9	20	22	AAH45318	Human MHC S DNA PC	C 928	52.9	24	22	AAV25992	Oligonucleotide ad
C 856	52.9	20	22	AAH45318	Human MHC S DNA PC	C 929	52.9	24	22	AAV25992	Oligonucleotide ad
C 857	52.9	20	22	AAH45318	Human MHC S DNA PC	C 930	52.9	24	22	AAV25992	Oligonucleotide ad
C 858	52.9	20	22	AAH45318	Human MHC S DNA PC	C 931	52.9	24	22	AAV25992	Oligonucleotide ad
C 859	52.9	20	22	AAH45318	Human MHC S DNA PC	C 932	52.9	24	22	AAV25992	Oligonucleotide ad
C 860	52.9	20	22	AAH45318	Human MHC S DNA PC	C 933	52.9	24	22	AAV25992	Oligonucleotide ad
C 861	52.9	20	22	AAH45318	Human MHC S DNA PC	C 934	52.9	24	22	AAV25992	Oligonucleotide ad
C 862	52.9	20	22	AAH45318	Human MHC S DNA PC	C 935	52.9	24	22	AAV25992	Oligonucleotide ad
C 863	52.9	20	22	AAH45318	Human MHC S DNA PC	C 936	52.9	24	22	AAV25992	Oligonucleotide ad
C 864	52.9	20	22	AAH45318	Human MHC S DNA PC	C 937	52.9	24	22	AAV25992	Oligonucleotide ad
C 865	52.9	20	22	AAH45318	Human MHC S DNA PC	C 938	52.9	24	22	AAV25992	Oligonucleotide ad
C 866	52.9	20	22	AAH45318	Human MHC S DNA PC	C 939	52.9	24	22	AAV25992	Oligonucleotide ad
C 867	52.9	20	22	AAH45318	Human MHC S DNA PC	C 940	52.9	24	22	AAV25992	Oligonucleotide ad
C 868	52.9	20	22	AAH45318	Human MHC S DNA PC	C 941	52.9	24	22	AAV25992	Oligonucleotide ad
C 869	52.9	20	22	AAH45318	Human MHC S DNA PC	C 942	52.9	24	22	AAV25992	Oligonucleotide ad
C 870	52.9	20	22	AAH45318	Human MHC S DNA PC	C 943	52.9	24	22	AAV25992	Oligonucleotide ad
C 871	52.9	20	22	AAH45318	Human MHC S DNA PC	C 944	52.9	24	22	AAV25992	Oligonucleotide ad
C 872	52.9	20	22	AAH45318	Human MHC S DNA PC	C 945	52.9	24	22	AAV25992	Oligonucleotide ad
C 873	52.9	20	22	AAH45318	Human MHC S DNA PC	C 946	52.9	24	22	AAV25992	Oligonucleotide ad
C 874	52.9	20	22	AAH45318	Human MHC S DNA PC	C 947	52.9	24	22	AAV25992	Oligonucleotide ad
C 875	52.9	20	22	AAH45318	Human MHC S DNA PC	C 948	52.9	24	22	AAV25992	Oligonucleotide ad
C 876	52.9	20	22	AAH45318	Human MHC S DNA PC	C 949	52.9	24	22	AAV25992	Oligonucleotide ad
C 877	52.9	20	22	AAH45318	Human MHC S DNA PC	C 950	52.9	24	22	AAV25992	Oligonucleotide ad
C 878	52.9	20	22	AAH45318	Human MHC S DNA PC	C 951	52.9	24	22	AAV25992	Oligonucleotide ad
C 879	52.9	20	22	AAH45318	Human MHC S DNA PC	C 952	52.9	24	22	AAV25992	Oligonucleotide ad
C 880	52.9	20	22	AAH45318	Human MHC S DNA PC	C 953	52.9	24	22	AAV25992	Oligonucleotide ad
C 881	52.9	20	22	AAH45318	Human MHC S DNA PC	C 954	52.9	24	22	AAV25992	Oligonucleotide ad
C 882	52.9	20	22	AAH45318	Human MHC S DNA PC	C 955	52.9	24	22	AAV25992	Oligonucleotide ad
C 883	52.9	20	22	AAH45318	Human MHC S DNA PC	C 956	52.9	24	22	AAV25992	Oligonucleotide ad
C 884	52.9	20	22	AAH45318	Human MHC S DNA PC	C 957	52.9	24	22	AAV25992	Oligonucleotide ad
C 885	52.9	20	22	AAH45318	Human MHC S DNA PC	C 958	52.9	24	22	AAV25992	Oligonucleotide ad

959	9	52.9	24	24	AB182867	Capture oligonucle
960	9	52.9	24	24	AB183042	Capture oligonucle
961	9	52.9	24	24	AB183043	Capture oligonucle
962	9	52.9	24	24	AB184634	Capture oligonucle
963	9	52.9	24	24	AB184635	Capture oligonucle
964	9	52.9	24	24	AB185126	Capture oligonucle
965	9	52.9	24	24	AB185127	Capture oligonucle
966	9	52.9	24	24	AB186728	Capture oligonucle
967	9	52.9	24	24	AB186729	Capture oligonucle
968	9	52.9	24	24	AB186796	Capture oligonucle
969	9	52.9	24	24	AB186797	Capture oligonucle
970	9	52.9	24	24	AB187204	Capture oligonucle
971	9	52.9	24	24	AB187205	Capture oligonucle
972	9	52.9	24	24	AB187794	Capture oligonucle
973	9	52.9	24	24	AB187795	Capture oligonucle
974	9	52.9	24	24	AB188446	Capture oligonucle
975	9	52.9	24	24	AB188447	Capture oligonucle
976	9	52.9	24	24	AB190236	Capture oligonucle
977	9	52.9	24	24	AB190237	Capture oligonucle
978	9	52.9	24	24	AB191942	Capture oligonucle
979	9	52.9	24	24	AB191943	Capture oligonucle
980	9	52.9	24	24	AB192132	Capture oligonucle
981	9	52.9	24	24	AB192133	Capture oligonucle
982	9	52.9	24	24	AB192308	Capture oligonucle
983	9	52.9	24	24	AB192309	Capture oligonucle
984	9	52.9	25	15	AA057362	Enzymatic RNA mole
985	9	52.9	25	17	AA184458	5' DNA primer TB2C
986	9	52.9	25	17	AA184458	Tomato phytoene de
987	9	52.9	25	17	AA184458	Human chemotactic
988	9	52.9	25	18	AA185301	Primer for beta-g
989	9	52.9	25	18	AA185301	Primer 443P for R.
990	9	52.9	25	19	AAV58794	Hepatitis E virus
991	9	52.9	25	19	AAV58795	Synthetic polypept
992	9	52.9	25	19	AAV58795	Oligonucleotide co
993	9	52.9	25	20	AAV58795	Human kinase KSP P
994	9	52.9	25	21	AA220821	Human Lhx3 genomic
995	9	52.9	25	21	AA220821	Bacteriophage 3A O
996	9	52.9	25	21	AA220821	Bacteriophage 3A O
997	9	52.9	25	21	AA220821	Bacteriophage 3A O
998	9	52.9	25	21	AA220821	Pseudomonas sp. W
999	9	52.9	25	21	AA220821	Alzheimer's disease
1000	9	52.9	25	21	AA220821	Alzheimer's disease

ALIGNMENTS

RESULT 1
ID ABR29246/c
ABR29246 standard; DNA; 22 BP.

AC ABR29246;
XX
DT 23-APR-2002 (first entry)
XX
DE Aspergillus auricomus probe.
XX
KM Fungal detection; bacterial detection; probe; primer; ss.
XX
OS Aspergillus auricomus.
XX
PD WO200196612-A2
XX
PD 20-DEC-2001.
XX
PF 13-JUN-2001; 2001WO-US18892.
XX
PR 13-JUN-2000; 2000US-0593012.
XX
PA (USSI) US ENVIRONMENTAL PROTECTION AGENCY.
XX
PI Haugland R, Vesper SJ;
XX

DR WPI; 2002-098078/13.
XX
PT Detecting and quantifying fungi and bacteria, involves obtaining a
PT sequence of the fungus, extracting the DNA from the sample, and
PT subjecting the DNA to polymerase chain reaction and fluorescent probe
PT analysis
XX
PS Disclosure; Page 23; 110pp; English.
XX
CC The invention relates to a method of detecting and quantifying fungi and
CC bacteria, involving obtaining a sequence of the microorganism to be
CC detected and quantified, extracting the DNA from the sample, and
CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
CC probe analysis. The method is useful for identifying and quantifying
CC specific fungi and bacteria using specific DNA sequences. The specific
CC DNA sequences are useful for the real time detection of PCR products with
CC a fluorescent probe system or other molecular probes like hybridisation.
CC ABR29246-ABR29247 represent fungal and bacterial PCR primers and probes
XX used in the method of the invention.
XX
SQ Sequence 22 BP; 7 A; 8 C; 6 G; 1 T; 0 other;
XX
Query Match 82.4%; Score 14; DB 24; Length 22;
Best Local Similarity 100.0%; Pred No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 14 GTTGCTTCGCGCGG 1

RESULT 2
ID ABR29280/c
ABR29280 standard; DNA; 22 BP.
XX
AC ABR29280;
XX
DT 23-APR-2002 (first entry)
XX
DE Aspergillus sclerotiorum probe.
XX
KM Fungal detection; bacterial detection; probe; primer; ss.
XX
OS Aspergillus sclerotiorum.
XX
PD WO200196612-A2.
XX
PD 20-DEC-2001.
XX
PF 13-JUN-2001; 2001WO-US18892.
XX
PR 13-JUN-2000; 2000US-0593012.
XX
PA (USSI) US ENVIRONMENTAL PROTECTION AGENCY.
XX
PI Haugland R, Vesper SJ;
XX
DR WPI; 2002-098078/13.
XX
PT Detecting and quantifying fungi and bacteria, involves obtaining a
PT sequence of the fungus, extracting the DNA from the sample, and
PT subjecting the DNA to polymerase chain reaction and fluorescent probe
PT analysis
XX
PS Claim 87; Page 25; 110pp; English.
XX
CC The invention relates to a method of detecting and quantifying fungi and
CC bacteria, involving obtaining a sequence of the microorganism to be
CC detected and quantified, extracting the DNA from the sample, and
CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
CC probe analysis. The method is useful for identifying and quantifying
CC specific fungi and bacteria using specific DNA sequences. The specific
CC DNA sequences are useful for the real time detection of PCR products with
CC a fluorescent probe system or other molecular probes like hybridisation.
CC ABR29280-ABR29281 represent fungal and bacterial PCR primers and probes
XX used in the method of the invention.
XX
SQ Sequence 22 BP; 7 A; 8 C; 6 G; 1 T; 0 other;
XX
Query Match 82.4%; Score 14; DB 24; Length 22;
Best Local Similarity 100.0%; Pred No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 14 GTTGCTTCGCGCGG 1

RESULT 1
ID ABR29246/c
ABR29246 standard; DNA; 22 BP.
XX
AC ABR29246;
XX
DT 23-APR-2002 (first entry)
XX
DE Aspergillus auricomus probe.
XX
KM Fungal detection; bacterial detection; probe; primer; ss.
XX
OS Aspergillus auricomus.
XX
PD WO200196612-A2
XX
PD 20-DEC-2001.
XX
PF 13-JUN-2001; 2001WO-US18892.
XX
PR 13-JUN-2000; 2000US-0593012.
XX
PA (USSI) US ENVIRONMENTAL PROTECTION AGENCY.
XX
PI Haugland R, Vesper SJ;
XX

CC a fluorogenic probe system or other molecular probes like hybridisation.
CC ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes
CC used in the method of the invention.

XX Sequence 22 BP; 7 A; 8 C; 6 G; 1 T; 0 other;

Query Match 82.4%; Score 14; DB 24; Length 22;

Best Local Similarity 100.0%; Pred. No. 4.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGCTTCGCGCGG 14

DB 14 GTTGCTTCGCGCGG 1

RESULT 3
ABK29289/c
ID ABK29289 standard; DNA; 22 BP.

XX ABK29289;

DT 23-APR-2002 (first entry)

XX Aspergillus wentii probe.

XX Fungal detection; bacterial detection; probe; primer; ss.

XX Aspergillus wentii.

XX WO200196612-A2.

XX 20-DEC-2001.

XX 13-JUN-2001; 2001WO-US18892.

XX 13-JUN-2000; 2000US-0593012.

XX (USST) US ENVIRONMENTAL PROTECTION AGENCY.

XX Haugland R, Vesper SJ;

XX WPI; 2002-098078/13.

XX Detecting and quantifying fungi and bacteria, involves obtaining a

XX sequence of the fungus, extracting the DNA from the sample, and

XX subjecting the DNA to polymerase chain reaction and fluorescent probe

XX analysis

XX Claim 90; Page 26; 110pp; English.

XX The invention relates to a method of detecting and quantifying fungi and

XX bacteria, involving obtaining a sequence of the microorganism to be

XX detected and quantified, extracting the DNA from the sample, and

XX subjecting the DNA to polymerase chain reaction (PCR) and fluorescent

XX probe analysis. The method is useful for identifying and quantifying

XX specific fungi and bacteria using specific DNA sequences. The specific

XX DNA sequences are useful for the real time detection of PCR products with

XX a fluorogenic probe system or other molecular probes like hybridisation.

XX ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes

XX used in the method of the invention.

XX Sequence 22 BP; 7 A; 8 C; 6 G; 1 T; 0 other;

Query Match 82.4%; Score 14; DB 24; Length 22;

Best Local Similarity 100.0%; Pred. No. 4.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGCTTCGCGCGG 14

DB 14 GTTGCTTCGCGCGG 1

RESULT 4

ABK29262
ID ABK29262 standard; DNA; 16 BP.

XX ABK29262;

XX 23-APR-2002 (first entry)

XX Aspergillus flavipes probe.

XX Fungal detection; bacterial detection; probe; primer; ss.

XX Aspergillus flavipes

XX WO200196612-A2.

XX 20-DEC-2001.

XX 13-JUN-2001; 2001WO-US18892.

XX 13-JUN-2000; 2000US-0593012.

XX (USST) US ENVIRONMENTAL PROTECTION AGENCY.

XX Haugland R, Vesper SJ;

XX WPI; 2002-098078/13.

XX Detecting and quantifying fungi and bacteria, involves obtaining a

XX sequence of the fungus, extracting the DNA from the sample, and

XX subjecting the DNA to polymerase chain reaction and fluorescent probe

XX analysis

XX Claim 81; Page 24; 110pp; English.

XX The invention relates to a method of detecting and quantifying fungi and

XX bacteria, involving obtaining a sequence of the microorganism to be

XX detected and quantified, extracting the DNA from the sample, and

XX subjecting the DNA to polymerase chain reaction (PCR) and fluorescent

XX probe analysis. The method is useful for identifying and quantifying

XX specific fungi and bacteria using specific DNA sequences. The specific

XX DNA sequences are useful for the real time detection of PCR products with

XX a fluorogenic probe system or other molecular probes like hybridisation.

XX ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes

XX used in the method of the invention.

XX Sequence 16 BP; 0 A; 6 C; 6 G; 4 T; 0 other;

Query Match 76.5%; Score 13; DB 24; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.7e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGCTTCGCGCGG 14

DB 1 TTGCTTCGCGCGG 13

RESULT 5

ABK29265

ID ABK29265 standard; DNA; 16 BP.

XX ABK29265;

XX 23-APR-2002 (first entry)

XX Aspergillus niveus probe.

XX Fungal detection; bacterial detection; probe; primer; ss.

XX Aspergillus niveus.

XX WO200196612-A2.

XX 20-DEC-2001.

XX PF 13-JUN-2001; 2001WO-US18892.
 XX 13-JUN-2000; 2000US-0593012.
 XX (USSI) US ENVIRONMENTAL PROTECTION AGENCY.
 XX Haugland R, Vesper SJ;
 XX WPI; 2002-098078/13.
 XX
 XX Detecting and quantifying fungi and bacteria, involves obtaining a
 PT sequence of the fungus, extracting the DNA from the sample, and
 PT subjecting the DNA to polymerase chain reaction and fluorescent probe
 PT analysis
 XX
 XX Claim 82; Page 24; 110pp; English.
 XX
 XX The invention relates to a method of detecting and quantifying fungi and
 CC bacteria, involving obtaining a sequence of the microorganism to be
 CC detected and quantified, extracting the DNA from the sample, and
 CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
 CC probe analysis. The method is useful for identifying and quantifying
 CC specific fungi and bacteria using specific DNA sequences. The specific
 CC DNA sequences are useful for the real time detection of PCR products with
 CC a fluorogenic probe system or other molecular probes like hybridisation.
 CC ABR29026-ABK29474 represent fungal and bacterial PCR primers and probes
 CC used in the method of the invention.
 CC
 XX Sequence 16 BP; 0 A; 6 C; 6 G; 4 T; 0 other;
 SQ
 Query Match 76.5%; Score 13; DB 24; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TTGCTTCGCGCGG 14
 Db 1 TTGCTTCGCGCGG 13
 DB
 RESULT 6
 ABR29249
 ID ABR29249 standard; DNA; 23 BP.
 XX
 XX ABR29249;
 XX
 XX 23-APR-2002 (first entry)
 XX
 XX Aspergillus caespitosus probe.
 XX
 XX Fungal detection; bacterial detection; probe; primer; ss.
 XX
 XX Aspergillus caespitosus.
 XX
 XX WO200196612-A2.
 XX
 XX 20-DEC-2001.
 XX
 XX 13-JUN-2001; 2001WO-US18892.
 XX
 XX 13-JUN-2000; 2000US-0593012.
 XX
 XX (USSI) US ENVIRONMENTAL PROTECTION AGENCY.
 XX
 XX Haugland R, Vesper SJ;
 XX
 XX WPI; 2002-098078/13.
 XX
 XX Detecting and quantifying fungi and bacteria, involves obtaining a
 PT sequence of the fungus, extracting the DNA from the sample, and
 PT subjecting the DNA to polymerase chain reaction and fluorescent probe
 PT analysis
 XX

PS Claim 77; Page 23; 110pp; English.
 XX
 XX The invention relates to a method of detecting and quantifying fungi and
 CC bacteria, involving obtaining a sequence of the microorganism to be
 CC detected and quantified, extracting the DNA from the sample, and
 CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
 CC probe analysis. The method is useful for identifying and quantifying
 CC specific fungi and bacteria using specific DNA sequences. The specific
 CC DNA sequences are useful for the real time detection of PCR products with
 CC a fluorogenic probe system or other molecular probes like hybridisation.
 CC ABR29026-ABK29474 represent fungal and bacterial PCR primers and probes
 CC used in the method of the invention.
 CC
 XX Sequence 23 BP; 3 A; 7 C; 8 G; 5 T; 0 other;
 SQ
 Query Match 75.3%; Score 12.8; DB 24; Length 23;
 Best Local Similarity 87.5%; Pred. No. 2.2e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GTTGCTTCGCGCGGAA 16
 Db 5 GTTGCTTCGCGCGAGA 20
 DB
 RESULT 7
 ABR29286
 ID ABR29286 standard; DNA; 23 BP.
 XX
 XX ABR29286;
 XX
 XX 23-APR-2002 (first entry)
 XX
 XX Aspergillus unguis probe.
 XX
 XX Fungal detection; bacterial detection; probe; primer; ss.
 XX
 XX Aspergillus unguis.
 XX
 XX WO200196612-A2.
 XX
 XX 20-DEC-2001.
 XX
 XX 13-JUN-2001; 2001WO-US18892.
 XX
 XX 13-JUN-2000; 2000US-0593012.
 XX
 XX (USSI) US ENVIRONMENTAL PROTECTION AGENCY.
 XX
 XX Haugland R, Vesper SJ;
 XX
 XX WPI; 2002-098078/13.
 XX
 XX Detecting and quantifying fungi and bacteria, involves obtaining a
 PT sequence of the fungus, extracting the DNA from the sample, and
 PT subjecting the DNA to polymerase chain reaction and fluorescent probe
 PT analysis
 XX
 XX Claim 89; Page 25; 110pp; English.
 XX
 XX The invention relates to a method of detecting and quantifying fungi and
 CC bacteria, involving obtaining a sequence of the microorganism to be
 CC detected and quantified, extracting the DNA from the sample, and
 CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
 CC probe analysis. The method is useful for identifying and quantifying
 CC specific fungi and bacteria using specific DNA sequences. The specific
 CC DNA sequences are useful for the real time detection of PCR products with
 CC a fluorogenic probe system or other molecular probes like hybridisation.
 CC ABR29026-ABK29474 represent fungal and bacterial PCR primers and probes
 CC used in the method of the invention.
 CC
 XX Sequence 23 BP; 3 A; 7 C; 8 G; 5 T; 0 other;
 SQ
 Query Match 75.3%; Score 12.8; DB 24; Length 23;

Best Local Similarity 87.5%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GTTGCTTCGGCGGGA 16
|||
DB 5 GTTGCTTCGGCGGGA 20

RESULT 8

ABN99623 ID ABN99623 standard; DNA; 15 BP.

AC ABN99623;

DT 05-AUG-2002 (first entry)

DE Fungi PCR primer SEQ ID NO 195.

KM Fungus; bacteria; quantification; detection; infection; gastroenteritis;
ulcer; asthma; allergy; sinusitis; PCR; primer; ss.

OS Trichoderma harzianum.

PN US6387652-B1.

PD 14-MAY-2002.

PF 13-JUN-2000; 2000US-0593012.

PR 15-APR-1998; 98US-081773P.

PS 14-APR-1999; 99US-0290990.

XX (USSI) US ENVIRONMENTAL PROTECTION AGENCY.

PI Haugland R. Vesper S;

XX WPI; 2002-462353/49.

PT Detection and quantification of specific fungi or bacteria useful e.g.
in medical diagnosis and treatment of fungal and bacterial conditions,
by hybridizing and amplifying DNA using sequences unique to the species
or group of species

PS Claim 65; Column 97; 55pp; English.

XX The invention relates to specific fungi or bacteria detected and
quantified in a sample by extracting and recovering DNA from the organism
in the sample and hybridizing and amplifying the DNA sequence using
sequences unique to the species/group of species but common to all
isolates of the species/group of species. The method especially employs
sequences selected from 225 fungal and bacterial primer and probe
sequences (ABN99429-ABN99653) for detection of specified fungi/fungal
groups or specified bacteria. The method enables detection and
quantification of specific fungi or bacteria, or groups of
fungal/bacterial species, useful medically for diagnosis and treatment of
fungi or bacteria associated with health problems such as infections,
gastroenteritis, ulcers, asthma, allergies and sinusitis. It is also
useful to detect and/or quantify microorganisms in the environment e.g.
to establish the risk of adverse health effects (e.g. pulmonary
haemorrhage from levels of Stachybotrys chartarum in air samples in
houses).

XX Sequence 15 BP; 1 A; 4 C; 6 G; 4 T; 0 other;

Query Match 72.9%; Score 12.4; DB 24; Length 15;

Best Local Similarity 92.9%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTGCTTCGGCGGGA 15
|||
DB 1 TTGCTTCGGCGGGA 14

RESULT 9

ABK29220 ID ABK29220 standard; DNA; 15 BP.

AC ABK29220;

DT 23-APR-2002 (first entry)

DE Trichoderma harzianum forward PCR primer.

KM Fungal detection; bacterial detection; probe; primer; ss.

OS Trichoderma harzianum.

PN WO200196612-A2.

PD 20-DEC-2001.

PF 13-JUN-2001; 2001WO-US18892.

PR 13-JUN-2000; 2000US-0593012.

XX (USSI) US ENVIRONMENTAL PROTECTION AGENCY.

PI Haugland R. Vesper S;

XX WPI; 2002-098078/13.

PT Detecting and quantifying fungi and bacteria, involves obtaining a
sequence of the fungus, extracting the DNA from the sample, and
subjecting the DNA to polymerase chain reaction and fluorescent probe
analysis

PS Claim 65; Page 21; 110pp; English.

XX The invention relates to a method of detecting and quantifying fungi and
bacteria, involving obtaining a sequence of the microorganism to be
detected and quantified, extracting the DNA from the sample, and
subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
probe analysis. The method is useful for identifying and quantifying
specific fungi and bacteria using specific DNA sequences. The specific
DNA sequences are useful for the real time detection of PCR products with
a fluorescent probe system or other molecular probes like hybridisation.
ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes
used in the method of the invention.

XX Sequence 15 BP; 1 A; 4 C; 6 G; 4 T; 0 other;

Query Match 72.9%; Score 12.4; DB 24; Length 15;

Best Local Similarity 92.9%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTGCTTCGGCGGGA 15
|||
DB 1 TTGCTTCGGCGGGA 14

RESULT 10

ABK29366/c ID ABK29366 standard; DNA; 16 BP.

AC ABK29366;

DT 23-APR-2002 (first entry)

DE Penicillium expansum reverse PCR primer.

KM Fungal detection; bacterial detection; probe; primer; ss.

OS Penicillium expansum.

XX WO200196612-A2.

CC The invention relates to specific fungi or bacteria detected and
 CC quantified in a sample by extracting and recovering DNA from the organism
 CC in the sample and hybridizing and amplifying the DNA sequence using
 CC sequences unique to the species/group of species but common to all
 CC isolates of the species/group of species. The method especially employs
 CC sequences selected from 225 fungal and bacterial primer and probe
 CC sequences (ABN99429-ABN99653) for detection of specified fungi/fungal
 CC groups or specified bacteria. The method enables detection and
 CC quantification of specific fungi or bacteria, or groups of
 CC fungi/bacterial species, useful medically for diagnosis and treatment of
 CC fungi or bacteria associated with health problems such as infections,
 CC gastroenteritis, ulcers, asthma, allergies and sinusitis. It is also
 CC useful to detect and/or quantify microorganisms in the environment e.g.
 CC to establish the risk of adverse health effects (e.g. pulmonary
 CC haemorrhage from levels of *Stachybotrys chartarum* in air samples in
 CC houses).

CC Sequence 21 BP, 3 A, 7 C, 7 G, 4 T, 0 other;
 SO

Query Match 72.9%; Score 12.4; DB 24; Length 21;
 Best Local Similarity 92.9%; Pred. No. 3.5e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTTGCTTCGGCGG 14
 |||||
 8 GTTGCTTCGGCGG 21

DB

RESULT 13
 ABN99631
 ID ABN99631 standard; DNA, 21 BP.
 AC
 XX ABN99631;
 XX
 DT 05-AUG-2002 (first entry)
 XX
 XX Fungi probe SEQ ID NO 203.
 DE
 XX Fungus; bacteria; quantification; detection; infection; gastroenteritis;
 XX ulcer; asthma; allergy; sinusitis; probe; ss.
 KW
 XX Trichoderma viride.
 OS Trichoderma atroviride.
 OS Trichoderma koningi.
 XX
 XX US6387652-B1.
 XX
 XX 14-MAY-2002.
 PD
 XX
 XX 13-JUN-2000; 2000US-0593012.
 PF
 XX 15-APR-1998; 98US-081773P.
 PR 14-APR-1999; 99US-0290990.
 XX
 XX (USSI) US ENVIRONMENTAL PROTECTION AGENCY.
 PA
 XX
 XX Haugland R, Vesper S;
 PI
 XX WPI, 2002-462353/49.
 DR
 XX
 XX Detection and quantification of specific fungi or bacteria useful e.g.
 PT in medical diagnosis and treatment of fungal and bacterial conditions,
 PT by hybridizing and amplifying DNA using sequences unique to the species
 PT or group of species -
 XX
 XX Claim 67; Column 98; 55pp; English.
 PS
 XX The invention relates to specific fungi or bacteria detected and
 CC quantified in a sample by extracting and recovering DNA from the organism
 CC in the sample and hybridizing and amplifying the DNA sequence using
 CC sequences unique to the species/group of species but common to all
 CC isolates of the species/group of species. The method especially employs
 CC sequences selected from 225 fungal and bacterial primer and probe

CC sequences (ABN99429-ABN99653) for detection of specified fungi/fungal
 CC groups or specified bacteria. The method enables detection and
 CC quantification of specific fungi or bacteria, or groups of
 CC fungi/bacterial species, useful medically for diagnosis and treatment of
 CC fungi or bacteria associated with health problems such as infections,
 CC gastroenteritis, ulcers, asthma, allergies and sinusitis. It is also
 CC useful to detect and/or quantify microorganisms in the environment e.g.
 CC to establish the risk of adverse health effects (e.g. pulmonary
 CC haemorrhage from levels of *Stachybotrys chartarum* in air samples in
 CC houses).

CC Sequence 21 BP, 3 A, 7 C, 7 G, 4 T, 0 other;
 SO

Query Match 72.9%; Score 12.4; DB 24; Length 21;
 Best Local Similarity 92.9%; Pred. No. 3.5e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTTGCTTCGGCGG 14
 |||||
 8 GTTGCTTCGGCGG 21

DB

RESULT 14
 ABK29216
 ID ABK29216 standard; DNA, 21 BP.
 AC
 XX ABK29216;
 XX
 DT 23-APR-2002 (first entry)
 XX
 XX Trichoderma asperellum/hamatum probe.
 DE
 XX Fungal detection; bacterial detection; probe; primer; ss.
 KW
 XX Trichoderma asperellum.
 OS Trichoderma hamatum.
 OS
 XX WO200196612-A2.
 PN
 XX 20-DEC-2001.
 PD
 XX
 XX 13-JUN-2001; 2001WO-US18892.
 PF
 XX 13-JUN-2000; 2000US-0593012.
 PR
 XX (USSI) US ENVIRONMENTAL PROTECTION AGENCY.
 PA
 XX
 XX Haugland R, Vesper SJ;
 PI
 XX WPI, 2002-098078/13.
 DR
 XX
 XX Detecting and quantifying fungi and bacteria, involves obtaining a
 PT sequence of the fungus, extracting the DNA from the sample, and
 PT subjecting the DNA to polymerase chain reaction and fluorescent probe
 PT analysis -
 XX
 XX Claim 63; Page 21; 110pp; English.
 PS
 XX The invention relates to a method of detecting and quantifying fungi and
 CC bacteria, involving obtaining a sequence of the microorganism to be
 CC detected and quantified, extracting the DNA from the sample, and
 CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
 CC probe analysis. The method is useful for identifying and quantifying
 CC specific fungi and bacteria using specific DNA sequences. The specific
 CC DNA sequences are useful for the real time detection of PCR products with
 CC a fluorescent probe system or other molecular probes like hybridisation.
 CC ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes
 CC used in the method of the invention.
 CC
 XX
 XX Sequence 21 BP, 3 A, 7 C, 7 G, 4 T, 0 other;
 SO

Query Match 72.9%; Score 12.4; DB 24; Length 21;
 Best Local Similarity 92.9%; Pred. No. 3.5e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTTGCTTCGGCGG 14
 |||||
 8 GTTGCTTCGGCGG 21

Db 8 GTTGCTTCGGCGG 21

RESULT 15
 ABRK29219
 ID ABRK29219 standard; DNA; 21 BP.
 XX
 AC ABRK29219;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Trichoderma asperillum/hamatum/viride probe.
 XX
 KM Fungal detection; bacterial detection; probe; primer; ss.
 XX
 OS Trichoderma asperillum.
 XX
 OS Trichoderma hamatum.
 XX
 PN WO200196612-A2.
 XX
 PD 20-DEC-2001.
 XX
 PF 13-JUN-2001; 2001WO-US18892.
 XX
 PR 13-JUN-2000; 2000US-0593012.
 XX
 PA (USST) US ENVIRONMENTAL PROTECTION AGENCY.
 XX
 PI Haugland R, Vesper SJ;
 XX
 DR WPI; 2002-098078/13.
 XX
 PT Detecting and quantifying fungi and bacteria, involves obtaining a
 PT sequence of the fungus, extracting the DNA from the sample, and
 PT subjecting the DNA to polymerase chain reaction and fluorescent probe
 PT analysis -
 XX
 PS Claim 64; Page 21; 110pp; English.
 XX
 CC The invention relates to a method of detecting and quantifying fungi and
 CC bacteria, involving obtaining a sequence of the microorganism to be
 CC detected and quantified, extracting the DNA from the sample, and
 CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
 CC probe analysis. The method is useful for identifying and quantifying
 CC specific fungi and bacteria using specific DNA sequences. The specific
 CC DNA sequences are useful for the real time detection of PCR products with
 CC a fluorogenic probe system or other molecular probes like hybridisation.
 CC ABRK29026-ABRK29474 represent fungal and bacterial PCR primers and probes
 CC used in the method of the invention.
 CC
 SQ Sequence 21 BP; 3 A; 7 C; 7 G; 4 T; 0 other;

Query Match 72.9%; Score 12.4; DB 24; Length 21;
 Best Local Similarity 92.9%; Pred. No. 3.5e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTTGCTTCGGCGG 14
 |||||
 8 GTTGCTTCGGCGG 21

Db 8 GTTGCTTCGGCGG 21

RESULT 16
 ABRK29228
 ID ABRK29228 standard; DNA; 21 BP.
 XX
 AC ABRK29228;
 XX
 DT 23-APR-2002 (first entry)

DE Trichoderma viride/atrovride/Koningii probe.
 XX
 KM Fungal detection; bacterial detection; probe; primer; ss.
 XX
 OS Trichoderma sp.
 XX
 OS WO200196612-A2.
 XX
 PN WO200196612-A2.
 XX
 PD 20-DEC-2001.
 XX
 PF 13-JUN-2001; 2001WO-US18892.
 XX
 PR 13-JUN-2000; 2000US-0593012.
 XX
 PA (USST) US ENVIRONMENTAL PROTECTION AGENCY.
 XX
 PI Haugland R, Vesper SJ;
 XX
 DR WPI; 2002-098078/13.
 XX
 PT Detecting and quantifying fungi and bacteria, involves obtaining a
 PT sequence of the fungus, extracting the DNA from the sample, and
 PT subjecting the DNA to polymerase chain reaction and fluorescent probe
 PT analysis -
 XX
 PS Claim 67; Page 22; 110pp; English.
 XX
 CC The invention relates to a method of detecting and quantifying fungi and
 CC bacteria, involving obtaining a sequence of the microorganism to be
 CC detected and quantified, extracting the DNA from the sample, and
 CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
 CC probe analysis. The method is useful for identifying and quantifying
 CC specific fungi and bacteria using specific DNA sequences. The specific
 CC DNA sequences are useful for the real time detection of PCR products with
 CC a fluorogenic probe system or other molecular probes like hybridisation.
 CC ABRK29026-ABRK29474 represent fungal and bacterial PCR primers and probes
 CC used in the method of the invention.
 CC
 SQ Sequence 21 BP; 3 A; 7 C; 7 G; 4 T; 0 other;

Query Match 72.9%; Score 12.4; DB 24; Length 21;
 Best Local Similarity 92.9%; Pred. No. 3.5e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTTGCTTCGGCGG 14
 |||||
 8 GTTGCTTCGGCGG 21

Db 8 GTTGCTTCGGCGG 21

RESULT 17
 ABRN99459
 ID ABRN99459 standard; DNA; 22 BP.
 XX
 AC ABRN99459;
 XX
 DT 05-AUG-2002 (first entry)
 XX
 DE Fungi probe SEQ ID NO 31.
 XX
 KM Fungus; bacteria; quantification; detection; infection; gastroenteritis;
 KM ulcer; asthma; allergy; sinusitis; probe; ss.
 XX
 OS Aspergillus ochraceus.
 XX
 OS Aspergillus ocellatus.
 XX
 OS Aspergillus auricomus.
 XX
 PN US6387652-B1.
 XX
 PD 14-MAY-2002.
 XX
 PF 13-JUN-2000; 2000US-0593012.
 XX
 PR 15-APR-1998; 98US-081773P.

PR 14-APR-1999; 99US-0290990.
 XX (USSI) US ENVIRONMENTAL PROTECTION AGENCY.
 XX
 PA Haugland R, Vesper S;
 XX WPI, 2002-462353/49.
 DR
 XX Detection and quantification of specific fungi or bacteria useful e.g.
 PT in medical diagnosis and treatment of fungal and bacterial conditions,
 PT by hybridizing and amplifying DNA using sequences unique to the species
 PT or group of species
 XX
 PS Claim 12, Column 91, 55pp, English.
 XX
 CC The invention relates to specific fungi or bacteria detected and
 CC quantified in a sample by extracting and recovering DNA from the organism
 CC in the sample and hybridizing and amplifying the DNA sequence using
 CC sequences unique to the species/group of species but common to all
 CC isolates of the species/group of species. The method especially employs
 CC sequences selected from 225 fungal and bacterial primer and probe
 CC sequences (ABN99429-ABN99653) for detection of specified fungi/fungal
 CC groups or specified bacteria. The method enables detection and
 CC quantification of specific fungi or bacteria, or groups of
 CC fungal/bacterial species, useful medically for diagnosis and treatment of
 CC fungi or bacteria associated with health problems such as infections,
 CC gastroenteritis, ulcers, asthma, allergies and sinusitis. It is also
 CC useful to detect and/or quantify microorganisms in the environment e.g.
 CC to establish the risk of adverse health effects (e.g. pulmonary
 CC haemorrhage from levels of Stachybotrys chartarum in air samples in
 CC houses).
 XX
 SQ Sequence 22 BP, 2 A; 8 C; 6 G; 6 T; 0 other;
 XX
 SQ
 Query Match 72.9%; Score 12.4; DB 24; Length 22;
 Best Local Similarity 92.9%; Pred. No. 3.5e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY
 1 GTTGCTTCGCGCGG 14
 |||||
 6 GTTGCTTCGCGCGG 19
 Db
 RESULT 18
 ABK29056
 ID ABK29056 standard; DNA; 22 BP.
 XX
 AC ABK29056;
 XX
 DT 23-APR-2002 (first entry)
 XX
 XX Aspergillus ochraceus/oslanus/auricomus probe.
 DE
 XX Fungal detection; bacterial detection; probe; primer; ss.
 KM
 XX Aspergillus sp.
 OS
 XX WO200196612-A2.
 PN
 XX 20-DEC-2001.
 PD
 XX 13-JUN-2001; 2001WO-US18892.
 PF
 XX 13-JUN-2000; 2000US-0593012.
 PR
 XX (USSI) US ENVIRONMENTAL PROTECTION AGENCY.
 PA
 XX Haugland R, Vesper SJ;
 PI
 XX WPI, 2002-098078/13.
 DR
 XX Detecting and quantifying fungi and bacteria, involves obtaining a
 PT sequence of the fungus, extracting the DNA from the sample, and

PT subjecting the DNA to polymerase chain reaction and fluorescent probe
 PT analysis
 XX
 XX Claim 12; Page 8; 110pp; English.
 PS
 XX The invention relates to a method of detecting and quantifying fungi and
 CC bacteria, involving obtaining a sequence of the microorganism to be
 CC detected and quantified, extracting the DNA from the sample, and
 CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
 CC probe analysis. The method is useful for identifying and quantifying
 CC specific fungi and bacteria using specific DNA sequences. The specific
 CC DNA sequences are useful for the real time detection of PCR products with
 CC a fluorescent probe system or other molecular probes like hybridisation.
 CC ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes
 CC used in the method of the invention.
 XX
 SQ Sequence 22 BP, 2 A; 8 C; 6 G; 6 T; 0 other;
 XX
 SQ
 Query Match 72.9%; Score 12.4; DB 24; Length 22;
 Best Local Similarity 92.9%; Pred. No. 3.5e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY
 1 GTTGCTTCGCGCGG 14
 |||||
 6 GTTGCTTCGCGCGG 19
 Db
 RESULT 19
 ABK29268
 ID ABK29268 standard; DNA; 22 BP.
 XX
 AC ABK29268;
 XX
 DT 23-APR-2002 (first entry)
 XX
 XX Aspergillus ochraceus probe.
 DE
 XX Fungal detection; bacterial detection; probe; primer; ss.
 KM
 XX Aspergillus ochraceus.
 OS
 XX WO200196612-A2.
 PN
 XX 20-DEC-2001.
 PD
 XX 13-JUN-2001; 2001WO-US18892.
 PF
 XX 13-JUN-2000; 2000US-0593012.
 PR
 XX (USSI) US ENVIRONMENTAL PROTECTION AGENCY.
 PA
 XX Haugland R, Vesper SJ;
 PI
 XX WPI, 2002-098078/13.
 DR
 XX Detecting and quantifying fungi and bacteria, involves obtaining a
 PT sequence of the fungus, extracting the DNA from the sample, and
 PT subjecting the DNA to polymerase chain reaction and fluorescent probe
 PT analysis
 XX
 PS Claim 83; Page 24; 110pp; English.
 XX
 CC The invention relates to a method of detecting and quantifying fungi and
 CC bacteria, involving obtaining a sequence of the microorganism to be
 CC detected and quantified, extracting the DNA from the sample, and
 CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
 CC probe analysis. The method is useful for identifying and quantifying
 CC specific fungi and bacteria using specific DNA sequences. The specific
 CC DNA sequences are useful for the real time detection of PCR products with
 CC a fluorescent probe system or other molecular probes like hybridisation.
 CC ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes
 CC used in the method of the invention.
 XX

PT Detection and quantification of specific fungi or bacteria useful e.g.
 PT in medical diagnosis and treatment of fungal and bacterial conditions,
 PT by hybridizing and amplifying DNA using sequences unique to the species
 PT or group of species
 PS Claim 41; Column 94; 55pp; English.
 CC The invention relates to specific fungi or bacteria detected and
 CC quantified in a sample by extracting and recovering DNA from the organism
 CC in the sample and hybridizing and amplifying the DNA sequence using
 CC sequences unique to the species/group of species but common to all
 CC isolates of the species/group of species. The method especially employs
 CC sequences selected from 325 fungal and bacterial primer and probe
 CC sequences (ABN99429-ABN99653) for detection of specified fungi/fungal
 CC groups or specified bacteria. The method enables detection and
 CC quantification of specific fungi or bacteria, or groups of
 CC fungal/bacterial species, useful medically for diagnosis and treatment of
 CC fungi or bacteria associated with health problems such as infections,
 CC gastroenteritis, ulcers, asthma, allergies and sinusitis. It is also
 CC useful to detect and/or quantify microorganisms in the environment e.g.
 CC to establish the risk of adverse health effects (e.g. pulmonary
 CC haemorrhage from levels of *Stachybotrys chartarum* in air samples in
 CC houses).
 CC Sequence 17 BP; 1 A; 5 C; 5 G; 6 T; 0 other;
 SQ
 Query Match 70.6%; Score 12; DB 24; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTGCTTCGGCG 12
 |||||
 5 GTTGCTTCGGCG 16
 Db
 RESULT 25
 ABK29145
 ID ABK29145 standard; DNA; 17 BP.
 XX
 XX ABK29145;
 AC
 XX
 XX 23-APR-2002 (first entry)
 DT
 XX Penicillium brevicompactum/alberechii forward PCR primer.
 DE
 XX Fungal detection; bacterial detection; probe; primer; ss.
 KM
 XX Penicillium brevicompactum.
 OS
 XX Penicillium alberechii.
 OS
 XX WO200196612-A2.
 PN
 XX
 XX 20-DEC-2001.
 PD
 XX 13-JUN-2001; 2001WO-US18992.
 PF
 XX 13-JUN-2000; 2000US-0593012.
 PR
 XX
 XX (USST) US ENVIRONMENTAL PROTECTION AGENCY.
 PA
 XX Haugland R, Vesper SJ;
 PI
 XX WPI, 2002-098078/13.
 DR
 XX
 XX Detecting and quantifying fungi and bacteria, involves obtaining a
 PT sequence of the fungus, extracting the DNA from the sample, and
 PT subjecting the DNA to polymerase chain reaction and fluorescent probe
 PT analysis
 XX
 XX Claim 41; Page 15; 110pp; English.
 CC The invention relates to a method of detecting and quantifying fungi and
 CC bacteria, involving obtaining a sequence of the microorganism to be

CC detected and quantified, extracting the DNA from the sample, and
 CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
 CC probe analysis. The method is useful for identifying and quantifying
 CC specific fungi and bacteria using specific DNA sequences. The specific
 CC DNA sequences are useful for the real time detection of PCR products with
 CC a fluorogenic probe system or other molecular probes like hybridisation.
 CC ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes
 CC used in the method of the invention.
 CC Sequence 17 BP; 1 A; 5 C; 5 G; 6 T; 0 other;
 SQ
 Query Match 70.6%; Score 12; DB 24; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTGCTTCGGCG 12
 |||||
 5 GTTGCTTCGGCG 16
 Db
 RESULT 26
 AA202872/C
 ID AA202872 standard; DNA; 20 BP.
 XX
 XX AA202872;
 AC
 XX
 XX 07-OCT-1999 (first entry)
 DT
 XX PCR primer used to amplify an ORF of *Chlamydia trachomatis*.
 DE
 XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 KM paratrachoma; inclusion conjunctivitis; genital disease; peritrophic;
 KM nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
 KM Bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
 XX
 XX Synthetic.
 OS
 XX *Chlamydia trachomatis*.
 OS
 XX WO9928475-A2.
 PN
 XX
 XX 10-JUN-1999.
 PD
 XX
 XX 27-NOV-1998; 98WO-IB01939.
 PF
 XX
 XX 04-NOV-1998; 98US-0107077.
 PR
 XX 28-NOV-1997; 97FR-0015041.
 PR
 XX 17-DEC-1997; 97FR-0016034.
 XX
 XX (GEST) GENSET.
 PA
 XX Griffais R;
 PI
 XX
 XX WPI, 1999-371125/31.
 DR
 XX
 XX Genome sequence of *Chlamydia trachomatis*
 PT
 XX
 XX Disclosure; Page 1560; 1755pp; English.
 PS
 XX
 XX PCR primers AA201426-206209 were used to amplify open reading frames
 CC (ORFs) of the genome of *Chlamydia trachomatis* (see AA201425). These ORFs
 CC encode polypeptides (see AA136754-Y37949) which can be used as vaccines
 CC against *Chlamydia trachomatis*. Antisense and ribozyme sequences
 CC can also be used to control growth of the microorganism. *Chlamydia*
 CC trachomatis is responsible for a large number of diseases, e.g. eye
 CC diseases such as conventional trachoma, nonendemic trachoma,
 CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
 CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis;
 CC peritrophic, Bartholinitis; pneumopathy in breast feeding infants;
 CC and venereal lymphogranulomatosis. The polypeptides of the
 CC invention may be of use in treating these diseases.
 CC
 CC Sequence 20 BP; 6 A; 7 C; 3 G; 4 T; 0 other;
 SQ

Query Match 70.6%; Score 12; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TTGCTTCGGCGG 13
 DB 14 TTGCTTCGGCGG 3

RESULT 27
 AAF61866
 ID AAF61866 standard; DNA; 19 BP.
 AC AAF61866;
 XX
 DT 26-JUL-2001 (first entry)
 XX
 DE Soybean lection PCR primer LECr1.
 XX
 KW Amplification; genetically modified organism; GMO; soya; maize; plant;
 KW detection; lection; invertase; 35S-promoter; NOS terminator; NPTII;
 KW nopaline synthase; neomycin phosphotransferase; EPSPS; CryIA(b);
 KW enol-pyruvyl-shikimate-3-phosphate synthase; PCR primer; ss.
 XX
 OS Glycine max.
 XX
 PN W0200132919-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 27-OCT-2000; 2000MO-AT00283.
 XX
 PR 29-OCT-1999; 99AT-0001820.
 XX
 PA (OSTP) OESTERR FORSCH SEIBERSDORF.
 PI Vollenhofer S, Mansfeld M, Kiroath H;
 XX
 DR MPI; 2001-308749/32.
 XX
 PT New primer pairs for polymerase chain reaction, useful for detecting
 PT genetically modified plant materials in e.g. foods, have high annealing
 PT temperature for increased sensitivity.
 PS
 XX
 PS Claim 10; Page 15; 37pp; German.
 XX
 CC This invention describes a novel group of primer pairs for polymerase
 CC chain reaction (PCR) amplification of at least one genetic element (A),
 CC introduced by genetic modification of soya, maize or other plants,
 CC present in crude plant materials or derived compositions. The new primers
 CC and probes are used (i) to detect and/or quantify genetically modified
 CC plant materials in seeds, animal and human foodstuffs, especially where
 CC these have been processed so that DNA is extensively degraded and (ii)
 CC for monitoring the amplification of (A). The probes may also be used to
 CC confirm a successful PCR amplification. The high annealing temperature of
 CC the primers ensures high specificity and sensitivity, even with badly
 CC degraded samples, and facilitates analysis by restriction analysis, since
 CC only inexpensive restriction enzymes are required, reducing costs and
 CC making the method suitable for routine use. The process reliably
 CC detects/quantifies even very small amounts of genetically modified
 CC materials. AAF61845-AAF61868 represent the PCR primers used in the method
 CC of the invention which amplify the soybean (Glycine max) lection gene, Zea
 CC mays invertase gene, Cauliflower Mosaic virus (CaMV) 35S-promoter,
 CC Agrobacterium tumefaciens NOS (nopaline synthase) terminator, an
 CC unidentified NPTII (neomycin phosphotransferase) gene, Petunia hybrida
 CC EPSPS (enol-pyruvyl-shikimate-3-phosphate synthase) CTP-fragment and the
 CC Bacillus thuringiensis modified CryIA(b) gene.
 XX
 SQ Sequence 19 BP; 3 A; 5 C; 5 G; 6 T; 0 other;

Query Match 69.4%; Score 11.8; DB 22; Length 19;
 Best Local Similarity 86.7%; Pred. No. 7.4e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 TGCTTCGGCGGAC 17
 DB 1 TGCTTCGGCGGAC 15

RESULT 28
 AAF69341/C
 ID AAF69341 standard; DNA; 20 BP.
 AC AAF69341;
 XX
 DT 18-APR-2001 (first entry)
 XX
 DE Integrin-linked kinase coding region targeted oligonucleotide #54.
 XX
 KW Antisense; integrin-linked kinase; htk; infection; tumour;
 KW inflammation; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6177273-B1.
 XX
 PD 23-JAN-2001.
 XX
 PF 26-OCT-1999; 99US-0428219.
 XX
 PR 26-OCT-1999; 99US-0428219.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Cowseert LM;
 XX
 DR MPI; 2001-137069/14.
 XX
 PT Novel antisense compounds capable of modulating expression of human
 PT integrin-linked kinase, useful for diagnosis, prophylaxis and treatment
 PT of disease, e.g. tumours, associated with expression of the kinase
 XX
 PS Claim 3; Column 43; 40pp; English.
 XX
 CC The present invention relates to an antisense compound 8 to
 CC 30 bases in length targeted to the 5' untranslated (UTR) region,
 CC the coding region or the 3' UTR region human integrin-linked
 CC kinase (htk). The antisense oligonucleotides are useful for
 CC inhibiting the expression of human htk in human cells or tissues,
 CC in vitro. The oligonucleotides can be utilized for diagnostics,
 CC therapeutics for the treatment of diseases associated with
 CC the expression of htk, prophylaxis e.g. to prevent or delay infection,
 CC inflammation or tumor formation and as research reagent.
 XX
 SQ Sequence 20 BP; 6 A; 8 C; 3 G; 3 T; 0 other;

Query Match 69.4%; Score 11.8; DB 22; Length 20;
 Best Local Similarity 86.7%; Pred. No. 7.4e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 TGCTTCGGCGGAC 17
 DB 18 TGCTTCGGCGGAC 4

RESULT 29
 AB194529/C
 ID AB194529 standard; DNA; 20 BP.
 AC AB194529;
 XX
 DT 16-FEB-2002 (first entry)
 XX
 XX Capture oligonucleotide zip ID#1616 oligo #9.
 DB Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 KW

KM ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KM infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
 KM cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
 KM environmental monitoring; food industry; feed industry; ss.
 OS Synthetic.
 XX
 PN WO200179548-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 04-APR-2001; 2001WO-US10958.
 XX
 PR 14-APR-2000; 2000US-197271P.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Barany F, Zivri M, Gerry NP, Favie R, Kliman R;
 XX
 DR WPI, 2002-034366/04.
 XX
 PT Designing capture oligonucleotide probes for use on a support to which
 PT complementary oligonucleotides hybridize with little mismatch -
 XX
 PS Example 5; Fig 29; 300pp; English.
 XX
 CC The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridize with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medinensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. AB182074 to
 CC AB197546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention.
 CC
 SQ Sequence 20 BP; 7 A; 6 C; 5 G; 2 T; 0 other;
 XX
 QY Query Match 69.4%; Score 11.8; DB 24; Length 20;
 Best Local Similarity 86.7%; Pred. No. 7.4e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 DB 20 TTGCTTCGGCGGAA 16
 20 TTGCTTCGGCGTCA 6
 RESULT 30
 AB185628/c
 ID AB185628 standard; DNA; 24 BP.
 XX
 AC AB185628;
 XX
 DT 15-FEB-2002 (first entry)
 XX
 DE Capture oligonucleotide zip ID#1616 oligo #1.
 XX
 KM Human; K-ras; PCR primer; probe; capture probe; mutation detection;

KM ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KM infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
 KM cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
 KM environmental monitoring; food industry; feed industry; ss.
 OS Synthetic.
 XX
 PN WO200179548-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 04-APR-2001; 2001WO-US10958.
 XX
 PR 14-APR-2000; 2000US-197271P.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Barany F, Zivri M, Gerry NP, Favie R, Kliman R;
 XX
 DR WPI, 2002-034366/04.
 XX
 PT Designing capture oligonucleotide probes for use on a support to which
 PT complementary oligonucleotides hybridize with little mismatch -
 XX
 PS Example 5; Fig 25; 300pp; English.
 XX
 CC The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridize with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medinensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. AB182074 to
 CC AB197546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention.
 CC
 SQ Sequence 24 BP; 7 A; 7 C; 7 G; 3 T; 0 other;
 XX
 QY Query Match 69.4%; Score 11.8; DB 24; Length 24;
 Best Local Similarity 86.7%; Pred. No. 7.4e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 DB 20 TTGCTTCGGCGGAA 16
 20 TTGCTTCGGCTGCA 6
 RESULT 31
 AB185629
 ID AB185629 standard; DNA; 24 BP.
 XX
 AC AB185629;
 XX
 DT 15-FEB-2002 (first entry)
 XX
 DE Capture oligonucleotide zip ID#1616 oligo #2.
 XX
 KM Human; K-ras; PCR primer; probe; capture probe; mutation detection;


```

OS      Synthetic.
XX      XX
XX      PN WO200179548-A2.
XX      PD 25-OCT-2001.
XX      PF 04-APR-2001; 2001WO-US10958.
XX      PR 14-APR-2000; 2000US-197271P.
XX      PA (CORR ) CORNELL RES FOUND INC.
XX      PI Barany F, Zivul M, Gerry NP, Favis R, Kliman R;
XX      PS WPI; 2002-034366/04.
XX      PT Designing capture oligonucleotide probes for use on a support to which
XX      PT complementary oligonucleotides hybridize with little mismatch -
XX      PS Example 5; Fig 25; 300pp; English.
XX      CC The present invention describes a method (M1) for designing capture
XX      CC oligonucleotide probes (I) for use on a support to which complementary
XX      CC oligonucleotide probes (II) will hybridise with little mismatch, where
XX      CC (I) have melting temperatures within a narrow range. The method is useful
XX      CC for detecting infectious diseases caused by bacterial infectious agents
XX      CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
XX      CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
XX      CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
XX      CC Epstein-Barr virus and polio virus, and parasitic infectious agents
XX      CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
XX      CC medinensis. The method is also useful for detecting genetic diseases such
XX      CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
XX      CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
XX      CC involved in DNA amplification, replication, recombination or repair, the
XX      CC cancer is specifically associated with a gene selected from BRCA1 gene,
XX      CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
XX      CC method is also used for environmental monitoring, forensics and the food
XX      CC and feed industry, detecting comprisess scanning (using e.g. a scanning
XX      CC electron microscope and infrared microscope) the support at the
XX      CC particular sites and identifying if ligation of the oligonucleotide probe
XX      CC sets occurred and correlating (using a computer) identified ligation to a
XX      CC presence or absence of the target nucleotide sequences. AB182074 to
XX      CC AB197546 represent oligonucleotide sequences used in the exemplification
XX      CC of the present invention.
XX      CC
XX      SQ Sequence 24 BP; 3 A; 7 C; 7 G; 7 T; 0 other;
XX
XX      Query Match 69.4%; Score 11.8; DB 24; Length 24;
XX      Best Local Similarity 86.7%; Pred. No. 7,4e+03;
XX      Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0.
XX
QY      2 TTGCTTCGGCGGAA 16
Db      5 TTGCTTCGGCGTCAA 19

```

XX	protein metabolism; carbohydrate metabolism; phytohormone biosynthesis;
KW	cell cycle regulation; transgenic plant; PCR primer; ss.
XX	
OS	Zea mays.
XX	
PN	MO200121783-A2.
XX	
PD	29-MAR-2001.
XX	
PF	22-SEP-2000; 2000MO-US26131.
XX	
PR	24-SEP-1999; 99US-0155859.
XX	
PA	(PION-) PIONEER HI-BRED INT INC.
XX	
PI	Jiao S, Habben JE, Niu X;
XX	
DR	WPI; 2001-257981/26.
XX	
PT	Novel seed-preferred promoter sequence useful for selectively
PT	expressing a first nucleotide sequence in a plant seed and for
XX	transgenic plant production
XX	
PS	Example 1; Page 19; 31pp; English.
XX	
CC	PCR primers AAB0067-69 were used to amplify a maize promoter that
CC	is capable of driving transcription in a seed-preferred manner. The
CC	promoter is isolated from a gene which is homologous to the barley pZ640
CC	gene. The seed-specific promoter is used for selectively expressing a
CC	nucleotide sequence encoding a polypeptide involved in fatty acid
CC	metabolism, protein metabolism, carbohydrate metabolism, phytohormone
CC	biosynthesis or in cell cycle regulation. The promoter may be used
CC	to produce transgenic plants. The genes of interest expressed by the
CC	promoter are also useful for varying the phenotype of seeds.
XX	
SQ	Sequence 25 BP; 5 A; 8 C; 6 G; 6 T; 0 other;
XX	
QY	2 TTGCTCGCGCGGNA 16
DB	15 TTGCTCGCGCGCGCA 1
XX	
RESULT 33	
AB061935/C	
ID	AB061935 standard; DNA; 25 BP.
XX	
AC	AB061935;
XX	
DT	03-OCT-2002 (first entry)
XX	
DE	Human aquaporin 5 (AQP5) gene oligonucleotide (OGN) chip PCR primer 674.
XX	
KW	Human; ss; PCR; primer; aquaporin; AQP5; AQP; water channel protein;
KW	oligonucleotide chip; OGN chip; cDNA chip; lung cancer;
KW	mutation detection; polymorphism detection; gene expression.
XX	
OS	Homo sapiens.
XX	
PN	WO200220787-A1.
XX	
PD	14-MAR-2002.
XX	
PF	10-SEP-2001; 2001WO-KR01528.
XX	
PR	09-SEP-2000; 2000KR-0053821.
XX	
PA	(GOOD-) GOODGENE INC.
PA	(MOON/) MOON W.
PA	(MOON/) MOON C.

XX Moon W, Moon C, Moon Y, Kim B, Kim D, Shin C, Um T, Kim H,
 PI Song M, Kim H, Song S;
 XX WPI; 2002-393647/42.
 XX Novel aquaporin 5 gene mutant useful for diagnosing lung, stomach,
 PT colon, prostate, or head or neck cancer -
 XX Claim 9; Fig 20; 154pp; English.
 XX The invention comprises a mutant form of the human aquaporin 5 (AQP5)
 CC gene. Aquaporin (AQP) is a family of water channel proteins, through
 CC which water is transported into and out of cells - ten types of mammalian
 CC AQP have been identified so far. The invention also comprises an
 CC oligonucleotide (OGN) chip having 902 oligonucleotide primer sequences
 CC and a cDNA chip comprising one or more sequences from the human AQP5
 CC gene. The mutant AQP5 gene is useful for diagnosing cancer (i.e. lung
 CC cancer). The OGN chip is useful for detecting mutations and polymorphisms
 CC in AQP5 and the cDNA chip is useful for analysis of gene expression. The
 CC present DNA sequence represents a human aquaporin 5 (AQP5) gene
 CC oligonucleotide (OGN) chip PCR primer.
 XX Sequence 25 BP; 3 A; 12 C; 6 G; 4 T; 0 other;
 SQ

Query Match 69.4%; Score 11.8; DB 24; Length 25;
 Best Local Similarity 86.7%; Pred. No. 7.5e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGGGA 15
 |||||
 DB 15 GTTGCTTCGGCGGGA 1

RESULT 34
 AAF51334/C
 ID AAF51334 standard; DNA; 15 BP.
 AC AAF51334;
 XX 30-MAR-2001 (first entry)
 DT IGF-1 oligonucleotide #2294.
 XX IGF-1 oligonucleotide #2294.
 DE
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KM cytostatic; dermatological; cardiac; vitreous; ophthalmological; keloid;
 KM skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KM IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KM growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;
 KM keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KM hyperneovascular condition; hyperplasia; kidney disease;
 KM neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS
 XX WO200078341-A1.
 PN
 XX 28-DEC-2000.
 PD
 XX 21-JUN-2000; 2000WO-AU00693.
 PF
 XX 21-JUN-1999; 99US-0140345.
 PR
 XX (MURDOCH CHILDRENS RES INST.
 PA Wright CJ, Werther GA, Edmondson SR,
 PI WPI; 2001-041421/05.
 DR
 XX ameliorating the effects of a disorder, e.g. psoriasis, by
 PT administering UV (ultra-violet) treatment (optional) and an antisense
 PT nucleic acid that inhibits or reduces growth factor mediated cell
 PT proliferation and/or inflammation -

XX Example 8; Page 75; 201pp; English.
 PS The present invention relates to a method for ameliorating the effects
 CC of skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor (IGF)-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation.
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF5151 and
 CC AAF5153-FAS151). The method is useful for ameliorating the effects of
 CC psoriasis, ichthyosis, pityriasis, ruba, pilaris, seborrhoea, keloids,
 CC keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
 CC skin, a hyperneovascular condition such as a neovascular condition of the
 CC retina, brain or skin, growth factor-mediated malignancies, other
 CC sclerotic disease, kidney disease, hyperproliferation of the inside of
 CC blood vessels or any other hyperplasia.
 XX Sequence 15 BP; 4 A; 5 C; 4 G; 2 T; 0 other;
 SQ

Query Match 67.1%; Score 11.4; DB 22; Length 15;
 Best Local Similarity 92.3%; Pred. No. 1.2e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGCTTCGGCGGGA 15
 |||||
 DB 15 TGCTTCGGCGGGA 3

RESULT 35
 AAF51335/C
 ID AAF51335 standard; DNA; 15 BP.
 AC AAF51335;
 XX 30-MAR-2001 (first entry)
 DT IGF-1 oligonucleotide #2295.
 XX IGF-1 oligonucleotide #2295.
 DE
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KM cytostatic; dermatological; cardiac; vitreous; ophthalmological; keloid;
 KM skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KM IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KM growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;
 KM keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KM hyperneovascular condition; hyperplasia; kidney disease;
 KM neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS
 XX WO200078341-A1.
 PN
 XX 28-DEC-2000.
 PD
 XX 21-JUN-2000; 2000WO-AU00693.
 PF
 XX 21-JUN-1999; 99US-0140345.
 PR
 XX (MURDOCH CHILDRENS RES INST.
 PA Wright CJ, Werther GA, Edmondson SR,
 PI WPI; 2001-041421/05.
 DR
 XX ameliorating the effects of a disorder, e.g. psoriasis, by
 PT administering UV (ultra-violet) treatment (optional) and an antisense
 PT nucleic acid that inhibits or reduces growth factor mediated cell
 PT proliferation and/or inflammation -
 XX Example 8; Page 75; 201pp; English.
 PS The present invention relates to a method for ameliorating the effects
 CC

CC of skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present cell proliferation is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and
CC AAF45153-F45161). The method is useful for ameliorating the effects of
CC psoriasis, ichthyosis, pityriasis, ruba, pilaris, seborrhea, keloids,
CC keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
CC skin, a hyperneovascular condition such as a neovascular condition of the
CC retina, brain or skin, growth factor-mediated malignancies, other
CC sclerotic disease, kidney disease, hyperproliferation of the inside of
CC blood vessels or any other hyperplasia.

Query Match 67.1%; Score 11.4; DB 22; Length 15;
Best Local Similarity 92.3%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGCTTCGGCGGGA 15
Db 14 TGCTTCGGCGTGA 2

RESULT 36
AAFS1336/c
ID AAF51336 standard; DNA, 15 BP.
XX AAF51336;
AC
XX 30-MAR-2001 (first entry)
DT
XX IGF-1 oligonucleotide #2296.
DE
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KM cytosarctic; dermatological; cardiant; vitruide; ophthalmological; keloid;
KM skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KM IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KM growth factor mediated cell proliferation; ichthyosis; seborrhea; ruba;
KM keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KM hyperneovascular condition; hyperplasia; kidney disease;
KM neovascular condition of the retina; ss.

OS Homo sapiens.
XX
XX WO200078341-A1.
PN
XX 28-DEC-2000.
PD
XX 21-JUN-2000; 2000WO-AU00693.
PF
XX 21-JUN-1999; 99US-0140345.
PR
XX (MURDOCH CHILDRENS RES INST.
PA
XX (MURDOCH CHILDRENS RES INST.
PI
XX Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
DR
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by
PT administering UV (ultra-violet) treatment (optional) and an antisense
PT nucleic acid that inhibits or reduces growth factor mediated cell
PT proliferation and/or inflammation -
XX
XX Example 8; Page 75; 20pp; English.
XX
XX The present invention relates to a method for ameliorating the effects
CC of skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and
CC AAF45153-F45161). The method is useful for ameliorating the effects of
CC psoriasis, ichthyosis, pityriasis, ruba, pilaris, seborrhea, keloids,
CC keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
CC skin, a hyperneovascular condition such as a neovascular condition of the
CC retina, brain or skin, growth factor-mediated malignancies, other
CC sclerotic disease, kidney disease, hyperproliferation of the inside of
CC blood vessels or any other hyperplasia.

Query Match 67.1%; Score 11.4; DB 22; Length 15;
Best Local Similarity 92.3%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGCTTCGGCGGGA 15
Db 13 TGCTTCGGCGTGA 1

RESULT 37
AAT05371
ID AAT05371 standard; DNA, 16 BP.
XX AAT05371;
AC
XX 04-JUN-1996 (first entry)
DT
XX
XX Fusarium spp. ITS primer JB577.
DE
XX
XX Plant pathogen; fungus; Septoria nodorum; Septoria tritici; Fusarium;
KM Pseudocercospora herpeticoides; Mycosphaerella filiensis; PCR;
KM Mycosphaerella muscicola; amplification; primer; ribosomal RNA gene;
KM internal transcribed region; strain; capture; colourimetric assay;
KM isolate; development; population; ss.

OS Synthetic.
XX
XX WO9529260-A2.
PN
XX 02-NOV-1995.
PD
XX 19-APR-1995; 95WO-US04712.
PF
XX 25-APR-1994; 94US-0233608.
PR
XX (CIBA) CIBA GEIGY AG.
PA
XX Beck J, Ligon JM;
PI
XX WPI; 1995-383005/49.
DR
XX
XX DNA encoding intervening transcribed sequence - used for detection
PT of plant fungal pathogens
PT
XX
XX Claim 3; Page 15; 65pp; English.
XX
XX A novel method for the detection of plant pathogenic strains of fungi
CC e.g. Septoria nodorum, S. tritici, Pseudocercospora herpeticoides,
CC Mycosphaerella filiensis, Muscicola or Fusarium spp. involves the PCR
CC amplification of sequences found in the internal transcribed region
CC (ITS) of the 18S, 5.8S and 28S ribosomal RNA genes by the primers
CC AA094359-93 and AAT05357-72. These primers are derived from the ITS
CC sequences of these fungi (AAT05394-T05404 and AA094398) and are strain
CC specific. The amplification products of the reactions using these
CC primers can be used with the capture primers AAT05378-93 in
CC colourimetric assays. The primers and ITS DNAs can be used for the
CC detection of specific fungal pathogen isolates and in monitoring disease
CC development in plant populations.
XX
XX Sequence 16 BP; 1 A; 5 C; 6 G; 4 T; 0 other;

Query Match 67.1%; Score 11.4; DB 16; Length 16;
 Best Local Similarity 92.3%; Pred. No. 1.2e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 GTTGCTTCGGCGG 13
 1 GTTGCTTCGGCGG 13
 Db 1 GTTGCTTCGGCGG 13

RESULT 38

AAT05364 standard; DNA, 16 BP.

XX AAT05364;
 XX AAT05364;
 XX 04-JUN-1996 (first entry)
 XX Fusarium spp. ITS primer JB570.
 XX Plant pathogen; fungus; Septoria nodorum; Septoria tritici; Fusarium;
 KM Pseudocercospora herpotrichoides; Mycosphaerella filijensis; PCR;
 KM Mycosphaerella muscicola; amplification; primer; ribosomal RNA gene;
 KM internal transcribed region; strain; capture; colourimetric assay;
 KM isolate; development; population; ss.
 XX Synthetic.
 XX OS
 XX WO9529260-A2.
 XX 02-NOV-1995.
 XX 19-APR-1995; 95WO-US04712.
 XX 25-APR-1994; 94US-0233608.
 XX (CIBA) CIBA GEIGY AG.
 XX Beck JJ, Liqon JM;
 XX WPI; 1995-383005/49.

PT DNA encoding intervening transcribed sequence - used for detection
 of plant fungal pathogens
 XX Claim 3; Page 15; 65pp; English.

CC A novel method for the detection of plant pathogenic strains of fungi
 e.g. Septoria nodorum, S.tritici, Pseudocercospora herpotrichoides,
 Mycosphaerella filijensis, M.muscicola or Fusarium spp, involves the PCR
 amplification of sequences found in the internal transcribed region
 (ITS) of the 18S, 5.8S and 28S ribosomal RNA genes by the primers
 AAQ9459-93 and AAT05357-72. These primers are derived from the ITS
 sequences of these fungi (AAT05394-105404 and AAQ94398) and are strain
 specific. The amplification products of the reactions using these
 CC primers can be used with the capture primers AAT05378-93 in
 CC colourimetric assays. The primers and ITS DNA can be used for the
 CC detection of specific fungal pathogen isolates and in monitoring disease
 CC development in plant populations.
 XX

Sequence 16 BP; 1 A; 4 C; 6 G; 5 T; 0 other;

Query Match 67.1%; Score 11.4; DB 16; Length 16;
 Best Local Similarity 92.3%; Pred. No. 1.2e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 GTTGCTTCGGCGG 13
 1 GTTGCTTCGGCGG 13
 Db 4 GTTGCTTCGGCGG 16

RESULT 39
 AAT55603/c

ID AAT55603 standard; RNA, 16 BP.
 XX AAT55603;
 AC 15-APR-1997 (first entry)
 XX Mouse rela hairpin ribozyme target sequence (nt. position 137).
 DE
 XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KM gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KM intercellular adhesion molecule; rel A; tumour necrosis factor;
 KM TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KM translocation; chronic myelogenous leukaemia; CML; cancer;
 KM Philadelphia chromosome; inflammation; autoimmune disease;
 KM atherosclerosis; myocardial infarction; stroke; revascular;
 KM transplant rejection; rheumatoid arthritis; psoriasis;
 KM myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KM human immunodeficiency virus; acquired immune deficiency syndrome;
 KM AIDS; ss.
 XX Mus musculus.
 OS
 XX WO9523225-A2.
 XX 31-AUG-1995.
 XX 23-FEB-1995; 95WO-IB00156.
 XX 30-JAN-1995; 95US-0380734.
 XX 23-FEB-1994; 94US-0201109.
 XX 22-MAR-1994; 94US-0218934.
 XX 04-APR-1994; 94US-0222795.
 XX 07-APR-1994; 94US-0224483.
 XX 15-APR-1994; 94US-0227958.
 XX 15-APR-1994; 94US-0228041.
 XX 18-MAY-1994; 94US-0245736.
 XX 06-JUL-1994; 94US-0271280.
 XX 15-AUG-1994; 94US-0291932.
 XX 16-AUG-1994; 94US-0291433.
 XX 17-AUG-1994; 94US-0292620.
 XX 19-AUG-1994; 94US-0293520.
 XX 02-SEP-1994; 94US-0300000.
 XX 08-SEP-1994; 94US-0303039.
 XX 23-SEP-1994; 94US-0311486.
 XX 28-SEP-1994; 94US-0311749.
 XX 03-OCT-1994; 94US-0316771.
 XX 07-OCT-1994; 94US-0319492.
 XX 11-OCT-1994; 94US-0321993.
 XX 04-NOV-1994; 94US-0334847.
 XX 10-NOV-1994; 94US-0337608.
 XX 28-NOV-1994; 94US-0345516.
 XX 16-DEC-1994; 94US-0357577.
 XX 23-DEC-1994; 94US-0363233.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Stinchcomb DT, Chowitra B, Dizenzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpelesky A, Kisich K, Matulic-Adamic J;
 PI McSwigen JA, Modak A, Pavco P, Beigelman L, Sullivan SM;
 PI Sweedler D, Thompson JD, Tracz D, Ueman N, Wincott FE;
 PI Woolf T;
 XX WPI; 1995-351090/45.
 XX Ribozymes having modified bases and methods for producing them
 PT for use in inhibiting disease related genes
 XX Claim 2; Page 240; 407pp; English.
 XX The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves rela
 CC mRNA at the nucleotide base position indicated in the DE line.

CC The relA gene product is a subunit of the transcriptional
 CC regulator NF-kappaB and is implicated specifically in the induction
 CC of inflammatory responses. Regions of the mRNA that do not form
 CC secondary folding structures and that contain potential hammerhead
 CC and hairpin ribozyme cleavage sites were identified by computer
 CC analysis. Ribozymes directed against these mRNA sequences were
 CC designed and synthesised with modifications that improve their
 CC nuclease resistance. The ribozymes are designed to cleave the
 CC target sequences and thereby inhibit relA expression, making them
 CC potentially useful for treating rheumatoid arthritis, restenosis
 CC and asthma as well as for increasing tolerance to transplanted
 CC tissues. The potential immunosuppressive properties of a ribozyme
 CC that cleaves relA mRNA means that uses are limited to local
 CC delivery, acute indications or ex vivo treatment.

SQ Sequence 16 BP; 7 A; 5 C; 4 G; 0 U; 0 other;

Query Match 67.1%; Score 11.4; DB 16; Length 16;
 Best Local Similarity 92.3%; Pred. No. 1.2e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 13
 DB 16 GTTGCTTCGGCTG 4

RESULT 40

AAV62556 AAV62556 standard; DNA; 16 BP.

AAV62556;

17-DEC-1998 (first entry)

Fusarium species specific primer JB577.

Internal transcribed spacer; ITS; ribosomal RNA; Fusarium avenaceum;
 Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant;
 Septoria avenae; Microdochium nivale; Fusarium poae; fungal pathogen;
 PCR; nucleic acid detection; PCR primer; ss.

Synthetic.

Fusarium sp.

US5814453-A.

29-SEP-1998.

02-JUL-1997; 97US-0887480.

02-JUL-1997; 97US-0887480.

19-APR-1995; 95WO-US04712.

15-OCT-1996; 96US-0722187.

(NOVS) NOVARTIS FINANCE CORP.

Beck JU;

WPI; 1998-541745/46.

DNA isolated from fungal RNA, and its internal transcribed spacer
 sequence - used for detecting fungal pathogens in plant tissue

Claim 3; Column 17; 56pp; English.

Sequences AAV62507 to AAV62566 represent species specific PCR primers
 for various fungal isolates used for fungal detection in the course of
 the invention. The primers are designed based on the internal
 transcribed spacer (ITS) sequences of the various fungal species. The
 invention provides a DNA molecule isolated from the ribosomal RNA gene
 region of a fungal pathogen, where the DNA molecule consists of an ITS
 sequence selected from ITS1 and ITS2 of Fusarium culmorum, Fusarium
 graminearum, Fusarium moniliforme, Septoria avenae or Microdochium

CC nivale. A method for detecting F. graminearum, F. culmorum, F.
 CC moniliforme, F. poae, F. avenaceum and M. nivale isolates is also
 CC provided which comprises isolating DNA from a plant leaf infected with at
 CC least one of the above pathogens and amplifying parts of the ITS sequence
 CC of the pathogen(s) by PCR using specific primers from within these
 CC sequences. The pathogen(s) are detected by visualising the amplified part
 CC of the ITS sequence.

SQ Sequence 16 BP; 1 A; 5 C; 6 G; 4 T; 0 other;

Query Match 67.1%; Score 11.4; DB 19; Length 16;
 Best Local Similarity 92.3%; Pred. No. 1.2e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 13
 DB 1 GTTGCTTCGGCGG 13

Search completed: June 7, 2003, 08:30:21
 Job time : 157.018 secs

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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 07:18:59 ; Search time 148.255 Seconds

(without alignments)
273.421 Million cell updates/sec

Title: US-10-080-959A-5

Perfect score: 18

Sequence: 1 ctggcgcgcgcgcgcgcgc 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 1698378

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: N_Geneseq_101002:.*
2: /SID2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
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4: /SID2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
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13: /SID2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
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19: /SID2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
20: /SID2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
21: /SID2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
22: /SID2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
23: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
25: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	24	ABN99616
2	18	100.0	18	24	ABK29213
3	12.8	71.1	17	24	ABN99534
4	12.8	68.9	15	22	ABK29131
5	12.4	68.9	15	22	AAFS1791
6	12.4	68.9	15	22	AAFS1792
7	12.4	68.9	24	24	AAAL42362
8	12.4	68.9	24	24	ABA96574
9	12.2	67.8	21	20	AAK59160

C	10	12.2	67.8	21	24	ABK94173	Endothelin recepto
C	11	12.2	67.8	21	24	ABK94174	Endothelin recepto
C	12	12.2	67.8	24	20	AAK24822	Oligonucleotide ZC
C	13	12.2	67.8	24	21	AAK4122	PCR primer for the
C	14	12.2	67.7	15	24	AAI19807	ASO primer #65 to
C	15	12	66.7	21	14	AAO40880	Apptase gene rever
C	16	12	66.7	21	15	AAO64130	Apptase gene PCR p
C	17	12	66.7	25	15	AAO61767	HEV strain BUR-121
C	18	12	66.7	25	17	AAAT27478	HEV ORF proteins e
C	19	12	66.7	25	19	AAV17688	Bacillus lichenifo
C	20	11.8	65.6	18	15	AAO68697	Alkaline protease
C	21	11.8	65.6	18	15	AAO68697	Human CDC27 gene 5
C	22	11.8	65.6	24	17	AAAT1772	Primer 48 for sequ
C	23	11.6	64.4	19	24	ABK98282	Human polymorphic
C	24	11.6	64.4	21	19	AAK26752	CAPL 3' splice sit
C	25	11.6	64.4	21	19	AAV41150	US5877308 Seq ID 2
C	26	11.6	64.4	21	20	AAK17717	Endothelin recepto
C	27	11.6	64.4	21	24	ABK94171	Endothelin recepto
C	28	11.6	64.4	21	24	ABK94172	Endothelin recepto
C	29	11.6	64.4	21	24	ABK94175	Endothelin recepto
C	30	11.6	64.4	21	24	ABK94176	Endothelin recepto
C	31	11.6	64.4	22	19	AAV41141	CAPL 3' splice sit
C	32	11.6	64.4	22	19	AAV41142	CAPL 3' splice sit
C	33	11.6	64.4	22	20	AAK17597	Antisense oligo to
C	34	11.6	64.4	22	20	AAK17598	Antisense oligo to
C	35	11.6	64.4	22	21	AAK58261	Human PRO212 hybr
C	36	11.6	64.4	23	22	AAH78624	PCR primer RFC780
C	37	11.4	63.3	15	22	AAFS1790	IGF-1 oligonucleot
C	38	11.4	63.3	19	19	AAV24277	Chimeric antibody
C	39	11.4	63.3	19	20	AAK00122	Human antibody PCR
C	40	11.4	63.3	19	21	AAK58902	PCR primer MBCLVR
C	41	11.4	63.3	19	22	AAH75095	Nucleotide sequenc
C	42	11.4	63.3	19	22	AAH74274	Nucleotide sequenc
C	43	11.4	63.3	19	22	AAH76633	Humanised anti-PTH
C	44	11.4	63.3	19	22	AAH69118	Human L chain V re
C	45	11.4	63.3	19	22	AAH69174	Human L chain V re
C	46	11.4	63.3	19	22	AAH69230	Human L chain V re
C	47	11.4	63.3	19	22	AAH694810	Joint disease rela
C	48	11.4	63.3	20	20	AAK06762	Lymphocyte activat
C	49	11.4	63.3	20	22	AAH6704	Human cytohesin-2
C	50	11.4	63.3	21	22	AAH65638	Human gene single
C	51	11.4	63.3	21	22	AAK02834	Grate subunit of AT
C	52	11.2	62.2	16	18	AAK62856	Granule bound star
C	53	11.2	62.2	17	21	AAK02847	Hammerhead ribozym
C	54	11.2	62.2	17	24	ABN00659	Human GDMMP-1 17-m
C	55	11.2	62.2	17	24	ABN00659	Human GDMMP-1 17-m
C	56	11.2	62.2	17	24	ABN00659	Human GDMMP-1 17-m
C	57	11.2	62.2	18	18	AAK62746	Human GDMMP-1 17-m
C	58	11.2	62.2	19	24	ABK99522	Granule bound star
C	59	11.2	62.2	19	24	ABK29119	Fungi probe SEQ ID
C	60	11.2	62.2	20	24	ABK96263	Membrane protein
C	61	11.2	62.2	21	21	AAK1937	Capture oligonucle
C	62	11.2	62.2	21	21	AAK1937	Sequence surroundi
C	63	11.2	62.2	22	19	AAV43066	Synthetic antisens
C	64	11.2	62.2	22	24	ABK35825	Amplification prim
C	65	11.2	62.2	23	19	AAV43100	Myotonic dystrophy
C	66	11.2	62.2	23	22	AAK04323	Primer B14 for 11
C	67	11.2	62.2	23	24	ABK28778	Dog leukocyte inte
C	68	11.2	62.2	24	24	ABK28778	HSV-1 capture sequ
C	69	11.2	62.2	24	24	ABK28778	Capture oligonucle
C	70	11.2	62.2	25	24	ABK28778	Capture oligonucle
C	71	11.2	62.2	25	24	ABK28778	Human GDMMP-1 25-m
C	72	11.2	62.2	25	24	ABK28778	Human GDMMP-1 25-m
C	73	11.2	62.2	25	24	ABK28778	Human GDMMP-1 25-m
C	74	11.2	62.2	25	24	ABK28778	Human GDMMP-1 25-m
C	75	11.2	62.2	25	24	ABK28778	Human GDMMP-1 25-m
C	76	11.2	62.2	25	24	ABK28778	Human GDMMP-1 25-m
C	77	11.2	62.2	25	24	ABK28778	Human GDMMP-1 25-m
C	78	11.2	62.2	25	24	ABK28778	Human GDMMP-1 25-m
C	79	11.2	62.2	25	24	ABK28778	Human GDMMP-1 25-m
C	80	11.2	62.2	25	24	ABK28778	Human GDMMP-1 25-m
C	81	11.2	62.2	25	24	ABK28778	Human GDMMP-1 25-m
C	82	11.2	62.2	25	24	ABK28778	Human GDMMP-1 25-m

C 83	11	61.1	25	10	AA97005	Herpes Simplex Vir
84	11	61.1	25	18	AA75208	Primer 1 used to a
85	11	61.1	25	18	AAV00130	Human glucose regu
86	11	61.1	25	18	AAV00095	Human glucose regu
87	11	61.1	25	18	AA755048	Human glucose regu
88	11	61.1	25	21	AA755048	PCR primer for hum
89	11	61.1	25	22	AA755048	Human glucose regu
90	10.8	60.0	18	22	AA755048	SNP specific lower
91	10.8	60.0	18	22	AA755048	Primer CDX2-0048P
92	10.8	60.0	18	24	AA755048	Fungi probe SEQ ID
93	10.8	60.0	18	24	AA755048	Human HLA genocyp
94	10.8	60.0	18	24	AA755048	Stachyotrys chart
95	10.8	60.0	19	11	AA755048	Oligonucleotide pr
96	10.8	60.0	19	18	AA755048	Rat liver derived
97	10.8	60.0	19	22	AA755048	Cyclin E ribozyme
98	10.8	60.0	19	22	AA755048	P HyBeacon probe f
99	10.8	60.0	19	22	AA755048	Cyclin E ribozyme
100	10.8	60.0	20	19	AA755048	HLA DQB1 typing pr
101	10.8	60.0	20	22	AA755048	Primer F3 used to
102	10.8	60.0	20	22	AA755048	Human BGR-1 transc
103	10.8	60.0	20	22	AA755048	Murine Bax-alpha c
104	10.8	60.0	20	22	AA755048	Oligonucleotide #5
105	10.8	60.0	21	21	AA755048	Human p52 PCR prim
106	10.8	60.0	21	21	AA755048	Human p52 PCR prim
107	10.8	60.0	21	21	AA755048	PCR primer for the
108	10.8	60.0	21	22	AA755048	Human gene single
109	10.8	60.0	21	22	AA755048	AB54 PCR primer.
110	10.8	60.0	24	13	AA755048	Human MIP-1 beta p
111	10.8	60.0	24	22	AA755048	Human BGR-1 transc
112	10.8	60.0	24	22	AA755048	DNA encoding VP16
113	10.8	60.0	24	22	AA755048	Oligonucleotide ad
114	10.8	60.0	24	22	AA755048	Oligonucleotide ad
115	10.8	60.0	24	24	AA755048	Transduced RACC ge
116	10.8	60.0	24	24	AA755048	M. tuberculosis st
117	10.8	60.0	24	24	AA755048	A. gossypii GUA2 p
118	10.8	60.0	25	17	AA755048	HLA DOB gene PCR p
119	10.8	60.0	25	20	AA755048	HLA DOB gene PCR p
120	10.8	60.0	25	21	AA755048	Neisseria meningit
121	10.8	60.0	25	21	AA755048	Neisseria meningit
122	10.8	60.0	25	22	AA755048	Rat catalase (CAT)
123	10.8	60.0	25	22	AA755048	N. meningitidis fu
124	10.8	60.0	25	22	AA755048	Human GDMPL-1 17-m
125	10.8	60.0	25	22	AA755048	Primer #2 for PCR/
126	10.8	60.0	25	22	AA755048	E. coli 16S rRNA s
127	10.8	60.0	25	22	AA755048	PCR primer used to
128	10.8	60.0	25	22	AA755048	Primer for amplify
129	10.8	60.0	25	22	AA755048	Human IGF-1 antisense
130	10.8	60.0	25	22	AA755048	Human mcpPCK phos
131	10.8	60.0	25	22	AA755048	Sense PCR primer u
132	10.8	60.0	25	22	AA755048	Corn zein 10 gene
133	10.8	60.0	25	22	AA755048	Oryza sativa 10 gene
134	10.8	60.0	25	22	AA755048	Human ACAT Related
135	10.8	60.0	25	22	AA755048	PCR primer to ampl
136	10.8	60.0	25	22	AA755048	PCR primer to ampl
137	10.8	60.0	25	22	AA755048	FR4 J-lambda 1 light
138	10.8	60.0	25	22	AA755048	PCR primer for Hox
139	10.8	60.0	25	22	AA755048	Corneodesmosin PCR
140	10.8	60.0	25	22	AA755048	Mouse Hoxc-9 gene
141	10.8	60.0	25	22	AA755048	Primer 50 for sequ
142	10.8	60.0	25	22	AA755048	Oligonucleotide ad
143	10.8	60.0	25	22	AA755048	Oligonucleotide ad
144	10.8	60.0	25	22	AA755048	Oligonucleotide ad
145	10.8	60.0	25	22	AA755048	Heavy chain variab
146	10.8	60.0	25	22	AA755048	Oligonucleotide us
147	10.8	60.0	25	22	AA755048	PCR primer for cod
148	10.8	60.0	25	22	AA755048	HLA DOB gene PCR p
149	10.8	60.0	25	22	AA755048	HLA DOB gene PCR p
150	10.8	60.0	25	22	AA755048	Human GDMPL-1 25-m
151	10.8	60.0	25	22	AA755048	Human GDMPL-1 25-m
152	10.8	60.0	25	22	AA755048	Human GDMPL-1 25-m
153	10.8	60.0	25	22	AA755048	Human GDMPL-1 25-m
154	10.8	60.0	25	22	AA755048	Human GDMPL-1 25-m
155	10.8	60.0	25	22	AA755048	Human GDMPL-1 25-m

156	10.6	58.9	25	24	ABN05518	Human GDMPL-1 25-m
157	10.6	58.9	25	24	ABN05519	Human GDMPL-1 25-m
158	10.6	58.9	25	24	ABN05520	Human GDMPL-1 25-m
159	10.6	58.9	25	24	ABN05521	Human GDMPL-1 25-m
160	10.6	58.9	25	24	ABN05522	Human GDMPL-1 25-m
161	10.6	58.9	25	24	ABN05523	Human GDMPL-1 25-m
162	10.6	58.9	25	24	ABN05524	Human GDMPL-1 25-m
163	10.6	58.9	25	24	ABN05525	Human GDMPL-1 25-m
164	10.6	58.9	25	24	ABN05526	Human GDMPL-1 25-m
165	10.6	58.9	25	24	ABN05527	Human GDMPL-1 25-m
166	10.6	58.9	25	24	ABN05528	Human GDMPL-1 25-m
167	10.6	58.9	25	24	ABN05529	Human GDMPL-1 25-m
168	10.6	58.9	25	24	ABN05530	Human GDMPL-1 25-m
169	10.6	58.9	25	24	ABN05531	Human GDMPL-1 25-m
170	10.6	58.9	25	24	ABN05532	Human GDMPL-1 25-m
171	10.6	58.9	25	24	ABN05533	Human GDMPL-1 25-m
172	10.6	58.9	25	24	ABN05534	Human GDMPL-1 25-m
173	10.6	58.9	25	24	ABN05535	Human GDMPL-1 25-m
174	10.6	58.9	25	24	ABN05536	Human GDMPL-1 25-m
175	10.6	58.9	25	24	ABN05537	Human GDMPL-1 25-m
176	10.6	58.9	25	24	ABN05538	Human GDMPL-1 25-m
177	10.6	58.9	25	24	ABN05539	Human GDMPL-1 25-m
178	10.6	58.9	25	24	ABN05540	Human GDMPL-1 25-m
179	10.6	58.9	25	24	ABN05541	Human GDMPL-1 25-m
180	10.6	58.9	25	24	ABN05542	Human GDMPL-1 25-m
181	10.6	58.9	25	24	ABN05543	Human GDMPL-1 25-m
182	10.6	58.9	25	24	ABN05544	Human GDMPL-1 25-m
183	10.6	58.9	25	24	ABN05545	Human GDMPL-1 25-m
184	10.6	58.9	25	24	ABN05546	Human GDMPL-1 25-m
185	10.6	58.9	25	24	ABN05547	Human GDMPL-1 25-m
186	10.6	58.9	25	24	ABN05548	Human GDMPL-1 25-m
187	10.6	58.9	25	24	ABN05549	Human GDMPL-1 25-m
188	10.6	58.9	25	24	ABN05550	Human GDMPL-1 25-m
189	10.6	58.9	25	24	ABN05551	Human GDMPL-1 25-m
190	10.6	58.9	25	24	ABN05552	Human GDMPL-1 25-m
191	10.6	58.9	25	24	ABN05553	Human GDMPL-1 25-m
192	10.6	58.9	25	24	ABN05554	Human GDMPL-1 25-m
193	10.6	58.9	25	24	ABN05555	Human GDMPL-1 25-m
194	10.6	58.9	25	24	ABN05556	Human GDMPL-1 25-m
195	10.6	58.9	25	24	ABN05557	Human GDMPL-1 25-m
196	10.6	58.9	25	24	ABN05558	Human GDMPL-1 25-m
197	10.6	58.9	25	24	ABN05559	Human GDMPL-1 25-m
198	10.6	58.9	25	24	ABN05560	Human GDMPL-1 25-m
199	10.6	58.9	25	24	ABN05561	Human GDMPL-1 25-m
200	10.6	58.9	25	24	ABN05562	Human GDMPL-1 25-m
201	10.6	58.9	25	24	ABN05563	Human GDMPL-1 25-m
202	10.6	58.9	25	24	ABN05564	Human GDMPL-1 25-m
203	10.6	58.9	25	24	ABN05565	Human GDMPL-1 25-m
204	10.6	58.9	25	24	ABN05566	Human GDMPL-1 25-m
205	10.6	58.9	25	24	ABN05567	Human GDMPL-1 25-m
206	10.6	58.9	25	24	ABN05568	Human GDMPL-1 25-m
207	10.6	58.9	25	24	ABN05569	Human GDMPL-1 25-m
208	10.6	58.9	25	24	ABN05570	Human GDMPL-1 25-m
209	10.6	58.9	25	24	ABN05571	Human GDMPL-1 25-m
210	10.6	58.9	25	24	ABN05572	Human GDMPL-1 25-m
211	10.6	58.9	25	24	ABN05573	Human GDMPL-1 25-m
212	10.6	58.9	25	24	ABN05574	Human GDMPL-1 25-m
213	10.6	58.9	25	24	ABN05575	Human GDMPL-1 25-m
214	10.6	58.9	25	24	ABN05576	Human GDMPL-1 25-m
215	10.6	58.9	25	24	ABN05577	Human GDMPL-1 25-m
216	10.6	58.9	25	24	ABN05578	Human GDMPL-1 25-m
217	10.6	58.9	25	24	ABN05579	Human GDMPL-1 25-m
218	10.6	58.9	25	24	ABN05580	Human GDMPL-1 25-m
219	10.6	58.9	25	24	ABN05581	Human GDMPL-1 25-m
220	10.6	58.9	25	24	ABN05582	Human GDMPL-1 25-m
221	10.6	58.9	25	24	ABN05583	Human GDMPL-1 25-m
222	10.6	58.9	25	24	ABN05584	Human GDMPL-1 25-m
223	10.6	58.9	25	24	ABN05585	Human GDMPL-1 25-m
224	10.6	58.9	25	24	ABN05586	Human GDMPL-1 25-m
225	10.6	58.9	25	24	ABN05587	Human GDMPL-1 25-m
226	10.6	58.9	25	24	ABN05588	Human GDMPL-1 25-m
227	10.6	58.9	25	24	ABN05589	Human GDMPL-1 25-m
228	10.6	58.9	25	24	ABN05590	Human GDMPL-1 25-m

Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1 25-m	Human GDMPL-1
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229	10.4	57.8	25	18	AAV00502	Human alpha-(2) su	c 302	10.2	56.7	20	21	AAAG92292	16S ribosomal DNA
230	10.4	57.8	25	19	AAV59348	zif10 primer ZC13	c 303	10.2	56.7	20	21	AAAG2647	Bacterial DNA PCR
231	10.4	57.8	25	19	AAV64971	Human c-myc protei	c 304	10.2	56.7	20	21	AAAI5486	PCR primer for 16S
232	10.4	57.8	25	21	AAZ92373	Primer used in con	c 305	10.2	56.7	20	21	AAAI5486	Hepatitis GB virus
233	10.4	57.8	25	22	AAZ92373	3' FTR 5' PCR prim	c 306	10.2	56.7	20	21	AAAI5486	Treponema socransk
234	10.4	57.8	25	24	AAI77922	Oligo #11 for clon	c 307	10.2	56.7	20	21	AAZ59415	Forward PCR primer
235	10.4	57.8	25	24	ABA03545	Relaxin/IGF/insuli	c 308	10.2	56.7	20	21	AAZ59415	PCR primer for L.
236	10.2	56.7	15	22	AAAF70003	Human TNFRSF1B ge	c 309	10.2	56.7	20	21	AAZ59415	PCR primer #1 for
237	10.2	56.7	15	22	AAAF45555	IGFBP2 oligonucleo	c 310	10.2	56.7	20	21	AAZ59415	Brevibacillus bore
238	10.2	56.7	15	22	AAAF45555	IGFBP2 oligonucleo	c 311	10.2	56.7	20	21	AAZ59415	PCR primer for 16S
239	10.2	56.7	16	18	AAV05767	Human chorionic go	c 312	10.2	56.7	20	22	AAH78560	Brevibacillus bore
240	10.2	56.7	16	20	AAV81285	PNA probe sequence	c 313	10.2	56.7	20	22	AAH78560	PCR primer for 16S
241	10.2	56.7	17	18	AAV45916	Granule bound star	c 314	10.2	56.7	20	22	AAH78560	Brevibacillus bore
242	10.2	56.7	17	19	AAV45916	Biosensor oligonuc	c 315	10.2	56.7	20	22	AAH78560	Human caspase 8 mr
243	10.2	56.7	17	20	AAV81920	PCR primer used to	c 316	10.2	56.7	20	22	AAH78560	Heart muscle cell
244	10.2	56.7	17	21	AAV81920	Hammerhead ribozym	c 317	10.2	56.7	20	22	AAH78560	MLC-2v PCR primer
245	10.2	56.7	17	21	AAV81920	Hepatitis B virus	c 318	10.2	56.7	20	22	AAH78560	Brevibacillus bore
246	10.2	56.7	17	21	AAV81920	Hepatitis B virus	c 319	10.2	56.7	20	22	AAH78560	PCR primer for 16S
247	10.2	56.7	17	21	AAV81920	Hepatitis B virus	c 320	10.2	56.7	20	22	AAH78560	Brevibacillus bore
248	10.2	56.7	17	22	AAV81920	Human ABC1 polymor	c 321	10.2	56.7	20	22	AAH78560	Human caspase 8 mr
249	10.2	56.7	17	22	AAV81920	Fungi probe SEQ ID	c 322	10.2	56.7	20	22	AAH78560	Heart muscle cell
250	10.2	56.7	17	24	ABN00658	Human GDMLP-1 17-m	c 323	10.2	56.7	20	22	AAH78560	MLC-2v PCR primer
251	10.2	56.7	17	24	ABN00658	Human GDMLP-1 17-m	c 324	10.2	56.7	20	22	AAH78560	Brevibacillus bore
252	10.2	56.7	17	24	ABN00658	Human GDMLP-1 17-m	c 325	10.2	56.7	20	22	AAH78560	PCR primer for 16S
253	10.2	56.7	17	24	ABN06404	Human GDMLP-1 17-m	c 326	10.2	56.7	20	22	AAH78560	Brevibacillus bore
254	10.2	56.7	17	24	ABN06404	Human GDMLP-1 17-m	c 327	10.2	56.7	20	22	AAH78560	Human caspase 8 mr
255	10.2	56.7	17	24	ABN06404	Human GDMLP-1 17-m	c 328	10.2	56.7	20	22	AAH78560	Heart muscle cell
256	10.2	56.7	17	24	ABK14159	Chlorinated ethyle	c 329	10.2	56.7	20	22	AAH78560	MLC-2v PCR primer
257	10.2	56.7	17	24	ABK29131	Bacterial 16S rRNA	c 330	10.2	56.7	20	22	AAH78560	Brevibacillus bore
258	10.2	56.7	17	24	ABK29131	Myrothecium vertiru	c 331	10.2	56.7	20	22	AAH78560	Human caspase 8 mr
259	10.2	56.7	18	19	AAV84821	Transforming growt	c 332	10.2	56.7	20	22	AAH78560	Heart muscle cell
260	10.2	56.7	18	19	AAV84821	Osteonin exon PCR	c 333	10.2	56.7	20	22	AAH78560	MLC-2v PCR primer
261	10.2	56.7	19	17	AAV84821	Primer #1 to ampl	c 334	10.2	56.7	20	22	AAH78560	Brevibacillus bore
262	10.2	56.7	19	18	AAV02915	Bacterial ribosoma	c 335	10.2	56.7	20	22	AAH78560	PCR primer for 16S
263	10.2	56.7	19	19	AAV29380	Bloom's syndrome a	c 336	10.2	56.7	20	22	AAH78560	Brevibacillus bore
264	10.2	56.7	19	19	AAV17991	Calcium ion channe	c 337	10.2	56.7	20	22	AAH78560	Human caspase 8 mr
265	10.2	56.7	19	20	AAV76739	Microorganism MO7	c 338	10.2	56.7	20	22	AAH78560	Heart muscle cell
266	10.2	56.7	19	20	AAV76739	PCR primer J11 for	c 339	10.2	56.7	20	22	AAH78560	MLC-2v PCR primer
267	10.2	56.7	19	20	AAV76739	5' primer used to	c 340	10.2	56.7	20	22	AAH78560	Brevibacillus bore
268	10.2	56.7	19	20	AAV76739	MO9922023 probe 62	c 341	10.2	56.7	20	22	AAH78560	Human caspase 8 mr
269	10.2	56.7	19	20	AAV76739	Strain MO7 16S rDN	c 342	10.2	56.7	20	22	AAH78560	Heart muscle cell
270	10.2	56.7	19	20	AAV76739	Strain MO7 16S rDN	c 343	10.2	56.7	20	22	AAH78560	MLC-2v PCR primer
271	10.2	56.7	19	22	AAV76739	Burkholderia sp. 1	c 344	10.2	56.7	20	22	AAH78560	Brevibacillus bore
272	10.2	56.7	19	22	AAV76739	Burkholderia sp. 1	c 345	10.2	56.7	20	22	AAH78560	PCR primer for 16S
273	10.2	56.7	19	24	AAV76739	Rhodococcus erythr	c 346	10.2	56.7	20	22	AAH78560	Hepatitis GB virus
274	10.2	56.7	19	24	AAV76739	Forward PCR primer	c 347	10.2	56.7	20	22	AAH78560	Treponema socransk
275	10.2	56.7	20	12	AAQ10065	Probe 1638 to the	c 348	10.2	56.7	20	22	AAH78560	Forward PCR primer
276	10.2	56.7	20	12	AAQ10065	Probe 1744 to the	c 349	10.2	56.7	20	22	AAH78560	PCR primer for L.
277	10.2	56.7	20	15	AAQ54376	LAB RNA gene prim	c 350	10.2	56.7	20	22	AAH78560	PCR primer #1 for
278	10.2	56.7	20	15	AAQ54376	PCR primer for amp	c 351	10.2	56.7	20	22	AAH78560	Brevibacillus bore
279	10.2	56.7	20	16	AAV01867	P. cepacia 16S rRNA	c 352	10.2	56.7	20	22	AAH78560	Human caspase 8 mr
280	10.2	56.7	20	16	AAV01867	Hepatitis GB virus	c 353	10.2	56.7	20	22	AAH78560	Heart muscle cell
281	10.2	56.7	20	16	AAV01867	16S rRNA forward a	c 354	10.2	56.7	20	22	AAH78560	MLC-2v PCR primer
282	10.2	56.7	20	17	AAV01867	Primer for amplif	c 355	10.2	56.7	20	22	AAH78560	Brevibacillus bore
283	10.2	56.7	20	17	AAV01867	Primer (1638) for	c 356	10.2	56.7	20	22	AAH78560	Human caspase 8 mr
284	10.2	56.7	20	18	AAV06352	Control scrambled	c 357	10.2	56.7	20	22	AAH78560	Heart muscle cell
285	10.2	56.7	20	19	AAV34336	Burkholderia casid	c 358	10.2	56.7	20	22	AAH78560	MLC-2v PCR primer
286	10.2	56.7	20	19	AAV34336	Nucleotide sequen	c 359	10.2	56.7	20	22	AAH78560	Brevibacillus bore
287	10.2	56.7	20	19	AAV58804	Primer 27F for bac	c 360	10.2	56.7	20	22	AAH78560	PCR primer for 16S
288	10.2	56.7	20	19	AAV58804	16S rRNA Becherich	c 361	10.2	56.7	20	22	AAH78560	Hepatitis GB virus
289	10.2	56.7	20	19	AAV34350	Eubacterial rRNA p	c 362	10.2	56.7	20	22	AAH78560	Treponema socransk
290	10.2	56.7	20	19	AAV34350	PCR primer UD SEQ	c 363	10.2	56.7	20	22	AAH78560	Forward PCR primer
291	10.2	56.7	20	20	AAV25448	Human Toso PCR pri	c 364	10.2	56.7	20	22	AAH78560	PCR primer for L.
292	10.2	56.7	20	20	AAV25448	Forward primer 27F	c 365	10.2	56.7	20	22	AAH78560	PCR primer #1 for
293	10.2	56.7	20	20	AAV211276	Forward primer for	c 366	10.2	56.7	20	22	AAH78560	Brevibacillus bore
294	10.2	56.7	20	20	AAV211276	Human Chiodoxin	c 367	10.2	56.7	20	22	AAH78560	Human caspase 8 mr
295	10.2	56.7	20	20	AAV89819	M. tuberculosis 16	c 368	10.2	56.7	20	22	AAH78560	Heart muscle cell
296	10.2	56.7	20	20	AAV89819	Human matrix metal	c 369	10.2	56.7	20	22	AAH78560	MLC-2v PCR primer
297	10.2	56.7	20	20	AAV92167	PCR primer used to	c 370	10.2	56.7	20	22	AAH78560	Brevibacillus bore
298	10.2	56.7	20	20	AAV76127	Human Toso protein	c 371	10.2	56.7	20	22	AAH78560	PCR primer for 16S
299	10.2	56.7	20	20	AAV16996	Forward primer for	c 372	10.2	56.7	20	22	AAH78560	Brevibacillus bore
300	10.2	56.7	20	20	AAV16996	PCR primer 1 used	c 373	10.2	56.7	20	22	AAH78560	Human caspase 8 mr
301	10.2	56.7	20	21	AAV87901	Pseudomonas sp. 01	c 374	10.2	56.7	20	22	AAH78560	Heart muscle cell

C 375	10.2	56.7	23	17	AA744282	5'-Guanosine-capped	C 448	10	55.6	20	22	AAH20679	Human telomeric re
C 376	10.2	56.7	23	21	AAJ39023	Unknown bacterial	C 449	10	55.6	20	22	AAH74084	Primer #18, Homo
C 377	10.2	56.7	23	21	ABL51612	Chemical polymers	C 450	10	55.6	20	22	AAH73059	Human dactyl inhibi
C 378	10.2	56.7	23	24	ABL51613	Chemical polymers	C 451	10	55.6	20	22	AAH73059	PCR primer specific
C 379	10.2	56.7	24	9	AAH80289	Sequence of Arg 15	C 452	10	55.6	20	22	AAH92460	Capture oligonucle
C 380	10.2	56.7	24	9	AAH80289	Sequence of Arg 15	C 453	10	55.6	21	14	AAQ35068	PCR primer #43 for
C 381	10.2	56.7	24	16	AAH80292	Primer for amplify	C 454	10	55.6	21	19	AAQ35068	Human polymorphic
C 382	10.2	56.7	24	16	AAH80292	Primer for amplify	C 455	10	55.6	21	19	AAH80292	Primer for human i
C 383	10.2	56.7	24	16	AAH80292	Primer for amplify	C 456	10	55.6	21	21	AAH80292	Human tumor suppr
C 384	10.2	56.7	24	18	AAH80293	Human cathepsin Y	C 457	10	55.6	21	21	AAH80293	Human gene single
C 385	10.2	56.7	24	19	AAH80293	M. catarrhalis str	C 458	10	55.6	21	22	AAH80293	Human gene single
C 386	10.2	56.7	24	19	AAH80293	Mismatch complemen	C 459	10	55.6	21	22	AAH80293	Primer 9 used in t
C 387	10.2	56.7	24	19	AAH80293	Primer used in pre	C 460	10	55.6	21	22	AAH80293	Barnase gene prime
C 388	10.2	56.7	24	22	AAH80293	Wild type 24-mer o	C 461	10	55.6	22	14	AAH80293	Barnase gene prime
C 389	10.2	56.7	24	22	AAH80293	Rice OsC1X2 PCR p	C 462	10	55.6	22	14	AAH80293	Barnase coding reg
C 390	10.2	56.7	24	24	ABO03269	Oligonucleotide ad	C 463	10	55.6	22	19	AAH80293	Barnase gene PCR p
C 391	10.2	56.7	24	24	ABO03269	Oligonucleotide ad	C 464	10	55.6	22	19	AAH80293	Barnase gene PCR p
C 392	10.2	56.7	24	24	ABO03269	Oligonucleotide ad	C 465	10	55.6	22	19	AAH80293	Barnase gene PCR p
C 393	10.2	56.7	24	24	ABO03269	Oligonucleotide ad	C 466	10	55.6	22	19	AAH80293	Barnase coding reg
C 394	10.2	56.7	24	24	ABO03269	Oligonucleotide ad	C 467	10	55.6	22	19	AAH80293	Vascular endotheli
C 395	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 468	10	55.6	22	20	AAH80293	Human lactoferrin
C 396	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 469	10	55.6	22	21	AAH80293	Human G-protein co
C 397	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 470	10	55.6	22	22	AAH80293	Primer #1, to ampl
C 398	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 471	10	55.6	22	22	AAH80293	Mouse interferon g
C 399	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 472	10	55.6	22	22	AAH80293	PCR primer, YYB-F
C 400	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 473	10	55.6	22	24	AAH80293	Megaspinaera cerevi
C 401	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 474	10	55.6	22	24	AAH80293	Transforming growt
C 402	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 475	10	55.6	23	19	AAH80293	Plasmid pHP PCR p
C 403	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 476	10	55.6	23	19	AAH80293	Primer used to iso
C 404	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 477	10	55.6	23	21	AAH80293	Primer used in con
C 405	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 478	10	55.6	23	21	AAH80293	Oleiferlin RT-PCR p
C 406	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 479	10	55.6	23	23	AAH80293	Interferon-gamma R
C 407	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 480	10	55.6	24	18	AAH80293	Murine xpc gene PC
C 408	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 481	10	55.6	24	20	AAH80293	PCR primer for his
C 409	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 482	10	55.6	24	20	AAH80293	PCR primer used to
C 410	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 483	10	55.6	24	21	AAH80293	Mouse KISS-1 PCR p
C 411	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 484	10	55.6	24	22	AAH80293	Human excitatory a
C 412	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 485	10	55.6	24	22	AAH80293	Human DNMT3L cDNA
C 413	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 486	10	55.6	24	22	AAH80293	Human GABA transpo
C 414	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 487	10	55.6	24	22	AAH80293	Alp1a (1) subunit
C 415	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 488	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 416	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 489	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 417	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 490	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 418	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 491	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 419	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 492	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 420	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 493	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 421	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 494	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 422	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 495	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 423	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 496	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 424	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 497	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 425	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 498	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 426	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 499	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 427	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 500	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 428	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 501	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 429	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 502	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 430	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 503	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 431	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 504	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 432	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 505	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 433	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 506	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 434	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 507	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 435	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 508	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 436	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 509	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 437	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 510	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 438	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 511	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 439	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 512	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 440	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 513	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 441	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 514	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 442	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 515	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 443	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 516	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 444	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 517	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 445	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 518	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 446	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 519	10	55.6	24	24	AAH80293	Oligonucleotide ad
C 447	10.2	56.7	24	24	ABO03269	Capture oligonucle	C 520	10	55.6	24	24	AAH80293	Oligonucleotide ad

521	9.8	54.4	15	17	AAT37716	Apo(a) mRNA (nt. p	C 594	9.8	54.4	20	20	AAV01433	Probe for Bacterol
522	9.8	54.4	15	17	AAT37626	Apo(a) mRNA (nt. p	595	9.8	54.4	20	21	AAV08766	Human FUT6 antisen
523	9.8	54.4	15	17	AAT37587	Apo(a) mRNA (nt. p	C 596	9.8	54.4	20	21	AAV40718	Mouse fibrinogen-1
524	9.8	54.4	15	17	AAT37564	Apo(a) mRNA (nt. p	C 597	9.8	54.4	20	21	AAV86872	16S rRNA PCR prime
525	9.8	54.4	15	17	AAT37566	Apo(a) mRNA (nt. p	C 598	9.8	54.4	20	22	AAV10991	Forward universal
526	9.8	54.4	15	17	AAT34531	Human Fas antigen	599	9.8	54.4	20	22	AAV03151	Human EPO primary
527	9.8	54.4	15	17	AAT34533	Human Fas antigen	C 600	9.8	54.4	20	22	AAV54839	Primer used for sp
C 528	9.8	54.4	15	22	AAV45522	IGFBP2 oligonucleo	C 601	9.8	54.4	20	22	AAV88343	Probe 432T. Unde
C 529	9.8	54.4	15	22	AAV45524	IGFBP2 oligonucleo	C 602	9.8	54.4	20	22	AAV67694	Oligonucleotide #5
C 530	9.8	54.4	15	22	AAV46672	IGFBP3 oligonucleo	C 603	9.8	54.4	20	22	AAV67695	Oligonucleotide #6
532	9.8	54.4	15	22	AAV46673	IGFBP3 oligonucleo	C 604	9.8	54.4	20	24	ABV55394	Eubacterial/univer
533	9.8	54.4	15	22	AAV46674	IGFBP3 oligonucleo	C 605	9.8	54.4	20	24	ABV83706	Arthrobacter sp. 1
534	9.8	54.4	15	24	AAV48092	Human neurotrophide	C 606	9.8	54.4	20	24	ABV80861	Human caspase 7 ph
535	9.8	54.4	16	16	AAV094570	RNA "clamp" used t	C 607	9.8	54.4	20	24	ABV68934	Rat phosphotyrlase
536	9.8	54.4	16	20	AAV00982	PCR primer for PGI	C 608	9.8	54.4	20	24	ABV69555	Rat phosphotyrlase
537	9.8	54.4	16	20	AAV390157	Detection probe SE	C 609	9.8	54.4	20	24	ABV69173	Human phosphotyrlas
C 538	9.8	54.4	16	24	ABV83104	HHA-QBI gene prob	C 610	9.8	54.4	20	24	AAV29926	Forward primer use
C 539	9.8	54.4	17	14	AAV039297	Glucocerebrosidase	C 611	9.8	54.4	20	24	ABV67074	Maniheta sp. 558
C 540	9.8	54.4	17	14	AAV048259	Glucocerebrosidase	C 612	9.8	54.4	20	16	AAV01017	Tomato exo-(1-4)de
C 541	9.8	54.4	17	18	AAV74687	Mouse fil-1 VEGF r	C 613	9.8	54.4	21	20	AAV23773	Vector pshuttle 3'
C 542	9.8	54.4	17	20	AAV87888	Novamyl loop-speci	C 614	9.8	54.4	21	22	AAV62469	GRAP polymorphism
C 543	9.8	54.4	17	20	AAV87889	Novamyl loop-speci	C 615	9.8	54.4	21	22	AAV62469	GRAP polymorphism
544	9.8	54.4	17	20	AAV92594	Human A-Raf subctr	C 616	9.8	54.4	21	22	AAV95460	Human gene single
545	9.8	54.4	17	21	AAV07163	Hammerhead ribozym	C 617	9.8	54.4	21	22	AAV96714	Human gene single
C 546	9.8	54.4	17	21	AAV07163	Hammerhead ribozym	C 618	9.8	54.4	21	24	ABV73315	TPO mimetic antibo
547	9.8	54.4	17	21	AAV07352	Hammerhead ribozym	C 619	9.8	54.4	21	24	ABV65766	Human single nucle
548	9.8	54.4	17	21	AAV07352	Hammerhead ribozym	C 620	9.8	54.4	22	18	AAV74816	Porcine retrovirus
549	9.8	54.4	17	24	ABV02589	Hepatitis B virus	C 621	9.8	54.4	22	18	AAV74816	Porcine retrovirus
550	9.8	54.4	17	24	ABV02590	Human GDMPL-1 17-m	C 622	9.8	54.4	22	18	AAV74816	Porcine retrovirus
551	9.8	54.4	17	24	ABV02591	Human GDMPL-1 17-m	C 623	9.8	54.4	22	18	AAV74817	Porcine retrovirus
552	9.8	54.4	17	24	ABV02592	Human GDMPL-1 17-m	C 624	9.8	54.4	22	18	AAV74817	Porcine retrovirus
553	9.8	54.4	17	24	ABV02592	Human GDMPL-1 17-m	C 625	9.8	54.4	22	20	AAV09309	Human macrophage s
C 554	9.8	54.4	18	13	AAV06544	Human HLA genotypi	C 626	9.8	54.4	22	21	AAV13227	PCR primer #8 used
C 555	9.8	54.4	18	15	AAV06544	Control probe #4 f	C 627	9.8	54.4	22	22	AAV73653	T cell receptor be
C 556	9.8	54.4	18	16	AAV084595	Type II procollage	C 628	9.8	54.4	22	22	AAV77732	Human MD36 CDNA PC
C 557	9.8	54.4	18	16	AAV084595	Cosmid 46C7-T7 pri	C 629	9.8	54.4	22	22	AAV77732	PCR primer #5. Un
C 558	9.8	54.4	18	17	AAV35870	Human DNA polymera	C 630	9.8	54.4	22	22	AAV77733	PCR primer #6. Un
C 559	9.8	54.4	18	18	AAV63304	Delta-9 desaturase	C 631	9.8	54.4	22	22	AAV77733	PCR primer #6. Un
560	9.8	54.4	18	19	AAV22170	DNA repeat unit 1	C 632	9.8	54.4	22	24	AAV77733	PCR primer #6. Un
561	9.8	54.4	18	20	AAV72038	Primer for amplify	C 633	9.8	54.4	22	24	ABV86116	T-cell antigen rec
C 562	9.8	54.4	18	20	AAV72038	Human CPG2 PCR pri	C 634	9.8	54.4	23	16	AAV82991	Human MD36 specific
563	9.8	54.4	18	20	AAV02155	Human IYS17 3'-acc	C 635	9.8	54.4	23	18	AAV82991	Human erythropoiet
564	9.8	54.4	18	20	AAV00323	Human leukocyte an	636	9.8	54.4	23	18	AAV59299	PCR primer HGH1 of
565	9.8	54.4	18	20	AAV00323	Human leukocyte an	637	9.8	54.4	23	18	AAV78932	Rose River virus N
566	9.8	54.4	18	20	AAV04794	Group-specific seq	C 638	9.8	54.4	23	18	AAV78932	Human stem cell an
567	9.8	54.4	18	21	AAV04798	Group-specific seq	C 639	9.8	54.4	23	18	AAV78932	Human stem cell an
568	9.8	54.4	18	21	AAV04798	Group-specific seq	C 640	9.8	54.4	23	19	AAV58813	Human mast protein
569	9.8	54.4	18	21	AAV04798	Group-specific seq	C 641	9.8	54.4	23	20	AAV58813	Human growth hormo
570	9.8	54.4	18	21	AAV04798	Group-specific seq	642	9.8	54.4	23	21	AAV58813	Human growth hormo
C 571	9.8	54.4	18	21	AAV04798	Group-specific seq	643	9.8	54.4	23	21	AAV58813	Human growth hormo
C 572	9.8	54.4	18	21	AAV04798	Group-specific seq	644	9.8	54.4	23	22	AAV58813	Human growth hormo
573	9.8	54.4	18	22	AAV04798	Group-specific seq	645	9.8	54.4	23	22	AAV58813	Human growth hormo
C 574	9.8	54.4	18	22	AAV04798	Group-specific seq	646	9.8	54.4	23	22	AAV58813	Human growth hormo
C 575	9.8	54.4	18	22	AAV04798	Group-specific seq	647	9.8	54.4	23	22	AAV58813	Human growth hormo
576	9.8	54.4	18	24	ABV58292	Human Smad7 phosph	648	9.8	54.4	23	23	ABV58292	Human ANK gene PCR
C 577	9.8	54.4	18	24	ABV58292	Human Smad7 phosph	649	9.8	54.4	23	24	ABV58292	Human growth hormo
578	9.8	54.4	19	18	AAV13331	Human GLUT 10 SSCP	C 650	9.8	54.4	23	24	ABV58292	Human growth hormo
C 579	9.8	54.4	19	18	AAV13331	Human GLUT 10 SSCP	C 651	9.8	54.4	23	24	ABV58292	Human growth hormo
C 580	9.8	54.4	19	21	AAV13331	Human GLUT 10 SSCP	C 652	9.8	54.4	24	16	AAV58292	Human growth hormo
C 581	9.8	54.4	20	15	AAV064102	Human GLUT 10 SSCP	C 653	9.8	54.4	24	16	AAV58292	Human growth hormo
C 582	9.8	54.4	20	15	AAV064102	Human GLUT 10 SSCP	C 654	9.8	54.4	24	17	AAV28899	Human growth hormo
583	9.8	54.4	20	18	AAV78479	Human GLUT 10 SSCP	C 655	9.8	54.4	24	17	AAV28899	Human growth hormo
584	9.8	54.4	20	18	AAV78479	Human GLUT 10 SSCP	C 656	9.8	54.4	24	18	AAV78490	Human growth hormo
585	9.8	54.4	20	18	AAV78479	Human GLUT 10 SSCP	C 657	9.8	54.4	24	19	AAV22263	Human growth hormo
586	9.8	54.4	20	18	AAV78479	Human GLUT 10 SSCP	C 658	9.8	54.4	24	19	AAV22263	Human growth hormo
587	9.8	54.4	20	19	AAV70000	Human GLUT 10 SSCP	C 659	9.8	54.4	24	20	AAV22263	Human growth hormo
C 588	9.8	54.4	20	19	AAV70000	Human GLUT 10 SSCP	C 660	9.8	54.4	24	21	AAV22263	Human growth hormo
C 589	9.8	54.4	20	19	AAV70000	Human GLUT 10 SSCP	C 661	9.8	54.4	24	22	AAV22263	Human growth hormo
C 590	9.8	54.4	20	19	AAV70000	Human GLUT 10 SSCP	C 662	9.8	54.4	24	22	AAV22263	Human growth hormo
C 591	9.8	54.4	20	19	AAV70000	Human GLUT 10 SSCP	C 663	9.8	54.4	24	22	AAV22263	Human growth hormo
C 592	9.8	54.4	20	19	AAV70000	Human GLUT 10 SSCP	C 664	9.8	54.4	24	24	ABV86841	Human growth hormo
C 593	9.8	54.4	20	19	AAV70000	Human GLUT 10 SSCP	C 665	9.8	54.4	24	24	ABV86841	Human growth hormo
							C 666	9.8	54.4	24	24	ABV86841	Human growth hormo

C 667	9.8	54.4	24	24	ABR99284	Primer 50 for sequ	740	9.6	53.3	20	13	AAQ31556	Sense primer for c
C 668	9.8	54.4	24	24	ABQ00975	Oligonucleotide ad	741	9.6	53.3	20	18	AA760474	MCSF PCR primer RM
C 669	9.8	54.4	24	24	ABQ001417	Oligonucleotide ad	C 742	9.6	53.3	20	18	AA760474	MCSF PCR primer RM
C 670	9.8	54.4	24	24	ABQ002727	Oligonucleotide ad	C 743	9.6	53.3	20	18	AA760476	MCSF PCR primer RM
C 671	9.8	54.4	24	24	ABQ005894	Oligonucleotide ad	C 744	9.6	53.3	20	18	AA760476	MCSF PCR primer RM
C 672	9.8	54.4	24	24	ABQ005935	Oligonucleotide ad	C 745	9.6	53.3	20	20	AA7231218	HCV NS5B DNA speci
C 673	9.8	54.4	24	24	ABQ06779	Oligonucleotide ad	C 746	9.6	53.3	20	20	AA723135	CXCR4 gene inhibit
C 674	9.8	54.4	24	24	ABQ06820	Oligonucleotide ad	C 747	9.6	53.3	20	20	AA701951	PCR primer used to
C 675	9.8	54.4	24	24	ABQ093432	Oligonucleotide ad	C 748	9.6	53.3	20	20	AA792522	PCR primer used to
C 676	9.8	54.4	24	24	ABQ093483	Oligonucleotide ad	C 749	9.6	53.3	20	20	AA792526	PCR primer used to
C 677	9.8	54.4	24	24	AB1869557	Capture oligonucle	C 750	9.6	53.3	20	21	AA792538	Forward primer #1.3
C 678	9.8	54.4	24	24	AB1869557	Capture oligonucle	C 751	9.6	53.3	20	21	AA792538	Forward primer TEF-46.
C 679	9.8	54.4	24	24	AA171439	Human excitatory a	C 752	9.6	53.3	20	21	AA773749	Primer F3c used to
C 680	9.8	54.4	25	17	AA170767	Yeast hls3 gene PC	C 753	9.6	53.3	20	22	AA7515213	Human bcl-x antisense
C 681	9.8	54.4	25	18	AA7559301	Human bcl-x antisense	C 754	9.6	53.3	20	22	AA7515213	Human bcl-x antisense
C 682	9.8	54.4	25	19	AA7559414	PCR primer ZC13449	C 755	9.6	53.3	20	22	AA7515213	Human bcl-x antisense
C 683	9.8	54.4	25	19	AA7559414	PCR primer ZC13449	C 756	9.6	53.3	20	22	AA7515213	Human bcl-x antisense
C 684	9.8	54.4	25	19	AA7559414	PCR primer ZC13449	C 757	9.6	53.3	20	22	AA7515213	Human bcl-x antisense
C 685	9.8	54.4	25	20	AA7559414	PCR primer ZC13449	C 758	9.6	53.3	20	22	AA7515213	Human bcl-x antisense
C 686	9.8	54.4	25	20	AA7559414	PCR primer ZC13449	C 759	9.6	53.3	20	22	AA7515213	Human bcl-x antisense
C 687	9.8	54.4	25	20	AA7559414	PCR primer ZC13449	C 760	9.6	53.3	20	24	AA743512	Human bcl-x antisense
C 688	9.8	54.4	25	20	AA7559414	PCR primer ZC13449	C 761	9.6	53.3	20	24	AA743512	Human bcl-x antisense
C 689	9.8	54.4	25	20	AA7559414	PCR primer ZC13449	C 762	9.6	53.3	20	24	AA743512	Human bcl-x antisense
C 690	9.8	54.4	25	21	AA7559414	PCR primer ZC13449	C 763	9.6	53.3	20	24	AA743512	Human bcl-x antisense
C 691	9.8	54.4	25	21	AA7559414	PCR primer ZC13449	C 764	9.6	53.3	20	24	AA743512	Human bcl-x antisense
C 692	9.8	54.4	25	21	AA7559414	PCR primer ZC13449	C 765	9.6	53.3	20	24	AA743512	Human bcl-x antisense
C 693	9.8	54.4	25	21	AA7559414	PCR primer ZC13449	C 766	9.6	53.3	20	24	AA743512	Human bcl-x antisense
C 694	9.8	54.4	25	21	AA7559414	PCR primer ZC13449	C 767	9.6	53.3	20	24	AA743512	Human bcl-x antisense
C 695	9.8	54.4	25	21	AA7559414	PCR primer ZC13449	C 768	9.6	53.3	20	24	AA743512	Human bcl-x antisense
C 696	9.8	54.4	25	22	AA7559414	PCR primer ZC13449	C 769	9.6	53.3	20	24	AA743512	Human bcl-x antisense
C 697	9.8	54.4	25	22	AA7559414	PCR primer ZC13449	C 770	9.6	53.3	20	24	AA743512	Human bcl-x antisense
C 698</													

C 813	9.6	53.3	24	20	AAx88475	Human MIP-1 beta p
814	9.6	53.3	24	21	AAc80372	Forward primer #14
815	9.6	53.3	24	21	AAz60283	Primer 2 used in t
C 816	9.6	53.3	24	21	AAz44726	Bovine c-Kit bK-1
C 817	9.6	53.3	24	21	AAz44738	Murine and human C
818	9.6	53.3	24	22	AAc85845	Primer 2 to const
819	9.6	53.3	24	22	AAc85851	Primer 8 to const
820	9.6	53.3	24	22	AAc85851	Nicotianamine amin
821	9.6	53.3	24	22	AAc87567	TGAT SFCIS element
822	9.6	53.3	24	24	AAJ39874	Human glycosyl-Hyd
C 823	9.6	53.3	24	24	ABK50798	Acid phosphatase 5
824	9.6	53.3	24	24	ABK67701	Transglutaminase 5
825	9.6	53.3	24	24	ABQ01511	Oligonucleotide ad
826	9.6	53.3	24	24	ABQ06955	Oligonucleotide ad
C 827	9.6	53.3	24	24	ABQ06956	Oligonucleotide ad
C 828	9.6	53.3	24	24	ABQ33423	Aspergillus oryzae
C 829	9.6	53.3	24	24	ABQ69574	Human thyroglobulin
C 830	9.6	53.3	24	24	ABJ84200	Capture oligonucle
C 831	9.6	53.3	24	24	ABJ84201	Capture oligonucle
C 832	9.6	53.3	24	24	ABJ85942	Capture oligonucle
C 833	9.6	53.3	24	24	ABJ85943	Capture oligonucle
C 834	9.6	53.3	24	24	ABJ87338	Capture oligonucle
C 835	9.6	53.3	24	24	ABJ87339	Capture oligonucle
C 836	9.6	53.3	24	24	ABJ87339	Capture oligonucle
837	9.6	53.3	24	24	ABJ87339	Capture oligonucle
838	9.6	53.3	24	24	ABJ90240	Capture oligonucle
C 839	9.6	53.3	24	24	ABJ90241	Capture oligonucle
C 840	9.6	53.3	24	24	ABJ91388	Capture oligonucle
841	9.6	53.3	24	24	ABJ91389	Capture oligonucle
842	9.6	53.3	25	19	AAV797480	Purified DNA of si
C 843	9.6	53.3	25	19	AAV79792	ECERO section 3 co
C 844	9.6	53.3	25	19	AAV79793	ECERO section 3 co
C 845	9.6	53.3	25	19	AAV31136	C-Jun amino acids
846	9.6	53.3	25	20	AAV33270	Probe used to dele
847	9.6	53.3	25	21	AAc80373	Forward primer #14
848	9.6	53.3	25	21	AAc95301	Oligonucleotide pr
C 849	9.6	53.3	25	21	AAz49603	PCR primer p57 for
C 850	9.6	53.3	25	21	AAz49604	PCR primer p58 for
851	9.6	53.3	25	21	AAz47421	Probe 5 used to co
C 852	9.6	53.3	25	22	AAJ16201	Human uPAR gene 5'
C 853	9.6	53.3	25	24	ABQ61280	Human aquaporin 5
854	9.6	53.3	25	24	ABQ61333	Human aquaporin 5
855	9.6	53.3	25	24	ABN03358	Human GDM-P-1 25-m
856	9.6	53.3	25	24	ABN03589	Human GDM-P-1 25-m
857	9.6	53.3	25	24	ABN05516	Human GDM-P-1 25-m
C 858	9.6	53.3	25	24	ABN07731	Human skin stress/
C 859	9.4	52.2	11	24	ABQ87738	Basidiomycetes deve
C 860	9.4	52.2	12	24	ABQ57398	HSV-1 blocker prob
861	9.4	52.2	12	24	ABK28806	Oligonucleotide PC
C 862	9.4	52.2	15	21	AAc55287	Reverse primer #74
863	9.4	52.2	15	21	AAc73366	IGFBP2 oligonucleo
864	9.4	52.2	15	22	AAc45551	IGFBP2 oligonucleo
865	9.4	52.2	15	22	AAc45552	IGFBP2 oligonucleo
866	9.4	52.2	15	22	AAc45553	IGFBP2 oligonucleo
C 867	9.4	52.2	15	22	AAc45554	IGFBP2 oligonucleo
C 868	9.4	52.2	15	22	AAc45555	IGFBP2 oligonucleo
C 869	9.4	52.2	15	22	AAc45556	IGFBP2 oligonucleo
C 870	9.4	52.2	15	22	AAc45557	IGFBP2 oligonucleo
C 871	9.4	52.2	15	22	AAc45558	IGFBP2 oligonucleo
872	9.4	52.2	15	22	AAc45559	IGFBP2 oligonucleo
873	9.4	52.2	15	22	AAc45560	IGFBP2 oligonucleo
874	9.4	52.2	15	22	AAc45561	IGFBP2 oligonucleo
875	9.4	52.2	15	22	AAc45562	IGFBP2 oligonucleo
876	9.4	52.2	15	22	AAc45563	IGFBP2 oligonucleo
877	9.4	52.2	15	22	AAc45564	IGFBP2 oligonucleo
C 878	9.4	52.2	15	22	AAc45565	IGFBP2 oligonucleo
C 879	9.4	52.2	15	22	AAc45566	IGFBP2 oligonucleo
C 880	9.4	52.2	15	22	AAc45567	IGFBP2 oligonucleo
C 881	9.4	52.2	15	22	AAc45568	IGFBP2 oligonucleo
882	9.4	52.2	15	22	AAc45569	IGFBP2 oligonucleo
C 883	9.4	52.2	15	22	AAc45570	IGFBP2 oligonucleo
C 884	9.4	52.2	15	22	AAc45571	IGFBP2 oligonucleo
C 885	9.4	52.2	15	22	AAc45572	IGFBP2 oligonucleo

C	959	9.4	52.2	20	22	AA545664	Human PAP-1 antis
C	960	9.4	52.2	20	22	AA012146	Rat PPIB antisens
C	961	9.4	52.2	20	22	AA012146	Canine SRP micros
C	962	9.4	52.2	20	22	AA012146	Plagelid vector PC
C	963	9.4	52.2	20	22	AA012146	Oligonucleotide #5
C	964	9.4	52.2	20	22	AA012146	Immunostimulatory
C	965	9.4	52.2	20	22	AA012146	Human PSA promoter
C	966	9.4	52.2	20	22	AA012146	Rat PPIB antisens
C	967	9.4	52.2	20	22	AA012146	Human caespase 7 ph
C	968	9.4	52.2	20	22	AA012146	CTB36 antigen pep
C	969	9.4	52.2	20	22	AA012146	Rat PPIB mRNA lev
C	970	9.4	52.2	20	22	AA012146	Rat secreted facto
C	971	9.4	52.2	20	22	AA012146	Human STAT3 antis
C	972	9.4	52.2	20	22	AA012146	Human vascular end
C	973	9.4	52.2	20	22	AA012146	Immunostimulatory
C	974	9.4	52.2	20	22	AA012146	Oligonucleotide Q1
C	975	9.4	52.2	20	22	AA012146	Plasmid construct
C	976	9.4	52.2	20	22	AA012146	Nocardiosis sp. p
C	977	9.4	52.2	20	22	AA012146	Lacto-N-biosidase
C	978	9.4	52.2	20	22	AA012146	PC-PSA promoter pr
C	979	9.4	52.2	20	22	AA012146	Primer for subclon
C	980	9.4	52.2	20	22	AA012146	Prostate specific
C	981	9.4	52.2	20	22	AA012146	SHOX gene exon 3'
C	982	9.4	52.2	20	22	AA012146	L-oncogene primer
C	983	9.4	52.2	20	22	AA012146	Chicken matrix met
C	984	9.4	52.2	20	22	AA012146	5' PCR primer used
C	985	9.4	52.2	20	22	AA012146	Rho GDI-alpha PCR
C	986	9.4	52.2	20	22	AA012146	Polylysylleucyl (K
C	987	9.4	52.2	20	22	AA012146	Polylysylleucyl (K
C	988	9.4	52.2	20	22	AA012146	Marine MSK-2 cDNA
C	989	9.4	52.2	20	22	AA012146	SNP specific upper
C	990	9.4	52.2	20	22	AA012146	Human gene single
C	991	9.4	52.2	20	22	AA012146	PCR primer #1 for
C	992	9.4	52.2	20	22	AA012146	Aspergillus niger
C	993	9.4	52.2	20	22	AA012146	Rat dipeptidyl pep
C	994	9.4	52.2	20	22	AA012146	Rab GDI alpha rela
C	995	9.4	52.2	20	22	AA012146	Rab3 GEP related P
C	996	9.4	52.2	20	22	AA012146	Mouse Skp2 promote
C	997	9.4	52.2	20	22	AA012146	PCR primer 1 used
C	998	9.4	52.2	20	22	AA012146	Histidinol selecti
C	999	9.4	52.2	20	22	AA012146	
C	1000	9.4	52.2	20	22	AA012146	

ALIGNMENTS

RESULT 1
ABN99616
ID ABN99616 standard; DNA; 18 BP.

XX	AC	ABN99616;
XX	DT	05-AUG-2002 (first entry)
XX	DE	Fungi probe SEQ ID NO 188.
XX	KW	Fungus; bacteria; quantification; detection; infection; gastroenteritis;
XX	KW	ulcer; asthma; allergy; sinusitis; probe; ss.
XX	OS	Stachybotrys chartarum.
XX	PN	US6387652-B1.
XX	PD	14-MAY-2002.
XX	PF	13-JUN-2000; 2000US-0593012.
XX	PR	15-APR-1996; 98US-081773P.
XX	PR	14-APR-1999; 99US-0290990.
XX	PA	(USSI) US ENVIRONMENTAL PROTECTION AGENCY.
XX	PS	

PI	Haugland R, Vesper S;
XX	WPI; 2002-462353/49.
DR	
XX	Detection and quantification of specific fungi or bacteria useful e.g.
PT	in medical diagnosis and treatment of fungal and bacterial conditions;
PT	by hybridizing and amplifying DNA using sequences unique to the species
PT	or group of species
XX	
PS	Claim 62; Column 97; 55pp; English.
XX	
CC	The invention relates to specific fungi or bacteria detected and
CC	quantified in a sample by extracting and recovering DNA from the organism
CC	in the sample and hybridizing and amplifying the DNA sequence using
CC	sequences unique to the species/group of species but common to all
CC	isolates of the species/group of species. The method especially employs
CC	sequences selected from 225 fungal and bacterial primer and probe
CC	sequences (ABN99429-ABN99653) for detection of specified fungi/fungal
CC	groups or specified bacteria. The method enables detection and
CC	quantification of specific fungi or bacteria, or groups of
CC	fungal/bacterial species, useful medically for diagnosis and treatment of
CC	infectious diseases, useful for health problems such as infections,
CC	gastroenteritis, ulcers, asthma, allergies and sinusitis. It is also
CC	useful to detect and/or quantify microorganisms in the environment e.g.
CC	to establish the risk of adverse health effects (e.g. pulmonary
CC	haemorrhage from levels of Stachybotrys chartarum in air samples in
CC	houses).
XX	
SO	Sequence 18 BP; 2 A; 8 C; 6 G; 2 T; 0 other;
	Query Match 100.0%; Score 18; DB 24; Length 18;
	Best Local Similarity 100.0%; Pred. No. 31;
	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 CTGCGCCCGATCCAGGC 18
DB	1 CTGCGCCCGATCCAGGC 18

RESULT 2
ABK29213
ID ABK29213 standard; DNA; 18 BP.

XX	AC	ABK29213;
XX	DT	23-APR-2002 (first entry)
XX	DE	Stachybotrys chartarum probe.
XX	KW	Fungal detection; bacterial detection; probe; primer; ss.
XX	OS	Stachybotrys chartarum.
XX	PN	WO200196612-A2.
XX	PD	20-DEC-2001.
XX	PF	13-JUN-2001; 2001WO-US18892.
XX	PR	13-JUN-2000; 2000US-0593012.
XX	PA	(USSI) US ENVIRONMENTAL PROTECTION AGENCY.
XX	PI	Haugland R, Vesper SJ;
XX	DR	WPI; 2002-098078/13.
XX	PT	Detecting and quantifying fungi and bacteria, involves obtaining a
XX	PT	sequence of the fungus, extracting the DNA from the sample, and
XX	PT	subjecting the DNA to polymerase chain reaction and fluorescent probe
XX	PS	analysis
XX	PS	Claim 62; Page 20; 110pp; English.

XX The invention relates to a method of detecting and quantifying fungi and
 CC bacteria, involving obtaining a sequence of the microorganism to be
 CC detected and quantified, extracting the DNA from the sample, and
 CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
 CC probe analysis. The method is useful for identifying and quantifying
 CC specific fungi and bacteria using specific DNA sequences. The specific
 CC DNA sequences are useful for the real time detection of PCR products with
 CC a fluorescent probe system or other molecular probes like hybridisation.
 CC ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes
 CC used in the method of the invention.

XX Sequence 18 BP, 2 A, 8 C, 6 G, 2 T, 0 other;

Query Match 100.0%; Score 18; DB 24; Length 18;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCGCCCGATCCAGGC 18
 Db 1 CTGCGCCCGATCCAGGC 18

RESULT 3

ABN9534/C
 ID ABN9534 standard; DNA; 17 BP.

AC ABN9534;

DT 05-AUG-2002 (first entry)

DE Fungal probe SEQ ID NO 106.

XX Fungus; bacteria; quantification; detection; infection; gastroenteritis;
 KM ulcer; asthma; allergy; sinusitis; probe; ss.

OS Myrothecium verrucaria.

XX Myrothecium torridum.

PN US6387652-B1.

PD 14-MAY-2002.

PF 13-JUN-2000; 2000US-0593012.

PR 15-APR-1998; 98US-081773P.

PR 14-APR-1999; 99US-0290990.

PT (USST) US ENVIRONMENTAL PROTECTION AGENCY.

PI Haugland R, Vesper S;

DR WPI, 2002-462353/49.

XX Detection and quantification of specific fungi or bacteria useful e.g.
 PT in medical diagnosis and treatment of fungal and bacterial conditions,
 PT by hybridizing and amplifying DNA using sequences unique to the species
 PT or group of species -

PS Claim 36; Column 94; 55pp; English.

XX The invention relates to specific fungi or bacteria detected and
 CC quantified in a sample by extracting and recovering DNA from the organism
 CC in the sample and hybridizing and amplifying the DNA sequence using
 CC sequences unique to the species/group of species but common to all
 CC isolates of the species/group of species. The method especially employs
 CC sequences selected from 225 fungal and bacterial primer and probe
 CC sequences (ABN9429-ABN9653) for detection of specified fungi/fungal
 CC groups or specified bacteria. The method enables detection and
 CC quantification of specific fungi or bacteria, or groups of
 CC fungi/bacterial species, useful medically for diagnosis and treatment of
 CC fungal or bacteria associated with health problems such as infections,
 CC gastroenteritis, ulcers, asthma, allergies and sinusitis. It is also

CC useful to detect and/or quantify microorganisms in the environment e.g.
 CC to establish the risk of adverse health effects (e.g. pulmonary
 CC hemorrhage from levels of Stachybotrys chartarum in air samples in
 CC houses).

XX Sequence 17 BP, 0 A, 8 C, 6 G, 3 T, 0 other;

Query Match 71.1%; Score 12.8; DB 24; Length 17;
 Best Local Similarity 87.5%; Pred. No. 8.4e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GCGCCCGATCCAGGC 18
 Db 17 GCGCCCGATCCAGGC 2

RESULT 4

ABK29131/C
 ID ABK29131 standard; DNA; 17 BP.

AC ABK29131;

DT 23-APR-2002 (first entry)

DE Myrothecium verrucaria/torridum probe.

XX Fungal detection; bacterial detection; probe; primer; ss.

OS Myrothecium verrucaria.

XX Myrothecium torridum.

PN WO200196612-A2.

PD 20-DEC-2001.

PF 13-JUN-2001; 2001WO-US18892.

PR 13-JUN-2000; 2000US-0593012.

PT (USST) US ENVIRONMENTAL PROTECTION AGENCY.

PI Haugland R, Vesper SJ;

DR WPI, 2002-098078/13.

XX Detecting and quantifying fungi and bacteria, involves obtaining a
 PT sequence of the fungus, extracting the DNA from the sample, and
 PT subjecting the DNA to polymerase chain reaction and fluorescent probe
 PT analysis -

PS Claim 36; Page 14; 110pp; English.

XX The invention relates to a method of detecting and quantifying fungi and
 CC bacteria, involving obtaining a sequence of the microorganism to be
 CC detected and quantified, extracting the DNA from the sample, and
 CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
 CC probe analysis. The method is useful for identifying and quantifying
 CC specific fungi and bacteria using specific DNA sequences. The specific
 CC DNA sequences are useful for the real time detection of PCR products with
 CC a fluorescent probe system or other molecular probes like hybridisation.
 CC ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes
 CC used in the method of the invention.

XX Sequence 17 BP, 0 A, 8 C, 6 G, 3 T, 0 other;

Query Match 71.1%; Score 12.8; DB 24; Length 17;
 Best Local Similarity 87.5%; Pred. No. 8.4e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GCGCCCGATCCAGGC 18
 Db 17 GCGCCCGATCCAGGC 2

RESULT 5
AAFS1791
ID AAF51791 standard; DNA; 15 BP.
XX
AC AAF51791;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-I oligonucleotide #2751.
XX
KM Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KM cytostatic; dermatological; cardiant; vituclide; ophthalmological; keloid;
KM skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KM IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KM growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KM keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KM hyperneovascular condition; hyperplasia; kidney disease;
KM neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU00693.
XX
PR 21-JUN-1999; 99US-0140345.
XX
PI (MURDOCH CHILDRENS RES INST.
XX
PA Wright CJ, Werther GA, Edmondson SR;
XX
PI WPI; 2001-041421/05.
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by
PT administering UV (ultra-violet) treatment (optional) and an antisense
PT nucleic acid that inhibits or reduces growth factor mediated cell
PT proliferation and/or inflammation -
XX
PS Example 8; Page 78; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects
CC of skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotide of the present invention (see AAF5151 and
CC AAF5153-F5161). The method is useful for ameliorating the effects of
CC psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids,
CC keratosis, neoplasia, scleroderma, wart, benign growths, cancers of the
CC skin, a hyperneovascular condition such as a neovascular condition of the
CC retina, brain or skin, growth factor-mediated malignancies, other
CC sclerotic disease, kidney disease, hyperproliferation of the inside of
CC blood vessels or any other hyperplasia.
XX
SQ Sequence 15 BP; 3 A; 5 C; 5 G; 2 T; 0 other;

Query Match 68.9%; Score 12.4; DB 22; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGATTCAGGC 18
DB 2 GCCCGATTTCAGGC 15

RESULT 6
AAFS1792
ID AAF51792 standard; DNA; 15 BP.

XX
AC AAF51792;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-I oligonucleotide #2752.
XX
KM Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KM cytostatic; dermatological; cardiant; vituclide; ophthalmological; keloid;
KM skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KM IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KM growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KM keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KM hyperneovascular condition; hyperplasia; kidney disease;
KM neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU00693.
XX
PR 21-JUN-1999; 99US-0140345.
XX
PI (MURDOCH CHILDRENS RES INST.
XX
PA Wright CJ, Werther GA, Edmondson SR;
XX
PI WPI; 2001-041421/05.
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by
PT administering UV (ultra-violet) treatment (optional) and an antisense
PT nucleic acid that inhibits or reduces growth factor mediated cell
PT proliferation and/or inflammation -
XX
PS Example 8; Page 78; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects
CC of skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotide of the present invention (see AAF5151 and
CC AAF5153-F5161). The method is useful for ameliorating the effects of
CC psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids,
CC keratosis, neoplasia, scleroderma, wart, benign growths, cancers of the
CC skin, a hyperneovascular condition such as a neovascular condition of the
CC retina, brain or skin, growth factor-mediated malignancies, other
CC sclerotic disease, kidney disease, hyperproliferation of the inside of
CC blood vessels or any other hyperplasia.
XX
SQ Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 other;

Query Match 68.9%; Score 12.4; DB 22; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGATTCAGGC 18
DB 1 GCCCGATTTCAGGC 14

RESULT 7
AA42362/c
ID AAL42362 standard; DNA; 24 BP.
XX
AC AAL42362;
XX
DT 28-JUN-2002 (first entry)

XX HBD 4-hydroxytamoxifen-responsive mutant oestrogen receptor PCR primer A.
 DE PCR; primer; ss; fusion protein; mutant oestrogen receptor; mouse;
 XX cytokine receptor; tamoxifen; selective proliferation; gene therapy;
 KW haematopoietic stem cell; hormone binding domain; HBD;
 KW 4-hydroxytamoxifen-responsive mutant oestrogen receptor.
 XX
 OS Mus sp.
 XX CA2309324-A1.
 PN 23-NOV-2001.
 XX 23-MAY-2000; 2000CA-2309324.
 XX 23-MAY-2000; 2000CA-2309324.
 XX 23-MAY-2000; 2000CA-2309324.
 XX (DNADV-) DNA VEC RES INC.
 PA Ueda Y, Sakata T, Hasegawa M, Ozawa K, Itoh K, Nagashima T;
 PI WPI, 2002-305122/35.
 XX
 DR New fusion protein, useful in gene therapy for selective expansion of
 XX transfectant cells, comprises mutant estrogen receptor and cytokine
 PT receptor fragment -
 XX
 PS Example 2; Page 21; 50pp; English.
 XX The invention relates to fusion proteins which comprises a mutant
 CC oestrogen receptor and a cytokine receptor that imparts proliferation
 CC activity to cells. The mutant oestrogen receptor does not respond to
 CC oestrogen, but does respond to tamoxifen. The fusion proteins are used to
 CC induce selective proliferation (in vivo or in vitro), of cells
 CC transformed to contain an exogenous gene. The fusion proteins of the
 CC invention are particularly useful in gene therapy where haematopoietic
 CC stem cells are being targeted. Selective proliferation of cells
 CC through fusion proteins allows effective gene therapy even where gene
 CC transfer efficiency is low. Also, since the fusion proteins can be
 CC expressed in various types of blood cells, the range of cells that can be
 CC targeted is enlarged. The present DNA sequence represents a PCR primer
 CC used in an example of the invention to amplify the coding sequence of the
 CC hormone binding domain (HBD) of the mouse 4-hydroxytamoxifen-responsive
 CC mutant oestrogen receptor.
 XX
 SO Sequence 24 BP; 5 A; 7 C; 8 G; 4 T; 0 other;
 Query Match 68.9%; Score 12.4; DB 24; Length 24;
 Best Local Similarity 92.9%; Pred. No. 1.3e+04;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GCGCCCGGATCCAG 16
 DB 14 GTGCCCGGATCCAG 1
 RESULT 8
 ABA96574
 ID ABA96574 standard; DNA; 24 BP.
 AC ABA96574;
 XX
 DT 19-MAR-2002 (first entry)
 XX
 DE Human thyroglobulin 11 RT-PCR primer, SEQ ID NO:4.
 XX
 KW Human; thyroglobulin 11; recombinant production; gene therapy;
 KW thyroid associated disease; goitre; thyroiditis; hypothyroidism;
 KW hyperthyroidism; struma nodosa; adenomatous goitre;
 KW reverse transcription-PCR; RT-PCR primer; ss.
 XX
 XX Homo sapiens.

XX WO200190166-A1.
 XX
 XX 29-NOV-2001.
 XX
 XX 08-MAY-2001; 2001WO-CN00696.
 XX
 XX 09-MAY-2000; 2000CN-0115631.
 XX
 XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
 XX
 XX Mao Y, Xie Y;
 XX
 XX WPI, 2002-106179/14.
 XX
 DR Human thyroglobulin 11 polynucleotide and polypeptide, useful in
 PT diagnosis and treatment of goiter, thyrotoxicosis, hypothyroidism, and
 PT hyperthyroidism -
 XX
 PS Example 2; Page 17; 38pp; Chinese.
 XX The invention relates to human thyroglobulin 11 (AAM53042), nucleic acids
 CC encoding it (ABA96572), and a method for the recombinant production of
 CC thyroglobulin 11. The protein has a molecular weight of 11 KD. The
 CC present invention additionally discloses an antagonist of thyroglobulin
 CC 11 for therapeutic use, and an antibody which specifically binds to
 CC thyroglobulin 11. Thyroglobulin 11, and nucleotides which encode it may
 CC be used for treating thyroid-associated diseases, such as goitre,
 CC thyroiditis, hypothyroidism, hyperthyroidism, and struma nodosa
 CC (adenomatous goitre). The protein may also be used to screen for
 CC modulators of its activity or for peptide fingerprinting identification.
 CC The polynucleotide can be used as a primer for nucleic acid amplification
 CC reactions or as a probe for hybridisation reactions, or in producing gene
 CC chips or microarrays. Sequences ABA96573-ABA96574 represent reverse
 CC transcription-PCR (RT-PCR) primers used in an exemplification of the
 CC invention to isolate human thyroglobulin 11 cDNA.
 XX
 SO Sequence 24 BP; 3 A; 11 C; 5 G; 5 T; 0 other;
 Query Match 68.9%; Score 12.4; DB 24; Length 24;
 Best Local Similarity 92.9%; Pred. No. 1.3e+04;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 GCGCCGATCCAGGC 18
 DB 5 GCGCTGATCCAGGC 18
 RESULT 9
 AAX59160
 ID AAX59160 standard; DNA; 21 BP.
 AC AAX59160;
 XX
 DT 06-SEP-1999 (first entry)
 XX
 DE Human soluble neurophilin-1 5' PCR primer.
 XX
 KW Neurophilin-1; human; vascular endothelial growth factor receptor;
 KW VEGF165R; inhibitor; metastasis; angiogenesis; inflammation;
 KW arthritis; diabetic retinopathy; cytotoxic; antiinflammatory;
 KW antiangiogenic; antidiabetic; ophthalmological; antiarthritic;
 KW PCR; primer; ss.
 XX
 XX Synthetic.
 OS Homo sapiens.
 XX
 XX WO9929858-A1.
 XX
 XX 17-JUN-1999.
 XX
 XX 09-DEC-1998; 98WO-US26138.

PR 09-SEP-1998; 98US-0099615.
PR 09-DEC-1997; 97US-0069155.
PR 12-DEC-1997; 97US-0069687.
PA (CHIL-) CHILDRENS MEDICAL CENT.
PI Gagnon ML, Klagesbrun M, Soker S;
XX WPI; 1999-394975/33.
XX
XX Soluble human neuropilins and related polynucleotides
PT
PS Example 2; Page 43; 98pp; English.
XX
XX This oligonucleotide was used as 5' primer in the RT-PCR
CC amplification of cDNA (see AAX59153) coding for a truncated,
CC soluble human neuropilin-1 polypeptide (see AY06319). The cDNA
CC was cloned from a PC3 library. Neuropilin-1 is a novel vascular
CC endothelial growth factor (VEGF) receptor that is expressed in
CC endothelial cells and motile metastatic cancer cells. Claimed
CC soluble neuropilin-1 polypeptides are useful for treatment of
CC diseases or disorders associated with VEGF, e.g. metastasis,
CC inappropriate angiogenesis, chronic inflammation, diabetic
CC retinopathy and arthritis. Solid tumors can also be treated.
SQ Sequence 21 BP; 2 A; 8 C; 6 G; 5 T; 0 other;
XX
XX Query Match 67.8%; Score 12.2; DB 20; Length 21;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 TGGCGCCGATCCAGGC 18
Db 5 TCTCTCGATCCAGGC 21
XX
XX RESULT 10
ABK94173/c
ID ABR94173 standard; DNA; 21 BP.
XX
XX ABR94173;
XX
XX 27-AUG-2002 (first entry)
XX
XX Endothelin receptor B (EDNRB) SNP detection PCR primer #15.
XX
XX Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;
XX EDNR; signaling system; cardiovascular disease; coronary heart disease;
XX hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;
XX diabetes; familial hypercholesterolaemia; forensic marker;
XX transgenic animal; solid support; cardiovascular regulator; SNP;
XX single nucleotide polymorphism; PCR; primer; ss.
XX
XX Synthetic.
XX
XX WO200224747-A2.
XX
XX 28-MAR-2002.
XX
XX 31-AUG-2001; 2001WO-EP10087.
XX
XX 19-SEP-2000; 2000EP-0120123.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Brinkmann U, Hoffmeyer S;
XX
XX WPI; 2002-435060/46.
XX
XX Novel polynucleotide of the endothelin/endothelin converting
XX enzyme/receptors of endothelin and endothelin converting enzyme
XX signaling system associated with cardiovascular disease, useful for
XX treating the disease

XX
XX Example 6; Page 59; 190pp; English.
XX
XX The invention describes a polynucleotide (I) of the endothelin
CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
CC signaling system which is associated with a cardiovascular disease. (I),
CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I),
CC or (II) is useful for producing cells capable of expressing a molecular
CC variant polypeptide which is associated with a cardiovascular disease.
CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing
CC a molecular variant gene comprising (I) is useful for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of the EDN/EDNR/ECE signaling system
CC or its gene product, or for identifying and obtaining an inhibitor of
CC the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
CC signaling system or its gene product. The isolated proteins and
CC polynucleotides encoding them are useful for preparation of a
CC pharmaceutical composition for treating a cardiovascular disease such as
CC coronary heart disease, hypertension, atherosclerosis, or related to
CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial
CC hypercholesterolaemia. The gene or a polynucleotide fragment of the
CC EDN/ECE/EDNR signaling system are useful as forensic markers, for
CC creating a transgenic animal and in creation of a solid support
CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or
CC host cells of the invention. This sequence represents a PCR primer used
CC to identify single nucleotide polymorphisms in DNA encoding
CC cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway.
SQ Sequence 21 BP; 5 A; 3 C; 9 G; 3 T; 1 other;
XX
XX Query Match 67.8%; Score 12.2; DB 24; Length 21;
Best Local Similarity 77.8%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CTGCGCCGATCCAGGC 18
Db 20 CTTCGCCAGATCCAGGC 3
XX
XX RESULT 11
ABK94174
ID ABR94174 standard; DNA; 21 BP.
XX
XX ABR94174;
XX
XX 27-AUG-2002 (first entry)
XX
XX Endothelin receptor B (EDNRB) SNP detection PCR primer #16.
XX
XX Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;
XX EDNR; signaling system; cardiovascular disease; coronary heart disease;
XX hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;
XX diabetes; familial hypercholesterolaemia; forensic marker;
XX transgenic animal; solid support; cardiovascular regulator; SNP;
XX single nucleotide polymorphism; PCR; primer; ss.
XX
XX Synthetic.
XX
XX WO200224747-A2.
XX
XX 28-MAR-2002.
XX
XX 31-AUG-2001; 2001WO-EP10087.
XX
XX 19-SEP-2000; 2000EP-0120123.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Brinkmann U, Hoffmeyer S;
XX
XX WPI; 2002-435060/46.
XX
XX Novel polynucleotide of the endothelin/endothelin converting

PT enzyme/receptor of endothelin and endothelin converting enzyme
PT signaling system associated with cardiovascular disease, useful for
PT treating the disease -

PS Example 6, Page 59, 190pp; English.

CC The invention describes a polynucleotide (I) of the endothelin
CC (EDN)/endothelin converting enzyme (ECE)/receptor of EDN and ECE (EDNR)
CC signaling system which is associated with a cardiovascular disease. (I),
CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)
CC or (II) is useful for producing cells capable of expressing a molecular
CC variant polypeptide which is associated with a cardiovascular disease.
CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing
CC a molecular variant gene comprising (I) is useful for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system
CC or its gene product, or for identifying and obtaining an inhibitor of
CC the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
CC signaling system or its gene product. The isolated proteins and
CC polynucleotides encoding them are useful for preparation of a
CC pharmaceutical composition for treating a cardiovascular disease such as
CC coronary heart disease, hypertension, atherosclerosis, or related to
CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial
CC hypercholesterolaemia. The gene or a polynucleotide fragment of the
CC EDN/ECE/EDNR signaling system are useful as forensic markers, for
CC creating a transgenic animal and in creation of a solid support
CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or
CC host cells of the invention. This sequence represents a PCR primer used
CC to identify single nucleotide polymorphisms in DNA encoding
CC cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway.

SO Sequence 21 BP; 3 A; 9 C; 3 G; 5 T; 1 other;

Query Match 67.8%; Score 12.2; DB 24; Length 21;
Best Local Similarity 77.8%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTGGCCCGGATCCAGC 18
Db 2 CTGGCCGAGNATCCAGC 19

RESULT 12

AAK24822/c
ID AAK24822 standard; DNA, 24 BP.

AC AAK24822;

DT 21-JUN-1999 (first entry)

DE Oligonucleotide ZC15035 used in zsig37 DNA amplification.

KW Adipocyte-specific protein; homologue; zsig37; human;
KW fatty acid metabolism; energy balance; nutrition; antimicrobial;
KW neurotransmitter; PCR; primer; ss.

OS Synthetic.

OS Homo sapiens.

PN WO9904000-A1.

PD 28-JAN-1999.

PF 17-JUL-1998; 98WO-US14864.

PR 18-JUL-1997; 97US-0053154.

PA (ZYMO) ZYMOGENETICS INC.

PI Sheppard PO;

PT WPI, 1999-132244/11.

PT New isolated adipocyte complement related polypeptides - used to
PT develop products for modulating energy balance in mammals;
PT protecting endothelial cells from injury or for antimicrobial or
PT neurotransmitter-modulated applications

PS Example 4, Page 118, 128pp; English.

CC Oligonucleotide ZC15035 was used as a primer, together with primer
CC ZC15721 (see AAK24821), in the PCR amplification of an 866 bp
CC fragment of human adipocyte-specific protein homologue zsig37 DNA
CC (see AAK24813). The PCR product was used in the creation of
CC mammalian expression vectors. zsig37 (see also AAW98013) can be used
CC to modulate energy balance in mammals or to protect endothelial
CC cells from injury. It can be used to modulate cellular metabolic
CC reactions including adipogenesis, gluconeogenesis, glycolysis,
CC lipogenesis, glucose uptake, protein synthesis, thermogenesis and
CC oxygen utilisation. zsig37 may also modulate acetylcholine and/or
CC norepinephrine release, and may find use as a neurotransmitter or
CC as modulator of neurotransmission, as an antimicrobial agent or to
CC modulate nutrient uptake.

SO Sequence 24 BP; 3 A; 6 C; 9 G; 6 T; 0 other;

Query Match 67.8%; Score 12.2; DB 20; Length 24;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGGCCCGGATCCAGC 17
Db 20 CCGAGCCCGGATCCAGC 4

RESULT 13

AAK64122/c
ID AAK64122 standard; DNA, 24 BP.

AC AAK64122;

DT 20-DEC-2000 (first entry)

DE PCR primer for the human zsig37 DNA fragment.

KW zsig37; adipocyte complement related protein; haemostasis inhibitor;
KW blood flow; thrombogenic activity; complement activity; angiopathy;
KW collagen-mediated platelet adhesion; vascular reconstruction; aneurysm;
KW coronary artery bypass graft; endarterectomy; microvascular repair;
KW anastomosis; trauma; stroke; ischemia; reperfusion; endarterectomy;
KW intestinal strangulation; cardiopulmonary bypass ischemia; resection;
KW myocardial infarction; post-trauma vasospasm; accidental vascular trauma;
KW percutaneous transluminal angioplasty; wound repair; wound healing;

OS Homo sapiens.

PN WO200048625-A2.

PD 24-AUG-2000.

PF 17-FEB-2000; 2000WO-US04161.

PR 19-FEB-1999; 99US-0253604.

PR 22-NOV-1999; 99US-0444794.

PA (ZYMO) ZYMOGENETICS INC.

PI Sheppard PO, Laser GW, Bishop PD,

PT WPI, 2000-565335/52.

PT Use of a human adipocyte complement related protein for promoting blood
PT flow in the vasculature, pacifying damaged collagenous tissues,
PT pacifying the surface of a prostatic biomaterial, and mediating wound
PT repair -

```
XX Example 4; Page 93; 102pp; English.
PS
XX PCR primers AAA64121-22 were used to amplify zsig37 gene fragment.
CC zsig37 polyepitide an adipocyte complement related protein, and is an
CC inhibitor of haemostasis and immune functions. The zsig37 protein is
CC useful for promoting blood flow in the vasculature, where the polypeptide
CC reduces thrombogenic and complement activity by the inhibition of the
CC complement pathway and inhibiting collagen-mediated platelet adhesion,
CC activation or aggregation. The methods are useful for treating injuries
CC due to, e.g. vascular reconstruction (angioplasty, coronary artery
CC bypass graft, endarterectomy, microvascular repair or anastomosis of a
CC vascular graft), trauma, stroke or aneurysm. The polypeptide is also
CC useful for pacifying damaged collagenous tissues due to injury
CC associated with ischemia and reperfusion (trauma injury ischemia,
CC intestinal strangulation, or injury associated with pre- and
CC post-vascular reconstruction of blood flow), cardiopulmonary bypass ischemia and
CC revascularization, myocardial infarction, or post-trauma vasospasm. In
CC particular, post-trauma vasospasm includes stroke, percutaneous
CC transluminal angioplasty, endarterectomy, accidental vascular trauma or
CC surgical-induced vascular trauma. The polypeptide may also be used for
CC pacifying the surface of a prosthetic biomaterial, where the surface of
CC the prosthetic biomaterial is coated with collagen or collagen
CC fragments, gelatin, fibrin or fibronectin. Finally, the polypeptide is
CC useful for mediating wound repair, where the polypeptide enhances the
CC progression of wound healing.
CC
XX Sequence 24 BP; 3 A; 6 C; 9 G; 6 T; 0 other;
SQ
Query Match 67.8%; Score 12.2; DB 21; Length 24;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1 CTGCCCCCGGATCCAG 17
Db 20 CCGAGCCCGGATCCAG 4
RESULT 14
AAS19807
ID AAS19807 standard; DNA; 15 BP.
AC AAS19807;
AT 08-MAY-2002 (first entry)
DE ASO primer #65 to detect human RANGAP1 gene polymorphisms.
EE
KM Human; single nucleotide polymorphism. SNP; RANGAP1; haplotyping
KW chromosome 22q13.2-q13.31; Ran GTPase activating protein 1; genotyping;
KW cancer; irregular cell cycle associated disorder; ASO; primer; ss;
KM allele-specific oligonucleotide.
XX
OS Homo sapiens.
FM WO200179240-A2.
PD 25-OCT-2001.
PF 17-APR-2001; 2001WO-US12455.
PR 17-APR-2000; 2000US-198072P.
PA (GENA-) GENAISSANCE PHARM. INC.
PI Chew A, Choi JY, Koshy B;
XX WPI, 2002-075068/10.
XX
PT Genotyping human Ran GTPase activating protein 1 gene of individual for
PT determining haplotype of individual, involves determining identity of
PT nucleotide pair at specific polymorphic sites for two copies of the
PT gene
```

```
XX Claim 15; Page 15; 148pp; English.
PS
XX The present invention relates to novel single nucleotide polymorphisms
CC (SNPs) in the human Ran GTPase activating protein 1 (RANGAP1) gene
CC located on chromosome 22q13.2-q13.31, and methods for haplotyping and/or
CC genotyping the RANGAP1 gene. The methods of the invention make use of
CC allele-specific oligonucleotides (ASOs) as probes and primers and/or
CC primer-extension oligonucleotides for detecting the RANGAP1 gene
CC polymorphisms. The polynucleotides and screened compounds are useful for
CC treatment of diseases associated with RANGAP1 activity, such as
CC cancer and other disorders associated with an irregular cell cycle.
CC AAS19743-AAS19820 represent ASO primers for detecting human RANGAP1
CC gene polymorphisms.
XX
SQ Sequence 15 BP; 0 A; 6 C; 6 G; 2 T; 1 other;
Query Match 66.7%; Score 12; DB 24; Length 15;
Best Local Similarity 85.7%; Pred. No. 2e+04;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy 3 GCGCCCGGATCCAG 16
Db 2 GCGCCCGGATCCAG 15
RESULT 15
AAQ40880
ID AAQ40880 standard; DNA; 21 BP.
AC AAQ40880;
AT 29-SEP-1993 (first entry)
DE Apyrase gene reverse primer.
EE
KM Shigella; entero-invasive E.coli; EIEC; virulence;
KW S. flexneri; S. dysenteriae; S. sonnei; S. boydii; ss.
XX
OS Synthetic.
FM GB2261878-A.
PD 02-JUN-1993.
PF 25-NOV-1992; 92GB-0024716.
PR 26-NOV-1991; 91IN-0000874.
PA (ASTR-) ASTRA AB.
PI Ramachandran V, Roy RK, Sankaran K, Subrahmanyam YVB;
XX WPI, 1993-177505/22.
DR
XX ATP di-phospho-hydrolase or apyrase DNA sequence and probe.
PT used for detection, therapy and protection against Shigella and
PT entero-invasive E.coli strains
XX
PS Example; Page 11; 40pp; English.
CC Plasmid DNA from clone PARC25 was used as a template to amplify
CC the apyrase gene, by PCR, using the primers in AAQ40879-80.
CC The apyrase enzyme is associated with the virulence of all species
CC of Shigella (e.g. S. flexneri, S. dysenteriae, S. sonnei, S. boydii)
CC and related entero-invasive E.coli (EIEC) strains. The apyrase
CC nucleotide sequence can be used in the detection of a virulence
CC determinant in pathogenic bacteria.
XX
SQ Sequence 21 BP; 3 A; 8 C; 7 G; 3 T; 0 other;
Query Match 66.7%; Score 12; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+04;
```

```

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 CCGATCCAGGC 18
   |||||
   2 CCGATCCAGGC 13
Db

RESULT 16
AA064130 standard; DNA; 21 BP.
XX AA064130;
XX 10-NOV-1994 (first entry)
XX
XX Apyrase gene PCR primer.
XX
XX Apyrase; ATP-diphosphohydrolase; virulence; Escherichia coli;
XX Shigella; probe; hybridization; plasmid PARC25; primer; PCR;
XX polymerase chain reaction; ss.
XX Synthetic.
XX
XX MO9412211-A.
XX
XX 09-JUN-1994.
XX
XX 19-NOV-1993; 93WO-SE00996.
XX
XX 23-NOV-1992; 92SE-0003506.
XX
XX (ASTR ) ASTRA AB.
XX
XX Ramachandran V, Roy RK, Sankaran K, Subrahmanyam YVBK;
XX WPI; 1994-199970/24.
XX
XX New DNA encoding virulence associated ATP di:phospho:hydrolase -
XX useful as hybridisation probe for specific detection of virulent
XX Shigella sp. and entero:invasive E. coli
XX
XX Disclosure; Page 26; 40pp; English.
XX
XX A DNA sequence (AA064128) encoding a virulence-associated apyrase
XX (ATP-diphosphohydrolase) in Shigella spp. and enteroinvasive Escherichia
XX coli was located in S. flexneri plasmid PARC25. The 20 N-terminal amino
XX acids of apyrase are given in sequence AAR54083 (positions 1-20 of the
XX full apyrase sequence, AAR54082). The gene encoding apyrase was
XX cloned by PCR amplification of PARC25 DNA using the primers given
XX
XX AA064129-30.
XX
XX Sequence 21 BP; 3 A; 8 C; 7 G; 3 T; 0 other;
SQ
Query Match 66.7%; Score 12; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 CCGATCCAGGC 18
   |||||
   2 CCGATCCAGGC 13
Db

RESULT 17
AA061767/c
XX AA061767 standard; cDNA; 25 BP.
XX
XX AA061767;
XX
XX 21-OCT-1994 (first entry)
XX
XX HEV strain BUR-121 primer D72.
XX
XX Hepatitis E virus; HEV; strain SAR-55; open reading frame; ORF; PCR;
XX

```

```

KM antibody; detection; diagnosis; primates; stool suspension; amplify;
KW polymerase chain reaction; primer; burma; strain BUR-121; ss.
XX
XX Synthetic.
XX
XX MO9406913-A.
XX
XX 31-MAR-1994.
XX
XX 17-SEP-1993; 93WO-US00849.
XX
XX 18-SEP-1992; 92US-0947263.
XX
XX (USSH ) US SEC DEPT HEALTH.
XX
XX Emerson SU, Purcell RH, Tsarev SA;
XX
XX WPI; 1994-118462/14.
XX
XX Purified hepatitis E strain SAR-55 virus - used to develop prods.
XX for use in detection, diagnosis, vaccines and therapy of
XX hepatitis E virus infection
XX
XX Example 1; Page 40; 114pp; English.
XX
XX The sequences given in AA045198-200 and AA061687-777 are primers which
XX were used in the isolation and amplification of the genomic sequence
XX of the hepatitis E virus (HEV) strain SAR-55. These primers were
XX based on sequences derived from the SAR-55 strain and a strain from
XX Burma (BUR-121). The amplified sequence contains three open reading
XX frames (ORFs). The proteins encoded by this sequence can be used to
XX stimulate the production of protective antibodies upon injection into
XX a mammal that would serve to protect the mammal upon challenge with
XX wild type HEV. The proteins can be used for detection and diagnosis
XX of HEV infection. This cDNA was isolated from primates inoculated
XX with stool suspensions obtained from hepatitis E patients.
XX
XX Sequence 25 BP; 4 A; 6 C; 10 G; 5 T; 0 other;
SQ
Query Match 66.7%; Score 12; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 CCGATCCAGGC 18
   |||||
   20 CCGATCCAGGC 9
Db

RESULT 18
AAT27478/c
XX AAT27478 standard; DNA; 25 BP.
XX
XX AAT27478;
XX
XX 27-NOV-1996 (first entry)
XX
XX HEV strain Burma-121 derived forward primer 72 (ORF-1).
XX
XX Hepatitis E virus; HEV; SAR-55 strain; enteric transmission;
XX structural region; antigen; detection; antibody; vaccine;
XX immunisation; infection; primer; Burma-121;
XX polymerase chain reaction; PCR; ss.
XX
XX Synthetic.
XX
XX MO9610580-A2.
XX
XX 11-APR-1996.
XX
XX 03-OCT-1995; 95WO-US13102.
XX
XX 03-OCT-1994; 94US-0316765.
XX

```

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Emerson SU, Purcell RH, Tearev SA;
 XX
 DR WPI, 1996-209320/21.
 XX
 PT Isolated and purified hepatitis E virus strain SAR-55 DNA - encodes
 PT antigenic protein useful in diagnosis, prophylaxis and treatment of
 PT hepatitis E virus infection
 XX
 PS Example 1; Page 44; 121pp; English.
 XX
 CC The present sequence is a hepatitis E virus (HEV) strain Burma-121
 CC derived primer, used in the isolation of the HEV strain SAR-55
 CC cDNA. The HEV strain SAR-55 was implicated in an enterically
 CC transmitted non-A, non-B hepatitis in Pakistan. The protein encoded
 CC by the structural region of the virus (i.e. ORF-2), which is
 CC capable of forming HEV like particles, is useful for the detection
 CC of HEV antibodies (pref. IgG or IgM) in blood, plasma, sera,
 CC cerebrospinal fluid, tissue, urine or pleural fluid. The protein,
 CC and anti-HEV antibodies generated using the protein, can also be
 CC used in vaccines for immunising an animal against HEV infection.
 CC The protein is identified as a band of greater than 50 kD
 CC following SDS-PAGE of cell lysates of insect cells infected with
 CC a HEV ORF-2 contg. baculovirus, i.e. the claimed recombinant
 CC expression vectors pPIC9-1779, -1780 and -1781.
 CC
 XX Sequence 25 BP; 4 A; 6 C; 10 G; 5 T; 0 other;
 SO
 Query Match 66.7%; Score 12; DB 17; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 CCGGATCCAGGC 18
 DB 20 CCGGATCCAGGC 9
 XX
 RESULT 19
 AAV71688/c
 ID AAV71688 standard; DNA; 25 BP.
 XX
 AC AAV71688;
 XX
 DT 02-FEB-1999 (first entry)
 XX
 DB HEV ORF proteins encoding DNA amplifying primer D 72 B.
 XX
 KM Hepatitis E virus; HEV; SAR-55; diagnostic agent; vaccine; antibody;
 KM passive immunisation; open reading frame; ORF; PCR primer; ss.
 XX
 OS Synthetic.
 OS Hepatitis E virus.
 XX
 PN WO9846761-A1.
 PD 22-OCT-1998.
 XX
 PF 09-APR-1998; 98WO-US07418.
 XX
 PR 11-APR-1997; 97US-0840316.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Emerson SU, Purcell RH, Robinson RA, Tearev SA;
 XX
 DR WPI, 1998-568733/48.
 XX
 PT New hepatitis E virus DNA from Pakistani strain SAR-55 - used for,
 PT e.g. developing products for diagnosis of, and vaccination against
 PT hepatitis E virus infection
 XX
 PS Example 1; Page 46; 204pp; English.

XX
 CC Sequences AAV71605 to AAV71698 represent primers used for PCR
 CC amplification of the hepatitis E virus (HEV) DNA SAR-55 encoding the open
 CC reading frame (ORF) proteins ORF-1, ORF-2 and ORF-3. A host organism
 CC transformed or transfected with a recombinant expression vector
 CC containing the SAR-55 nucleic acid can be used to produce the HEV
 CC proteins, especially ORF-2 protein. The recombinant HEV proteins can be
 CC used as diagnostic agents and as vaccines for use against HEV infection.
 CC The detection of antibodies specific for HEV can be used for the
 CC diagnosis of infection and diseases caused by HEV, and for monitoring the
 CC progression of such disease. Such methods are also useful for monitoring
 CC the efficacy of therapeutic agents during the course of treatment of HEV
 CC infection and disease in a mammal. The antibodies can be used for
 CC detection or for passive immunisation of mammals.
 CC
 XX Sequence 25 BP; 4 A; 6 C; 10 G; 5 T; 0 other;
 SO
 Query Match 66.7%; Score 12; DB 19; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 CCGGATCCAGGC 18
 DB 20 CCGGATCCAGGC 9
 XX
 RESULT 20
 AA068697/c
 ID AA068697 standard; DNA; 18 BP.
 XX
 AC AA068697;
 XX
 DT 20-FEB-1995 (first entry)
 XX
 DE Bacillus licheniformis alkaline protease N-terminal probe.
 XX
 KM Pullulanase; recombinant production; pullulan, amylopectin;
 KM hydrolysis; alpha-1,6-glycosidic bond; starch saccharification;
 KM alkaline protease; ss.
 XX
 OS Synthetic.
 OS
 PN EP605040-A.
 PD 06-JUL-1994.
 XX
 PF 20-DEC-1993; 93EP-0203593.
 XX
 PR 28-DEC-1992; 92BE-0001156.
 PR 15-JUL-1993; 93BE-0000744.
 PR 19-NOV-1993; 93BE-0001278.
 XX
 PA (SOLV) SOLVAY SA.
 XX
 PI AMORY A, DeWeer P;
 XX
 DR WPI; 1994-210291/26.
 XX
 PT New pullulanase from Bacillus deramificans - for starch
 PT saccharification etc., with good stability over wide temp. and pH
 PT ranges, also related DNA vectors, transformed cells etc.
 XX
 PS Example 15; Page 20; 61pp; French.
 XX
 CC A probe was constructed which corresponded to the N-terminal part
 CC of the alkaline protease (AP) gene of Bacillus licheniformis SE2.
 CC The probe (AA068697) localised the N-terminal part of the gene to a
 CC 5.5kb PstI fragment as part of a procedure for preparing a deletion
 CC plasmid for deleting the AP gene from B. licheniformis SE2.
 CC
 XX Sequence 18 BP; 2 A; 6 C; 7 G; 3 T; 0 other;
 SO
 Query Match 65.6%; Score 11.8; DB 15; Length 18;

Best Local Similarity 86.7%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGCGCCGATCCA 15
|||
DB 16 CTGGCGCCAGAGCCA 2

RESULT 21
AA080932/c
AA080932 standard; DNA; 18 BP.

AC AA080932;
DT 02-AUG-1995 (first entry)
DE Alkaline protease N-terminus probe.

XX Xylanase; endo-1,4-beta-D-xylanase; wood pulp; pulping;
KM biobleaching; bleaching; Bacillus licheniformis;
KW probe; hybridization; alkaline protease; ss.

XX Synthetic.
OS
XX GB2279955-A.
PN
PD 18-JAN-1995.
XX
PF 15-JUL-1993; 93GB-0014780.
XX
PR 15-JUL-1993; 93GB-0014780.
XX
XX (SOLV) SOLVAY SA.
PA (SOLV) SOLVAY & CIE.

PI Amory A, Andre C, De Buyt E, Detroz R, Lahaye A;
PI Ledoux P;
XX
XX WPI; 1995-039214/06.

PT Purified xylanase from Bacillus pumilus PRL B12 - esp. produced
PT in transformed Bacillus licheniformis, and related DNA, vectors,
PT etc.; used for pre-treatment of wood pulp to reduce chlorine or
PT ozone consumption in subsequent bleaching

PS Example 23; Page 55; 97p; English.

XX The C- and N-terminal portions of the Bacillus licheniformis
CC SE2 alkaline protease gene were cloned by hybridization to
CC the probe given in AA090831-32, respectively.

XX Sequence 18 BP; 2 A; 6 C; 7 G; 3 T; 0 other;

QY Query Match 65.6%; Score 11.8; DB 16; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGCGCCGATCCA 15
|||
DB 16 CTGGCGCCAGAGCCA 2

RESULT 22
AAT41772
AAT41772 standard; DNA; 24 BP.

AC AAT41772;

XX 24-JAN-1997 (first entry)

DE Human CDC27 gene 5' PCR primer.

KM CDC27, mitotic destruction complex; cell cycle regulatory protein;

KM CCRP; inhibitor; apoptosis; cell differentiation; primer; PCR;
KM polymerase chain reaction; ss.

OS Synthetic.
XX
XX WO9633286-A1.
PN
XX
XX
PD 24-OCT-1996.

PF 19-APR-1996; 96WO-US05643.
XX
PR 20-APR-1995; 95US-0425299.

PA (HARD) HARVARD COLLEGE.

PI King RW, Kirschner MW, Peters J;
PI
DR WPI; 1996-485790/48.

XX Detecting inhibitors of ubiquitin-mediated proteolysis of CCRPs -
PT used in the treatment of proliferative and/or differentiation
PT diseases, and in modulation of apoptosis

XX Example 1; Page 24; 63p; English.

XX PCR primers (AAT41772 and AAT41773) were used to amplify the coding
CC sequence (AAT41774) for CDC27 (AA00364) from a human cDNA library.
CC The amplified cDNA was cloned into vector pRSET and used to
CC transfect E. coli JM109 for the prodn. of poly(His)-tagged CDC27
CC fusion protein. CDC27 can be used in novel cell-free ubiquitin-
CC conjugating systems for the detection of inhibitors of ubiquitin-
CC mediated proteolysis of cell cycle regulatory proteins.

XX Sequence 24 BP; 3 A; 7 C; 10 G; 4 T; 0 other;

QY Query Match 65.6%; Score 11.8; DB 17; Length 24;
Best Local Similarity 86.7%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGCGCGATCCAGG 17
|||
DB 1 GCGCGCGATCCATG 15

RESULT 23
ABA98282/c

ID ABA98282 standard; DNA; 19 BP.

AC ABA98282;

XX 18-JUN-2002 (first entry)

DE Primer 48 for sequencing of pcu.

XX PHBA; para-Hydrobenzoate; liquid crystal polymer; LCP;
KM toluene monooxygenase; TMO; pcu gene; p-creosol; PCR primer; ss.

XX Pseudomonas mendocina KR-1.

XX WO200192539-A2.

XX 06-DEC-2001.

XX 22-MAY-2001; 2001WO-US16574.

XX 01-JUN-2000; 2000US-0585174.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Ben-Bassat A, Cattermole M, Gatenby AA, Gibson KJ;
PI Ramos-Gonzales MI, Ramos JL, Sarielani S;

XX WPI; 2002-171436/22.

XX New nucleic acid fragments encoding bacterial toluene monooxygenase
PT enzyme pathway, useful for isolating genes encoding proteins from the
PT same or other microbial species, and for producing para-hydroxybenzoate
XX
XX
PS Example 1, Page 81, 97pp; English.
XX
CC The invention relates to an isolated nucleic acid fragment encoding a
CC bacterial toluene monooxygenase enzyme pathway. The nucleic acid
CC fragments of the invention may be used to isolate genes encoding
CC proteins from the same or other microbial species. Bacterial strains
CC transformed with the p-cresol utilizing (pcu) genes are useful for
CC producing para-hydroxybenzoate (PHBA) which can be used for
CC synthesizing liquid crystal polymers (LCP). The sequences given in
CC ABA98235-ABA98331 represent primers for; pcu sequencing; cloning of the
CC p. putida pchC gene, sequencing tmox, cloning pcu for insertion into
CC pMC3, construction of plasmids pPCU1 and 2, mapping the transcript
CC initiation site of tmox, and the identification of pchA and B genes.
XX
SQ Sequence 19 BP; 2 A; 5 C; 7 G; 5 T; 0 other;
Query Match 64.4%; Score 11.6; DB 24; Length 19;
Best Local Similarity 77.8%; Pred. No. 3e+04; 4; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CTGGCGCCGGATCCAGGC 18
DB 18 CAGCACCCTGATCAAGGC 1
RESULT 24
AA226752/c
ID AA226752 standard; DNA; 21 BP.
XX
XX AA226752;
AC
XX 30-NOV-1999 (first entry)
DT
XX Human polymorphic region 941.
DE
XX
XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
XX cell viability; loss of heterozygosity; precancerous condition; ASI;
XX allele specific inhibitor; somatic cell; diagnosis; prevention;
XX atherosclerotic plaque; premalignant metastatic lesion; endometriosis;
XX dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
XX graft versus host disease; malignant cell removal; bone marrow; ss.
XX
XX Homo sapiens.
OS
XX
XX MO9841648-A2.
PN
XX
XX 24-SEP-1998.
PD
XX
XX 19-MAR-1998; 98WO-US05419.
PF
XX
XX 20-MAR-1997; 97US-0041057.
PR
XX
XX (VARI-) VARIAGENICS INC.
PA
XX
XX Housman D, Ledley FD, Stanton VP;
PI
XX
XX WPI; 1998-521232/44.
DR
XX
XX Identifying target genes for allele-specific drugs - used for
PT diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic
PT plaque, dysplastic lesions, endometriosis or graft versus host disease
XX
XX Disclosure; Figure 7, 605pp; English.
PS
XX This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is
CC active on a gene vital for cell growth or viability, and where the gene

CC is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can
CC be used in the diagnosis, prevention and treatment of LOH disorders,
CC e.g. cancers, atherosclerotic plaques, premalignant metastatic or
CC dysplastic lesions, benign tumours, endometriosis, polycystic kidney
CC disease, and graft versus host disease. The method can also be used to
CC remove malignant cells from bone marrow transplants. AA25812-226825
CC represent human polymorphic sites described in the method of the
CC invention.
XX
SQ Sequence 21 BP; 4 A; 8 C; 7 G; 2 T; 0 other;
Query Match 64.4%; Score 11.6; DB 19; Length 21;
Best Local Similarity 77.8%; Pred. No. 3e+04; 4; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CTGGCGCCGGATCCAGGC 18
DB 18 CTGGCGCCGGATTCATGC 1
RESULT 25
AAV41150/c
ID AAV41150 standard; cDNA; 21 BP.
XX
XX AAV41150;
AC
XX
XX 02-OCT-1998 (first entry)
DT
XX
XX CAPL 3' splice site.
DE
XX
XX CAPL, inhibitor; human; calcium-binding protein; S100 family; therapy;
XX metastatic cancer; 3' splice site; ss.
XX
XX Homo sapiens.
OS
XX
XX US5789248-A.
PN
XX
XX 04-AUG-1998.
PD
XX
XX 16-FEB-1996; 96US-0602036.
PF
XX
XX 16-FEB-1996; 96US-0602036.
PR
XX
XX 17-FEB-1995; 95US-0391375.
PR
XX
XX (HYBR-) HYBRIDON INC.
PA
XX
XX (NORA-) NORWEGIAN RADIIUM HOSPITAL RES FOUND.
PI
XX
XX Agrawal S, Engebraaten O, Fodstad O, Hovig E, Maelandemo G;
DR
XX
XX WPI; 1998-446090/38.
DR
XX
XX Oligo:nucleotides inhibiting expression of CAPL mRNA - useful for
PT treating metastatic cancer
PT
XX
XX Disclosure; Column 6; 28pp; English.
PS
XX This sequence represents a 3' splice site from the human CAPL gene, and
CC is targeted by the oligonucleotide of the invention. The oligonucleotide
CC inhibits expression of mRNA encoding CAPL (a calcium-binding protein of
CC the S100 family) and has a sequence complementary to a sequence of the
CC CAPL mRNA. The oligonucleotide may be used for inhibiting expression of
CC CAPL mRNA in a cell-free reaction mixture or in a cell in vitro or for
CC treating metastatic cancer. The oligonucleotide provides a novel method
CC for blocking the metastatic cascade.

50 Sequence 21 BP, 5 A, 3 C, 10 G, 3 T, 0 other;

Query Match 64.4%; Score 11.6; DB 19; Length 21;
 Best Local Similarity 77.8%; Pred. No. 3e+04;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 1 CTGGCCCCGATCCAGGC 18
 18 CTGCTCCAGATCCTGAC 1

RESULT 26

AAK17717/C
 ID AAK17717 standard; DNA, 21 BP.

XX
 XX AAK17717;
 XX
 XX 10-MAY-1999 (first entry)
 XX
 XX US5877308 Seq ID 23.
 XX
 XX Human; CAPL; RNA splicing; antisense; metastatic cancer; ss.
 XX
 XX Synthetic.
 XX
 XX US5877308-A.
 XX
 XX 02-MAR-1999.
 XX
 XX 03-MAY-1996; 96US-0642407.
 XX
 XX 16-FEB-1996; 96US-0602036.
 XX
 XX 19-FEB-1995; 95US-0391375.
 XX
 XX 03-MAY-1996; 96US-0642407.
 XX
 XX (HYBR-) HYBRIDON INC.
 XX
 XX (NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.
 XX
 XX Agrawal S, Engestraten O, Fodstad O, Hovig E, Maelandemo G;
 XX Von Hofe E;
 XX WPI; 1999-189725/16.

XX
 XX New synthetic oligonucleotides complementary to human CAPL mRNA -
 XX PT useful for inhibiting expression of s100 calcium binding protein for
 XX PT the treatment of metastatic cancer
 XX
 XX Disclosure; Column 37; 27pp; English.

XX
 XX The invention provides synthetic oligonucleotides which are complementary
 XX to and inhibit expression of human CAPL mRNA that includes the 3' or 5'-
 XX splice site or the translational start site. The oligonucleotides prevent
 XX translation and splicing of RNA and can be used as antisense or triple-
 XX helix forming oligonucleotides to treat metastatic cancer.

XX Sequence 21 BP, 5 A, 3 C, 10 G, 3 T, 0 other;

Query Match 64.4%; Score 11.6; DB 20; Length 21;
 Best Local Similarity 77.8%; Pred. No. 3e+04;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 1 CTGGCCCCGATCCAGGC 18
 18 CTGCTCCAGATCCTGAC 1

RESULT 27

ABK94171/c
 ID ABK94171 standard; DNA, 21 BP.

XX
 XX ABK94171;
 XX
 XX 27-AUG-2002 (first entry)

XX Endothelin receptor B (EDNRB) SNP detection PCR primer #13.

XX Endothelin; EDN, endothelin converting enzyme; ECE; endothelin receptor;
 XX EDNR; signaling system; cardiovascular disease; coronary heart disease;
 XX hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;
 XX diabetes; familial hypercholesterolemia; forensic marker;
 XX transgenic animal; solid support; cardiovascular regulator; SNP;
 XX single nucleotide polymorphism; PCR; primer; ss.

XX Synthetic.

XX WO200224747-A2.

XX 28-MAR-2002.

XX 31-AUG-2001; 2001WO-EP10087.

XX 19-SEP-2000; 2000EP-0120123.

XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

XX Brinkmann U, Hoffmeyer S;

XX WPI; 2002-435060/46.

XX Novel polynucleotide of the endothelin/endothelin converting
 XX PT enzyme/receptors of endothelin and endothelin converting enzyme
 XX PT signaling system associated with cardiovascular disease, useful for
 XX PT treating the disease

XX Example 6; Page 59; 190pp; English.

XX The invention describes a polynucleotide (I) of the endothelin
 XX (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
 XX CC signaling system which is associated with a cardiovascular disease. (I),
 XX CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)
 XX CC or (II) is useful for producing cells capable of expressing a molecular
 XX CC variant polypeptide which is associated with a cardiovascular disease.
 XX CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing
 XX CC a molecular variant gene comprising (I) is useful for identifying and
 XX CC obtaining a pro-drug or drug capable of modulating the activity of a
 XX CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system
 XX CC or its gene product, or for identifying and obtaining an inhibitor of
 XX CC the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
 XX CC signaling system or its gene product. The isolated proteins and
 XX CC polynucleotides encoding them are useful for preparation of a
 XX CC pharmaceutical composition for treating a cardiovascular disease such as
 XX CC coronary heart disease, hypertension, atherosclerosis, or related to
 XX CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial
 XX CC hypercholesterolemia. The gene or a polynucleotide fragment of the
 XX CC EDN/ECE/EDNR signaling system are useful as forensic markers, for
 XX CC creating a transgenic animal and in creation of a solid support
 XX CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or
 XX CC host cells of the invention. This sequence represents a PCR primer used
 XX CC to identify single nucleotide polymorphisms in DNA encoding
 XX CC cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway.

XX Sequence 21 BP, 6 A, 3 C, 9 G, 3 T, 0 other;

Query Match 64.4%; Score 11.6; DB 24; Length 21;
 Best Local Similarity 77.8%; Pred. No. 3e+04;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 CTGGCCCCGATCCAGGC 18
 20 CTTCGCCAGATCCAGGC 3

RESULT 28

ABK94172
 ID ABK94172 standard; DNA, 21 BP.

XX

AC ABK94172,
XX
DT 27-AUG-2002. (first entry)
XX
DE Endothelin receptor B (EDNRB) SNP detection PCR primer #14.
XX
KW Endothelin; EDN: endothelin converting enzyme; ECE: endothelin receptor;
KW EDNR; signaling system; cardiovascular disease; coronary heart disease;
KW hyperextension; atherosclerosis; angiogenesis; fatty acid metabolism;
KW diabetes; familial hypercholesterolemia; forensic marker;
KW transgenic animal; solid support; cardiovascular regulator; SNP;
KW single nucleotide polymorphism; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO200224747-A2.
XX
PD 28-MAR-2002.
XX
PF 31-AUG-2001; 2001WO-EPI0087.
XX
PR 19-SEP-2000; 2000EP-0120123.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Brinkmann U, Hoffmeyer S;
XX WPI; 2002-435060/46.
XX
DR Novel polynucleotide of the endothelin/endothelin converting
PT enzyme/receptors of endothelin and endothelin converting enzyme
PT signaling system associated with cardiovascular disease, useful for
PT treating the disease -
XX
PS Example 6; page 59; 19ppp; English.

The invention describes a polynucleotide (I) of the endothelin (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR) signaling system which is associated with a cardiovascular disease. (I), the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I) or (II) is useful for producing cells capable of expressing a molecular variant polypeptide which is associated with a cardiovascular disease. (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing a molecular variant gene comprising (I) is useful for identifying and obtaining a pro-drug or drug capable of modulating the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system or its gene product, or for identifying and obtaining an inhibitor of the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system or its gene product. The isolated proteins and polynucleotides encoding them are useful for preparation of a pharmaceutical composition for treating a cardiovascular disease such as coronary heart disease, hypertension, atherosclerosis, or related to abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial hypercholesterolemia. The gene or a polynucleotide fragment of the EDN/ECE/EDNR signaling system are useful as forensic markers, for creating a transgenic animal and in creation of a solid support comprising polynucleotides, genes, vectors, polypeptides, antibodies or host cells of the invention. This sequence represents a PCR primer used to identify single nucleotide polymorphisms in DNA encoding cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway.

```

Query Match      64.4%; Score 11.6; DB 24; Length 21;
Best Local Similarity 77.8%; Pred. NO.3e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy      1 CTGCGCCCGGATCCAGGC 18
        ||||| ||||| ||
Db      2 CTGCGCCAGTATCCAGC 19

RESULT 29

```

ABK94175/c	ABK94175 standard; DNA; 21 BP.
ABK94175;	
27-AUG-2002	(first entry)
Endothelin receptor B (EDNRB)	SNP detection PCR primer #17.
Endothelin; EDN;	endothelin converting enzyme; ECE; endothelin receptor;
EDNR;	signaling system; cardiovascular disease; coronary heart disease;
hyperemia; atherosclerosis;	angiogenesis; fatty acid metabolism;
diabetes; familial hypercholesterolemia;	forensic marker;
transgenic animal; solid support;	cardiovascular regulator; SNP;
single nucleotide polymorphism; PCR; primer; ss.	
Synthetic.	
WO200224747-A2.	
28-MAR-2002.	
31-AUG-2001;	2001WO-EP10087.
19-SEP-2000;	2000EP-0120123.
(EPID-)	EPIDAUROS BIOTECHNOLOGIE AG.
Brinkmann U,	Hofmeyer S;
WPI;	2002-435060/46.
Novel polynucleotide of the endothelin/endothelin converting	
enzyme/receptors of endothelin and endothelin converting enzyme	
signaling system associated with cardiovascular disease, useful for	
treating the disease	

CC	Claim 1, Page 59; 190pp; English.	
XX		
CC	The invention describes a polynucleotide (I) of the endothelin	
CC	(EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)	
CC	signaling system which is associated with a cardiovascular disease. (I),	
CC	the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)	
CC	or (II) is useful for producing cells capable of expressing a molecular	
CC	variant polypeptide which is associated with a cardiovascular disease.	
CC	(II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing	
CC	a molecular variant gene comprising (I) is useful for identifying and	
CC	obtaining a pro-drug or drug capable of modulating the activity of a	
CC	molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system	
CC	or its gene product, or for identifying and obtaining an inhibitor of	
CC	the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE	
CC	signaling system or its gene product. The isolated proteins and	
CC	polynucleotides encoding them are useful for preparation of a	
CC	pharmaceutical composition for treating a cardiovascular disease such as	
CC	coronary heart disease, hypertension, atherosclerosis, or related to	
CC	abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial	
CC	hypercholesterolaemia. The gene or a polynucleotide fragment of the	
CC	EDN/ECE/EDNR signaling system are useful as forensic markers, for	
CC	creating a transgenic animal and in creation of a solid support	
CC	comprising polynucleotides, genes, vectors, polypeptides, antibodies or	
CC	host cells of the invention. This sequence represents a PCR primer used	
CC	to identify single nucleotide polymorphisms in DNA encoding	
CC	cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway.	
XX		
SO	Sequence 21 BP, 5 A; 3 C; 10 G; 3 T; 0 other;	
Query Match	64.4%; Score 11.6; DB 24; Length 21;	
Best Local Similarity	77.8%; Pred. No. 3e+04;	
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;		
07	1 CTGGCGCCGATCCAGGC 18	
DB	20 CTTCGACGATCCAGCG 3	

RESULT 30
ID ABR94176 standard; DNA; 21 BP.
XX ABR94176;
XX
XX 27-AUG-2002 (first entry)
XX
XX Endothelin receptor B (EDNRB) SNP detection PCR primer #18.
XX
XX Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;
XX EDNR; signaling system; cardiovascular disease; coronary heart disease;
XX hyperhomocysteinemia; atherosclerosis; angiogenesis; fatty acid metabolism;
XX diabetes; familial hypercholesterolemia; forensic marker;
XX transgenic animal; solid support; cardiovascular regulator; SNP;
XX single nucleotide polymorphism; PCR; primer; ss.
XX
XX Synthetic.
XX
XX WO200224747-A2.
XX
XX 26-MAR-2002.
XX
XX 31-AUG-2001; 2001WO-EP10087.
XX
XX 19-SEP-2000; 2000EP-0120123.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Brinkmann U, Hoffmeyer S;
XX WPI; 2002-435060/46.
XX
XX Novel polynucleotide of the endothelin/endothelin converting
XX enzyme/receptor of endothelin and endothelin converting enzyme
XX signaling system associated with cardiovascular disease, useful for
XX treating the disease -
XX
XX Claim 1; Page 59; 190pp; English.
XX
XX The invention describes a polynucleotide (I) of the endothelin
XX (EDN)/endothelin converting enzyme (ECE)/receptor of EDN and ECE (EDNR)
XX signaling system which is associated with a cardiovascular disease. (I),
XX the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)
XX or (II) is useful for producing cells capable of expressing a molecular
XX variant polypeptide which is associated with a cardiovascular disease.
XX (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing
XX a molecular variant gene comprising (I) is useful for identifying and
XX obtaining a pro-drug or drug capable of modulating the activity of a
XX molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system
XX or its gene product, or for identifying and obtaining an inhibitor of
XX the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
XX signaling system or its gene product. The isolated proteins and
XX polynucleotides encoding them are useful for preparation of a
XX pharmaceutical composition for treating a cardiovascular disease such as
XX coronary heart disease, hypertension, atherosclerosis, or related to
XX abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial
XX hypercholesterolemia. The gene or a polynucleotide fragment of the
XX EDN/ECE/EDNR signaling system are useful as forensic markers, for
XX creating a transgenic animal and in creation of a solid support
XX comprising polynucleotides, genes, vectors, polypeptides, antibodies or
XX host cells of the invention. This sequence represents a PCR primer used
XX to identify single nucleotide polymorphisms in DNA encoding
XX cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway.
XX
XX Sequence 21 BP; 3 A; 10 C; 3 G; 5 T; 0 other;
SQ

Query Match 64.4%; Score 11.6; DB 24; Length 21;
Best Local Similarity 77.8%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CTGCGCCCGATCCAGGC 18
Db 2 CTGCGCCAGATCCAGGC 19

RESULT 31
ID AAV41141/c
XX AAV41141 standard; cDNA; 22 BP.
XX
XX AAV41141;
XX
XX 02-OCT-1998 (first entry)
XX
XX CAPL 3' splice site.
XX
XX CAPL; inhibitor; human; calcium-binding protein; S100 family; therapy;
XX metastatic cancer; 3' splice site; ss.
XX
XX Homo sapiens.
XX
XX US5789248-A.
XX
XX 04-AUG-1998.
XX
XX 16-FEB-1996; 96US-0602036.
XX
XX 16-FEB-1996; 96US-0602036.
XX 17-FEB-1995; 95US-0391375.
XX
XX (HYBR-) HYBRIDON INC.
XX (NORA-) NORWEGIAN RADIIUM HOSPITAL RES FOUND.
XX
XX Agrawal S, Engestraten O, Fodstad O, Hovig E, Maelandsmo G;
XX WPI; 1998-446090/38.
XX
XX Oligonucleotides inhibiting expression of CAPL mRNA - useful for
XX treating metastatic cancer
XX
XX Claim 1; Column 6; 28pp; English.
XX
XX This sequence represents a 3' splice site from the human CAPL gene, and
XX is targeted by the oligonucleotide of the invention. The oligonucleotide
XX inhibits expression of mRNA encoding CAPL (a calcium-binding protein of
XX the S100 family) and has a sequence complementary to a sequence of the
XX CAPL mRNA. The oligonucleotide may be used for inhibiting expression of
XX CAPL mRNA in a cell-free reaction mixture or in a cell in vitro or for
XX treating metastatic cancer. The oligonucleotide provides a novel method
XX for blocking the metastatic cascade.
XX
XX Sequence 22 BP; 5 A; 3 C; 11 G; 3 T; 0 other;
SQ

Query Match 64.4%; Score 11.6; DB 19; Length 22;
Best Local Similarity 77.8%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CTGCGCCCGATCCAGGC 18
Db 18 CTGCTCCAGATCCTGAC 1

RESULT 32
ID AAV41142/c
XX AAV41142 standard; RNA; 22 BP.
XX
XX AAV41142;
XX
XX 02-OCT-1998 (first entry)
XX
XX CAPL 3' splice site.
XX
XX CAPL; inhibitor; human; calcium-binding protein; S100 family; therapy;
XX metastatic cancer; 3' splice site; ss.
XX

XX Homo sapiens.
 OS
 XX US5789248-A.
 PN
 XX 04-AUG-1998.
 PD
 XX
 PF 16-FEB-1996; 96US-0602036.
 XX
 PR 16-FEB-1996; 96US-0602036.
 XX
 PR 17-FEB-1995; 95US-0391375.
 XX
 PA (HYBR-) HYBRIDON INC.
 XX (NORA-) NORWEGIAN RADIIUM HOSPITAL RES FOUND.
 XX
 PI Agrawal S, Engebraten O, Fodstad O, Hovig E, Maelandemo G;
 XX WPI, 1998-446090/38.
 DR
 XX Oligo:nucleotides inhibiting expression of CAPL mRNA - useful for
 PT treating metastatic cancer
 XX
 PS Claim 1, Column 6; 28pp; English.
 XX
 CC This sequence represents a 3' splice site from the human CAPL gene, and
 CC is targeted by the oligonucleotide of the invention. The oligonucleotide
 CC inhibits expression of mRNA encoding CAPL (a calcium-binding protein of
 CC the S100 family) and has a sequence complementary to a sequence of the
 CC CAPL mRNA. The oligonucleotide may be used for inhibiting expression of
 CC CAPL mRNA in a cell-free reaction mixture or in a cell in vitro or for
 CC treating metastatic cancer. The oligonucleotide provides a novel method
 CC for blocking the metastatic cascade.
 CC
 XX
 SQ Sequence 22 BP; 5 A; 3 C; 11 G; 3 U; 0 other;
 Query Match 64.4%; Score 11.6; DB 19; Length 22;
 Best Local Similarity 77.8%; Pred. No. 3e+04;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CTGGCGCCCGATCCAGGC 18
 DB 18 CTGCTCCAGATCTGTAC 1
 RESULT 33
 AAX17697/C
 ID AAX17697 standard; DNA; 22 BP.
 XX
 AC AAX17697;
 XX
 DT 10-MAY-1999 (first entry)
 XX
 DE Antisense oligo for human CAPL.
 XX
 KW Human; CAPL; RNA splicing; antisense; metastatic cancer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 PN US5877308-A.
 XX
 PD 02-MAR-1999.
 XX
 PF 03-MAY-1996; 96US-0642407.
 XX
 PR 16-FEB-1996; 96US-0602036.
 XX
 PR 19-FEB-1995; 95US-0391375.
 XX
 PR 03-MAY-1996; 96US-0642407.
 XX
 PA (HYBR-) HYBRIDON INC.
 XX (NORA-) NORWEGIAN RADIIUM HOSPITAL RES FOUND.
 XX
 PI Agrawal S, Engebraten O, Fodstad O, Hovig E, Maelandemo G;

PI Von Hofe E;
 XX
 DR WPI; 1999-189725/16.
 XX
 PT New synthetic oligonucleotides complementary to human CAPL mRNA -
 PT useful for inhibiting expression of s100 calcium binding protein for
 PT the treatment of metastatic cancer
 XX
 PS Claim 2; Columns 27; 27pp; English.
 XX
 CC The invention provides synthetic oligonucleotides which are complementary
 CC to and inhibit expression of human CAPL mRNA that includes the 3' or 5'
 CC splice site or the translational start site. The oligonucleotides prevent
 CC translation and splicing of RNA and can be used as antisense or triple-
 CC helix forming oligonucleotides to treat metastatic cancer.
 CC
 XX
 SQ Sequence 22 BP; 5 A; 3 C; 11 G; 3 T; 0 other;
 Query Match 64.4%; Score 11.6; DB 20; Length 22;
 Best Local Similarity 77.8%; Pred. No. 3e+04;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CTGGCGCCCGATCCAGGC 18
 DB 18 CTGCTCCAGATCTGTAC 1
 RESULT 34
 AAX17698/C
 ID AAX17698 standard; RNA; 22 BP.
 XX
 AC AAX17698;
 XX
 DT 10-MAY-1999 (first entry)
 XX
 DE Antisense oligo for human CAPL.
 XX
 KW Human; CAPL; RNA splicing; antisense; metastatic cancer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 PN US5877308-A.
 XX
 PD 02-MAR-1999.
 XX
 PF 03-MAY-1996; 96US-0642407.
 XX
 PR 16-FEB-1996; 96US-0602036.
 XX
 PR 19-FEB-1995; 95US-0391375.
 XX
 PR 03-MAY-1996; 96US-0642407.
 XX
 PA (HYBR-) HYBRIDON INC.
 XX (NORA-) NORWEGIAN RADIIUM HOSPITAL RES FOUND.
 XX
 PI Agrawal S, Engebraten O, Fodstad O, Hovig E, Maelandemo G;
 XX Von Hofe E;
 XX WPI, 1999-189725/16.
 DR
 XX
 PT New synthetic oligonucleotides complementary to human CAPL mRNA -
 PT useful for inhibiting expression of s100 calcium binding protein for
 PT the treatment of metastatic cancer
 XX
 PS Claim 2; Columns 27; 27pp; English.
 XX
 CC The invention provides synthetic oligonucleotides which are complementary
 CC to and inhibit expression of human CAPL mRNA that includes the 3' or 5'
 CC splice site or the translational start site. The oligonucleotides prevent
 CC translation and splicing of RNA and can be used as antisense or triple-
 CC helix forming oligonucleotides to treat metastatic cancer.
 CC
 XX
 SQ Sequence 22 BP; 5 A; 3 C; 11 G; 3 U; 0 other;

Query Match 64.4%; Score 11.6; DB 20; Length 22;
Best Local Similarity 77.8%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 1 CTGCGCCCGATCCAGGC 18
18 CTGCTCCCGATCCTGAC 1

RESULT 35
AAC58261
ID AAC58261 standard; DNA; 22 BP.
AC AAC58261;
XX
XX 29-JAN-2001 (first entry)
DE Human PRO212 hybridisation probe SEQ ID NO:80.
XX
XX Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
XX proliferation; tumourigenesis; identification; cancer; PCR primer;
XX hybridisation; probe; cytostatic; neurotropic; neuroprotective;
XX antiinflammatory; immunosuppressive; immunostimulant; angiogenic;
XX leukaemia; lymphoid malignancy; neuronal disorder; glial disorder;
XX astrocytal disorder; hypothalamic disorder; glandular disorder;
XX macrophagal disorder; epithelial disorder; stromal disorder;
XX blastocoele disorder; inflammatory disorder; angiogenic;
XX immunologic disorder; ss.
XX Homo sapiens.
XX WO200053755-A2.
XX
XX 14-SEP-2000.
XX
XX 06-JAN-2000; 2000WO-US00376.
XX
XX 08-MAR-1999; 99MO-US05028.
XX 02-JUN-1999; 99MO-US12252.
XX 23-JUN-1999; 99US-0141037.
XX 07-JUL-1999; 99US-0143048.
XX 26-JUL-1999; 99US-0145698.
XX 30-NOV-1999; 99MO-US28313.
XX 20-DEC-1999; 99MO-US30911.
XX 05-JAN-2000; 2000WO-US00219.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
XX Watanabe CK, Wood WI, WPI, 2000-572270/53.
XX
XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
XX treatment, diagnosis and prevention of cancer -
XX
XX Example 23; Page 133; 286pp; English.

The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO345, PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO1055, PRO1030, PRO1037, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187, PRO1281, PRO23, PRO33, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The PRO polypeptides and nucleotides are useful in the treatment, diagnosis and prevention of cancer. The antibodies and other anti-tumour compounds may be used to treat various conditions, including those characterised by overexpression and/or activation of the amplified PRO genes. Exemplary conditions or disorders to be treated with such antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic

CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours),
CC leukaemias and lymphoid malignancies, other disorders such as neuronal,
CC glial, astrocytal, hypothalamic and other glandular, macrophagal,
CC epithelial, stromal and blastocoele disorders, and inflammatory,
CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
CC primers and hybridisation probes used in the isolation of the human PRO
CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
CC PRO polynucleotide and protein sequences given in the exemplification of
CC the present invention.
XX
XX Sequence 22 BP; 2 A; 10 C; 5 G; 5 T; 0 other;
SQ

Query Match 64.4%; Score 11.6; DB 21; Length 22;
Best Local Similarity 77.8%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 1 CTGCGCCCGATCCAGGC 18
3 CTGTGCACTGATCCTGGC 20

RESULT 36
AAH78624/C
ID AAH78624 standard; DNA; 23 BP.
AC AAH78624;
XX
XX 10-DEC-2001 (first entry)
DE PCR primer RFC780(9) for amplification of human RFC gene exon 3.
XX
XX Human; reduced folate carrier gene; RFC gene; cancer;
XX antifolate chemotherapy; folate metabolism; PCR primer; ss.
XX
XX Homo sapiens.
XX WO200165994-A2.
XX
XX 13-SEP-2001.
XX
XX 06-MAR-2001; 2001WO-IL00212.
XX
XX 06-MAR-2000; 2000US-0519673.
XX
XX (TECR) TECHNION RES & DEV POUND LTD.
XX
XX Assaraf Y, Dvori S;
XX WPI, 2001-589905/66.
XX
XX Assessing responsiveness of a cancer patient to antifolate-containing
XX chemotherapy, comprising searching for mutation or mutations in a gene
XX associated with folate metabolism or uptake in cells derived from the
XX patient
XX
XX Example; Page 59; 122pp; English.

PCR primers AAH78624-25 were used to amplify exon 3 of the human reduced folate carrier (RFC) gene. Detection of mutations associated with the RFC gene are used to assess the responsiveness of a cancer patient to antifolate chemotherapy. The RFC gene is associated with folate metabolism. The method is useful for assessing the responsiveness of a cancer patient to antifolate chemotherapy.

Sequence 23 BP; 4 A; 8 C; 8 G; 3 T; 0 other;
SQ

Query Match 64.4%; Score 11.6; DB 22; Length 23;
Best Local Similarity 77.8%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 1 CTGCGCCCGATCCAGGC 18
20 CTGGCCCGATTCATGC 3

RESULT 37
AAFS1790
ID AAFS1790 standard; DNA; 15 BP.
XX
AC AAFS1790;
XX
30-MAR-2001 (first entry)
XX
IGF-1 oligonucleotide #2750.
XX
Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytoskeletal; dermatological; cardiac; vitruide; ophthalmological; keloid;
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX Homo sapiens.
XX MO200078341-A1.
XX 28-DEC-2000.
XX 21-JUN-2000; 2000MO-AU00693.
XX 21-JUN-1999; 99US-0140345.
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX Ameliorating the effects of a disorder, e.g. psoriasis, by
XX administering UV (ultra-violet) treatment (optional) and an antisense
XX nucleic acid that inhibits or reduces growth factor mediated cell
XX proliferation and/or inflammation -
XX
XX Example 8; Page 78; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects
XX of skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and
XX AAF45153-F45161). The method is useful for ameliorating the effects of
XX psoriasis, ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids,
XX keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
XX skin, a hyperneovascular condition such as a neovascular condition of the
XX retina, brain or skin, growth factor-mediated malignancies, other
XX sclerotic disease, kidney disease, hyperproliferation of the inside of
XX blood vessels or any other hyperplasia.
XX
XX Sequence 15 BP; 3 A; 5 C; 5 G; 2 T; 0 other;
XX
Query Match 63.3%; Score 11.4; DB 22; Length 15;
Best Local Similarity 92.3%; Pred. No. 3.8e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 5 CCGCGATCCAGG 17
DB 3 CCGCGATTCAGG 15

RESULT 38
AAFS1793
ID AAFS1793 standard; DNA; 15 BP.
XX
AC AAFS1793;
XX
30-MAR-2001 (first entry)
XX
IGF-1 oligonucleotide #2753.
XX
Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytoskeletal; dermatological; cardiac; vitruide; ophthalmological; keloid;
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX Homo sapiens.
XX MO200078341-A1.
XX 28-DEC-2000.
XX 21-JUN-2000; 2000MO-AU00693.
XX 21-JUN-1999; 99US-0140345.
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX Ameliorating the effects of a disorder, e.g. psoriasis, by
XX administering UV (ultra-violet) treatment (optional) and an antisense
XX nucleic acid that inhibits or reduces growth factor mediated cell
XX proliferation and/or inflammation -
XX
XX Example 8; Page 78; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects
XX of skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and
XX AAF45153-F45161). The method is useful for ameliorating the effects of
XX psoriasis, ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids,
XX keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
XX skin, a hyperneovascular condition such as a neovascular condition of the
XX retina, brain or skin, growth factor-mediated malignancies, other
XX sclerotic disease, kidney disease, hyperproliferation of the inside of
XX blood vessels or any other hyperplasia.
XX
XX Sequence 15 BP; 3 A; 6 C; 4 G; 2 T; 0 other;
XX
Query Match 63.3%; Score 11.4; DB 22; Length 15;
Best Local Similarity 92.3%; Pred. No. 3.8e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 6 CCGCGATCCAGG 18
DB 1 CCGCGATTCAGG 13

RESULT 39
AAV24277/C
ID AAV24277 standard; DNA; 19 BP.
XX
AC AAV24277;
XX

DT 03-SEP-1998 (first entry)
 XX Chimeric antibody against hPTRP human L chain PCR primer MBCLVRL.
 DE Chimeric antibody against hPTRP human L chain PCR primer MBCLVRL.
 XX Chimeric antibody against hPTRP human L chain PCR primer MBCLVRL.
 KW L chain; H chain; hypercalcaemia; cancer; malignant lymphoma; CDR;
 KW hypophosphataemia; pathogen; vitamin D resistance; V region; C region;
 KW humanised; PCR primer ss.
 XX Synthetic.
 OS Homo sapiens.
 XX MO981338-A1.
 PN 02-APR-1998.
 XX 24-SEP-1997; 97WO-JP03382.
 PF 24-JUL-1997; 97JP-0214168.
 PR 26-SEP-1996; 96JP-0255196.
 XX (CHUS) CHUGAI SEIYAKU KK.
 PA Sato K, Wakahara Y, Yabuta N;
 PI MPI; 1998-230640/20.
 DR New chimeric antibodies against human parathormone related
 XX peptide(s) - useful for, e.g. treatment of hypercalcaemia and other
 XX disorders caused by malignant neoplasm(s)
 PS Example 3; Page 107; 182pp; Japanese.
 CC New antibodies have been developed which are specific for human
 CC parathormone related peptides (hPTRP). The antibodies comprise chimeric
 CC L and/or H chains, where the C region is of human and L region of mouse,
 CC origin. The present sequence represents a PCR primer used in an example
 CC of the present invention. Host cells, transformed with vectors
 CC containing DNA encoding antibodies of the invention, can be used to
 CC produce the antibodies. The antibodies may be used to treat
 CC hypercalcaemia, especially that due to a malignancy, e.g. cancers of
 CC pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver,
 CC breast, kidney, bladder, womb or prostate or malignant lymphoma. They
 CC may also be used for treatment of hypophosphataemia such as that due to
 CC pathogens or to vitamin D resistance.
 CC
 SQ Sequence 19 BP; 2 A; 6 C; 6 G; 5 T; 0 other;
 Query Match 63.3%; Score 11.4; DB 19; Length 19;
 Best Local Similarity 92.3%; Pred. No. 3.8e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 GCCCGATCCAG 17
 DB 13 GCCCGATCCAG 1
 RESULT 40
 ID AAX00122/C
 AC AAX00122; standard; DNA; 19 BP.
 XX
 DT 14-APR-1999 (first entry)
 XX Human antibody PCR primer MBCLVRL.
 DE Human antibody PCR primer MBCLVRL.
 KW Human; parathyroid hormone related protein; PTHrP; cachexia; cancer;
 KW inhibitor; humanised; PCR primer; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX

PN MO9851329-A1.
 XX 19-NOV-1998.
 PD 13-MAY-1998; 98WO-JP02116.
 PF 18-JUL-1997; 97JP-0194445.
 PR 15-MAY-1997; 97JP-0125505.
 XX (CHUS) CHUGAI SEIYAKU KK.
 PA Ishii K, Sato K, Tunemari T;
 PI MPI; 1999-070101/06.
 DR Inhibitors of binding of parathyroid hormone related peptide to its
 XX receptor - useful for, e.g. treatment of cachexia arising from
 XX cancer or other diseases
 PS Example 4; Page 68; 125pp; Japanese.
 CC The present invention describes compositions for the treatment of
 CC cachexia containing a substance which inhibits the binding of a
 CC parathyroid hormone related peptide (PTHrP) to its receptor, as an
 CC active component. This substance may be an antagonist to the receptor,
 CC or an antibody (preferably monoclonal) or antibody fragment,
 CC recognising PTHrP. The antibody is preferably humanised or chimeric.
 CC The present invention also describes a humanised antibody prepared
 CC by hybridoma 23-57-137-1 (FERM BP-5631). The composition is used for
 CC the treatment of cachexia arising in connection with diseases such as
 CC cancer, thereby improving the quality of life of the patient. The
 CC present sequence represents a PCR primer used in an example from the
 CC present invention.
 CC
 SQ Sequence 19 BP; 2 A; 6 C; 6 G; 5 T; 0 other;
 Query Match 63.3%; Score 11.4; DB 20; Length 19;
 Best Local Similarity 92.3%; Pred. No. 3.8e+04;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 GCCCGATCCAG 17
 DB 13 GCCCGATCCAG 1

Search completed: June 7, 2003, 08:30:51
 Job time : 162.255 secs

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C 67	10.8	63.5	23	6	AR090572	AR090572 Sequence	C 140	9.8	57.6	17	6	AX262748	AX262748 Sequence	
C 68	10.8	63.5	23	6	AR197607	AR197607 Sequence	C 141	9.8	57.6	17	6	AX262749	AX262749 Sequence	
C 69	10.8	63.5	23	6	AX458827	AX458827 Sequence	C 142	9.8	57.6	18	6	AR098815	AR098815 Sequence	
C 70	10.8	63.5	24	6	AX049485	AX049485 Sequence	C 143	9.8	57.6	18	6	AR110538	AR110538 Sequence	
C 71	10.6	62.4	20	6	AR116457	AR116457 Sequence	C 144	9.8	57.6	18	6	AR110541	AR110541 Sequence	
C 72	10.6	62.4	21	6	AR070874	AR070874 Sequence	C 145	9.8	57.6	18	6	AR110543	AR110543 Sequence	
C 73	10.6	62.4	22	6	AR053409	AR053409 Sequence	C 146	9.8	57.6	18	6	AR110545	AR110545 Sequence	
C 74	10.6	62.4	22	6	E11228	E11228 PCR primer	C 147	9.8	57.6	18	6	AR148407	AR148407 Sequence	
C 75	10.6	62.4	24	6	AX291927	AX291927 Sequence	C 148	9.8	57.6	18	6	AR151758	AR151758 Sequence	
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C 77	10.6	62.4	25	6	AB2665	AB2665 Sequence 10	C 150	9.8	57.6	18	6	AR151763	AR151763 Sequence	
C 78	10.4	61.2	19	6	AX106965	AX106965 Sequence	C 151	9.8	57.6	18	6	AR151765	AR151765 Sequence	
C 79	10.4	61.2	20	6	AR022549	AR022549 Sequence	C 152	9.8	57.6	18	6	AR156704	AR156704 Sequence	
C 80	10.4	61.2	20	6	AR099519	AR099519 Sequence	C 153	9.8	57.6	18	6	E34000	E34000 Sequence	
C 81	10.4	61.2	20	6	AR099522	AR099522 Sequence	C 154	9.8	57.6	19	6	AR067855	AR067855 Sequence	
C 82	10.4	61.2	20	6	AR124957	AR124957 Sequence	C 155	9.8	57.6	19	6	AR067855	AR067855 Sequence	
C 83	10.4	61.2	20	6	AR178800	AR178800 Sequence	C 156	9.8	57.6	19	6	AR168087	AR168087 Sequence	
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C 87	10.4	61.2	20	6	AX095608	AX095608 Sequence	C 160	9.8	57.6	19	6	E09196	E09196 Oligonucleo	
C 88	10.4	61.2	21	6	AX095608	AX095608 Sequence	C 161	9.8	57.6	19	6	E09966	E09966 Primer for	
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C 92	10.2	60.0	18	6	AR202731	AR202731 Sequence	C 165	9.8	57.6	20	6	AR178819	AR178819 Sequence	
C 93	10.2	60.0	20	6	AB3990	AB3990 Sequence 11	C 166	9.8	57.6	20	6	AR195428	AR195428 Sequence	
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C 96	10.2	60.0	21	6	A62036	A62036 Sequence 22	C 169	9.8	57.6	20	6	AX077181	AX077181 Sequence	
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C 98	10.2	60.0	21	6	AR043702	AR043702 Sequence	C 171	9.8	57.6	20	6	E05990	E05990 PCR primer	
C 99	10.2	60.0	21	6	AR043703	AR043703 Sequence	C 172	9.8	57.6	20	6	115638	115638 Sequence 52	
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C 112	10.2	58.8	17	6	AR210245	AR210245 Sequence	C 185	9.8	57.6	22	6	AR137691	AR137691 Sequence	
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C 128	10.2	58.8	20	6	AX297463	AX297463 Sequence	C 201	9.8	57.6	25	6	AX146521	AX146521 Sequence	
C 129	10.2	58.8	21	6	A23590	A23590 CE gene mut	C 202	9.8	57.6	25	6	AX343026	AX343026 Sequence	
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C 131	10.2	58.8	21	6	AX095303	AX095303 Sequence	C 204	9.8	57.6	25	6	AX068305	AX068305 Sequence	
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C 133	10.2	58.8	21	6	AX402753	AX402753 Sequence	C 206	9.8	57.6	25	6	AB069250	AB069250 Synthetic	
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C 215	9.6	56.5	20	6	BD003460	BD003460 A gene re	C 288	9.4	55.3	21	6	AR043693	AR043693 Sequence
C 216	9.6	56.5	20	6	E16974	E16974 PCR primer	C 289	9.4	55.3	21	6	AR052430	AR052430 Sequence
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C 220	9.6	56.5	21	6	AX487177	AX487177 Sequence	C 293	9.4	55.3	21	6	AX060905	AX060905 Sequence
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C 232	9.6	56.5	24	6	AR072787	AR072787 Sequence	C 305	9.4	55.3	22	6	I32033	I32033 Sequence 44
C 233	9.6	56.5	24	6	AR134685	AR134685 Sequence	C 306	9.4	55.3	22	6	I32717	I32717 Sequence 44
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C 235	9.6	56.5	24	6	AR207687	AR207687 Sequence	C 308	9.4	55.3	22	6	I64763	I64763 Sequence 18
C 236	9.6	56.5	24	6	AX205068	AX205068 Sequence	C 309	9.4	55.3	23	6	AX110640	AX110640 Sequence
C 237	9.6	56.5	24	6	AX289422	AX289422 Sequence	C 310	9.4	55.3	23	6	A02544	A02544 Nucleotide
C 238	9.6	56.5	24	6	AX43562	AX43562 Sequence	C 311	9.4	55.3	24	6	AX151751	AX151751 Sequence
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C 247	9.6	56.5	25	6	AX043212	AX043212 Sequence	C 320	9.4	55.3	25	6	I59883	I59883 Sequence 10
C 248	9.6	56.5	25	6	AX354444	AX354444 Sequence	C 321	9.4	55.3	25	6	I68664	I68664 Sequence 29
C 249	9.6	56.5	25	6	BD005585	BD005585 Sequence	C 322	9.4	55.3	25	6	I96741	I96741 Sequence 10
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C 253	9.4	55.3	14	6	E38194	E38194 Expression	C 326	9.2	54.1	15	6	AX281895	AX281895 Sequence
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C 262	9.4	55.3	16	6	A65530	A65530 Sequence 26	C 335	9.2	54.1	17	6	AX325813	AX325813 Sequence
C 263	9.4	55.3	17	6	AR036945	AR036945 Sequence	C 336	9.2	54.1	17	6	AX325837	AX325837 Sequence
C 264	9.4	55.3	17	6	AR097280	AR097280 Sequence	C 337	9.2	54.1	17	6	I46295	I46295 Sequence 27
C 265	9.4	55.3	18	6	A12953	A12953 Nucleotide	C 338	9.2	54.1	17	6	I53864	I53864 Sequence 16
C 266	9.4	55.3	18	6	AR073377	AR073377 Sequence	C 339	9.2	54.1	17	6	I55143	I55143 Sequence 7
C 267	9.4	55.3	18	6	AR092844	AR092844 Sequence	C 340	9.2	54.1	17	6	AR043153	AR043153 Sequence
C 268	9.4	55.3	18	6	AR162294	AR162294 Sequence	C 341	9.2	54.1	18	6	AR074653	AR074653 Sequence
C 269	9.4	55.3	18	6	AX395468	AX395468 Sequence	C 342	9.2	54.1	18	6	AX192837	AX192837 Sequence
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C 272	9.4	55.3	19	6	AX130985	AX130985 Sequence	C 345	9.2	54.1	19	6	A39750	A39750 Sequence 18
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C 275	9.4	55.3	20	6	AR163994	AR163994 Sequence	C 348	9.2	54.1	19	6	AX035666	AX035666 Sequence
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C 277	9.4	55.3	20	6	AX104665	AX104665 Sequence	C 350	9.2	54.1	19	6		
C 278	9.4	55.3	20	6	AX286797	AX286797 Sequence	C 351	9.2	54.1	19	6		
C 279	9.4	55.3	20	6	AX293546	AX293546 Sequence	C 352	9.2	54.1	19	6		
C 280	9.4	55.3	20	6	AX355397	AX355397 Sequence	C 353	9.2	54.1	19	6		
C 281	9.4	55.3	20	6	AX355398	AX355398 Sequence	C 354	9.2	54.1	19	6		
C 282	9.4	55.3	20	6	AX402880	AX402880 Sequence	C 355	9.2	54.1	19	6		
C 283	9.4	55.3	20	6	E07661	E07661 Primer. 9/1	C 356	9.2	54.1	19	6		
C 284	9.4	55.3	20	6			C 357	9.2	54.1	19	6		

C 504	9	52.9	18	6	AR112300	AR113300 Sequence	C 577	9	52.9	24	6	AX288473	AX288473 Sequence
C 505	9	52.9	18	6	AR203563	AR203563 Sequence	C 578	9	52.9	24	6	AX288561	AX288561 Sequence
C 506	9	52.9	18	6	AX428585	AX428585 Sequence	C 579	9	52.9	24	6	AX289357	AX289357 Sequence
C 507	9	52.9	18	6	BD003523	BD003523 A gene re	C 580	9	52.9	24	6	AX289603	AX289603 Sequence
C 508	9	52.9	18	6	BD003523	BD003523 A gene re	C 581	9	52.9	24	6	AX290404	AX290404 Sequence
C 509	9	52.9	19	6	AG1201	AG1201 Sequence 38	C 582	9	52.9	24	6	AX290438	AX290438 Sequence
C 510	9	52.9	19	6	AR076583	AR076583 Sequence	C 583	9	52.9	24	6	AX290642	AX290642 Sequence
C 511	9	52.9	19	6	AR076585	AR076585 Sequence	C 584	9	52.9	24	6	AX290937	AX290937 Sequence
C 512	9	52.9	19	6	AX359802	AX359802 Sequence	C 585	9	52.9	24	6	AX291263	AX291263 Sequence
C 513	9	52.9	19	6	AX472012	AX472012 Sequence	C 586	9	52.9	24	6	AX292188	AX292188 Sequence
C 514	9	52.9	20	6	AS8995	AS8995 Sequence 3	C 587	9	52.9	24	6	AX342202	AX342202 Sequence
C 515	9	52.9	20	6	AR023394	AR023394 Sequence	C 588	9	52.9	24	6	AX343612	AX343612 Sequence
C 516	9	52.9	20	6	AR089470	AR089470 Sequence	C 589	9	52.9	24	6	AX444222	AX444222 Sequence
C 517	9	52.9	20	6	AR116524	AR116524 Sequence	C 590	9	52.9	24	6	AX444724	AX444724 Sequence
C 518	9	52.9	20	6	AR121006	AR121006 Sequence	C 591	9	52.9	24	6	AX445018	AX445018 Sequence
C 519	9	52.9	20	6	AR167955	AR167955 Sequence	C 592	9	52.9	24	6	AX445187	AX445187 Sequence
C 520	9	52.9	20	6	AX066405	AX066405 Sequence	C 593	9	52.9	24	6	AX445452	AX445452 Sequence
C 521	9	52.9	20	6	AX073513	AX073513 Sequence	C 594	9	52.9	24	6	AX445730	AX445730 Sequence
C 522	9	52.9	20	6	AX073513	AX073513 Sequence	C 595	9	52.9	24	6	AX445877	AX445877 Sequence
C 523	9	52.9	20	6	AX148927	AX148927 Sequence	C 596	9	52.9	24	6	AX445912	AX445912 Sequence
C 524	9	52.9	20	6	AX148928	AX148928 Sequence	C 597	9	52.9	24	6	AX445950	AX445950 Sequence
C 525	9	52.9	20	6	AX293106	AX293106 Sequence	C 598	9	52.9	24	6	AX446476	AX446476 Sequence
C 526	9	52.9	20	6	AX293194	AX293194 Sequence	C 599	9	52.9	24	6	AX447473	AX447473 Sequence
C 527	9	52.9	20	6	AX293990	AX293990 Sequence	C 600	9	52.9	24	6	AX488489	AX488489 Sequence
C 528	9	52.9	20	6	AX294236	AX294236 Sequence	C 601	9	52.9	24	6	BD000091	BD000091 Novel ol1
C 529	9	52.9	20	6	AX295037	AX295037 Sequence	C 602	9	52.9	24	6	BD011176	BD011176 Human tel
C 530	9	52.9	20	6	AX295071	AX295071 Sequence	C 603	9	52.9	24	6	E36925	E36925 Human telom
C 531	9	52.9	20	6	AX295570	AX295570 Sequence	C 604	9	52.9	24	6	I30971	I30971 Sequence 3
C 532	9	52.9	20	6	AX295896	AX295896 Sequence	C 605	9	52.9	24	6	I30975	I30975 Sequence 7
C 533	9	52.9	20	6	AX296821	AX296821 Sequence	C 606	9	52.9	24	6	I30978	I30978 Sequence 10
C 534	9	52.9	20	6	AX297174	AX297174 Sequence	C 607	9	52.9	24	6	I30981	I30981 Sequence 13
C 535	9	52.9	20	6	AX298864	AX298864 Sequence	C 608	9	52.9	24	6	I30987	I30987 Sequence 19
C 536	9	52.9	20	6	AX356929	AX356929 Sequence	C 609	9	52.9	24	6	I30987	M59524 Mouse T-cell
C 537	9	52.9	20	6	AX351246	AX351246 Sequence	C 610	9	52.9	24	10	MUSTCGXAP	AX031455 Sequence
C 538	9	52.9	20	6	E36214	E36214 Japanese cl	C 611	9	52.9	24	13	AX031455	AX031459 Sequence
C 539	9	52.9	20	6	E36214	E36214 Japanese cl	C 612	9	52.9	24	13	AX031462	AX031462 Sequence
C 540	9	52.9	20	6	E38877	E38877 Chimeric an	C 613	9	52.9	24	13	AX031465	AX031465 Sequence
C 541	9	52.9	20	12	AB069027	AB069027 Synthetic	C 614	9	52.9	24	13	AX031471	AX031471 Sequence
C 542	9	52.9	21	6	AR031457	AR031457 Sequence	C 615	9	52.9	25	6	A57005	AX031455 Sequence
C 543	9	52.9	21	6	AR112754	AR112754 Sequence	C 616	9	52.9	25	6	AR084194	AX031459 Sequence
C 544	9	52.9	21	6	AR118869	AR118869 Sequence	C 617	9	52.9	25	6	AR085004	AX031459 Sequence
C 545	9	52.9	21	6	AR162648	AR162648 Sequence	C 618	9	52.9	25	6	AR090657	AX031459 Sequence
C 546	9	52.9	21	6	AX006711	AX006711 Sequence	C 619	9	52.9	25	6	AR141420	AR141420 Sequence
C 547	9	52.9	21	6	AX094960	AX094960 Sequence	C 620	9	52.9	25	6	AR197692	AR197692 Sequence
C 548	9	52.9	21	6	AX095231	AX095231 Sequence	C 621	9	52.9	25	6	AX077734	AX077734 Sequence
C 549	9	52.9	21	6	AX095841	AX095841 Sequence	C 622	9	52.9	25	6	AX133809	AX133809 Sequence
C 550	9	52.9	21	6	AX417512	AX417512 Sequence	C 623	9	52.9	25	6	AX197216	AX197216 Sequence
C 551	9	52.9	21	6	II1760	II1760 Sequence 48	C 624	9	52.9	25	6	AX211751	AX211751 Sequence
C 552	9	52.9	21	6	II19431	II19431 Sequence 48	C 625	9	52.9	25	6	AX249886	AX249886 Sequence
C 553	9	52.9	22	6	A08339	A08339 Oligonucleo	C 626	9	52.9	25	6	AX278991	AX278991 Sequence
C 554	9	52.9	22	6	AR179906	AR179906 Sequence	C 627	9	52.9	25	6	AX279123	AX279123 Sequence
C 555	9	52.9	22	6	AR182279	AR182279 Sequence	C 628	9	52.9	25	6	AX447594	AX447594 Sequence
C 556	9	52.9	22	6	I46957	I46957 Sequence 50	C 629	9	52.9	25	6	AX448188	AX448188 Sequence
C 557	9	52.9	23	6	A00103	A00103 Nucleotide	C 630	9	52.9	25	6	AX476757	AX476757 Sequence
C 558	9	52.9	23	6	AR043240	AR043240 Sequence	C 631	9	52.9	25	6	AX476758	AX476758 Sequence
C 559	9	52.9	23	6	AR074895	AR074895 Sequence	C 632	9	52.9	25	6	AX476759	AX476759 Sequence
C 560	9	52.9	23	6	AR090741	AR090741 Sequence	C 633	9	52.9	25	6	AX476760	AX476760 Sequence
C 561	9	52.9	23	6	AR197776	AR197776 Sequence	C 634	9	52.9	25	6	AX476761	AX476761 Sequence
C 562	9	52.9	23	6	AX082174	AX082174 Sequence	C 635	9	52.9	25	6	AX476762	AX476762 Sequence
C 563	9	52.9	23	6	I82091	I82091 Sequence 28	C 636	9	52.9	25	6	AX476763	AX476763 Sequence
C 564	9	52.9	24	6	AG2489	AG2489 Sequence 4	C 637	9	52.9	25	6	AX476764	AX476764 Sequence
C 565	9	52.9	24	6	AR055632	AR055632 Sequence	C 638	9	52.9	25	6	AX476765	AX476765 Sequence
C 566	9	52.9	24	6	AR091182	AR091182 Sequence	C 639	9	52.9	25	6	E12501	E12501 Primer. 4/1
C 567	9	52.9	24	6	AR174261	AR174261 Sequence	C 640	9	52.9	25	6	E15861	E15861 PCR primer
C 568	9	52.9	24	6	AR198217	AR198217 Sequence	C 641	9	52.9	25	6	E31897	E31897 Method for
C 569	9	52.9	24	6	AR208336	AR208336 Sequence	C 642	9	52.9	25	12	SYNANVAN	E31109 Protein par
C 570	9	52.9	24	6	AX031345	AX031345 Sequence	C 643	9	52.9	25	12	SYNANVAN	ME0083 Avian neovl
C 571	9	52.9	24	6	AX031349	AX031349 Sequence	C 644	9	51.8	12	6	A46084	A46084 Sequence 9
C 572	9	52.9	24	6	AX031352	AX031352 Sequence	C 645	9	51.8	12	6	AR027677	AR027677 Sequence
C 573	9	52.9	24	6	AX031355	AX031355 Sequence	C 646	9	51.8	13	6	A89148	A89148 Sequence 12
C 574	9	52.9	24	6	AX031361	AX031361 Sequence	C 647	9	51.8	14	6	AR148601	AR148601 Sequence
C 575	9	52.9	24	6	AX060697	AX060697 Sequence	C 648	9	51.8	14	6	AX358009	AX358009 Sequence
C 576	9	52.9	24	6	AX288378	AX288378 Sequence	C 649	9	51.8	14	6	I46934	I46934 Sequence 27

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654	8.8	51.8	15	6	AX040890	Sequence	727	8.8	51.8	20	6	AX146439	Sequence
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662	8.8	51.8	16	6	AX285815	Sequence	735	8.8	51.8	20	6	AX488431	Sequence
663	8.8	51.8	16	6	AR480515	Sequence	736	8.8	51.8	20	6	E07135	Sequence
664	8.8	51.8	17	4	GS4J789	Sequence	737	8.8	51.8	20	6	E08654	Sequence
665	8.8	51.8	17	6	AR66913	Sequence	738	8.8	51.8	20	6	E08790	Sequence
666	8.8	51.8	17	6	AR66943	Sequence	739	8.8	51.8	20	6	E17267	Sequence
667	8.8	51.8	17	6	AR67043	Sequence	740	8.8	51.8	20	6	E17268	Sequence
668	8.8	51.8	17	6	AR67045	Sequence	741	8.8	51.8	20	6	E38874	Sequence
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671	8.8	51.8	17	6	AR67045	Sequence	744	8.8	51.8	20	6	E49528	Sequence
672	8.8	51.8	17	6	AR67045	Sequence	745	8.8	51.8	20	6	E49528	Sequence
673	8.8	51.8	17	6	AR67045	Sequence	746	8.8	51.8	20	6	E49528	Sequence
674	8.8	51.8	17	6	AR67045	Sequence	747	8.8	51.8	20	6	E49528	Sequence
675	8.8	51.8	17	6	AR67045	Sequence	748	8.8	51.8	20	6	E49528	Sequence
676	8.8	51.8	17	6	AR67045	Sequence	749	8.8	51.8	20	6	E49528	Sequence
677	8.8	51.8	18	6	AR67045	Sequence	750	8.8	51.8	20	12	AB068988	Sequence
678	8.8	51.8	18	6	AR67045	Sequence	751	8.8	51.8	21	6	AR07666	Sequence
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680	8.8	51.8	18	6	AR034582	Sequence	753	8.8	51.8	21	6	AR022540	Sequence
681	8.8	51.8	18	6	AR036933	Sequence	754	8.8	51.8	21	6	AR099913	Sequence
682	8.8	51.8	18	6	AR054937	Sequence	755	8.8	51.8	21	6	AR100586	Sequence
683	8.8	51.8	18	6	AR092864	Sequence	756	8.8	51.8	21	6	AR157641	Sequence
684	8.8	51.8	18	6	AR092864	Sequence	757	8.8	51.8	21	6	AR096968	Sequence
685	8.8	51.8	18	6	AR092864	Sequence	758	8.8	51.8				

796	8.8	51.8	22	23	Bd007696																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
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942 8.6 50.6 21 6 AR111126 Sequence
943 8.6 50.6 21 6 AR123012 Sequence
944 8.6 50.6 21 6 AR149503 Sequence
945 8.6 50.6 21 6 AR160932 Sequence
946 8.6 50.6 21 6 AR004426 Sequence
947 8.6 50.6 21 6 AR022063 Sequence
948 8.6 50.6 21 6 AX096704 Sequence
949 8.6 50.6 21 6 AX096814 Sequence
950 8.6 50.6 21 6 AX097307 Sequence
951 8.6 50.6 21 6 AX375726 Sequence
952 8.6 50.6 21 6 AX375727 Sequence
953 8.6 50.6 21 6 E21986 Sequence
954 8.6 50.6 21 6 E26005 Sequence
955 8.6 50.6 21 6 E29435 Sequence
956 8.6 50.6 21 6 I75042 Sequence
957 8.6 50.6 21 6 I93340 Sequence
958 8.6 50.6 21 8 PTRRND04
959 8.6 50.6 22 6 A09899
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961 8.6 50.6 22 6 A86783
962 8.6 50.6 22 6 AR019664
963 8.6 50.6 22 6 AR030176
964 8.6 50.6 22 6 AR080244
965 8.6 50.6 22 6 AR093695
966 8.6 50.6 22 6 AR128062
967 8.6 50.6 22 6 AR177038
968 8.6 50.6 22 6 AR181077
969 8.6 50.6 22 6 AR210070
970 8.6 50.6 22 6 AX011595
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972 8.6 50.6 22 6 AX048135
973 8.6 50.6 22 6 AX081800
974 8.6 50.6 22 6 AX098591
975 8.6 50.6 22 6 AX191001
976 8.6 50.6 22 6 AX268978
977 8.6 50.6 22 6 AX375728
978 8.6 50.6 22 6 E06853
979 8.6 50.6 22 6 I12812
980 8.6 50.6 22 6 I30875
981 8.6 50.6 22 6 I30876
982 8.6 50.6 22 6 I46334
983 8.6 50.6 22 6 I46335
984 8.6 50.6 22 6 I88037
985 8.6 50.6 23 6 A80535
986 8.6 50.6 23 6 AR026776
987 8.6 50.6 23 6 AR049202
988 8.6 50.6 23 6 AR065460
989 8.6 50.6 23 6 AR069859
990 8.6 50.6 23 6 AX023932
991 8.6 50.6 23 6 AX046193
992 8.6 50.6 23 6 AX076940
993 8.6 50.6 23 6 AX253407
994 8.6 50.6 23 6 AX278690
995 8.6 50.6 23 6 AX403785
996 8.6 50.6 23 6 AX468808
997 8.6 50.6 23 6 E33021
998 8.6 50.6 24 1 S58561
999 8.6 50.6 24 6 AR000509
1000 8.6 50.6 24 6 AR059918

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ALIGNMENTS

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RESULT 1
LOCUS AX402771/c 22 bp DNA linear PAT 07-JUN-2002
DEFINITION Sequence 255 from Patent WO0196612.
ACCESSION AX402771
VERSION AX402771.1 GI:21387762
KEYWORDS Aspergillus sclerotiorum.
SOURCE Aspergillus sclerotiorum.
ORGANISM Aspergillus sclerotiorum

```

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REFERENCE
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 255 20-DEC-2001;
UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
FEATURES
SOURCE 1. .22
/organism="Aspergillus sclerotiorum"
/db_xref="taxon:138282"
BASE COUNT 7 a 8 c 1 t
ORIGIN
Query Match 82.4%; Score 14; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
14 GTTGCTTCGGCGG 1

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RESULT 2
LOCUS AX402778/c 22 bp DNA linear PAT 07-JUN-2002
DEFINITION Sequence 262 from Patent WO0196612.
ACCESSION AX402778
VERSION AX402778.1 GI:21387769
KEYWORDS Aspergillus wentii.
SOURCE Aspergillus wentii.
ORGANISM Aspergillus wentii.
REFERENCE
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 262 20-DEC-2001;
UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
FEATURES
SOURCE 1. .22
/organism="Aspergillus wentii"
/db_xref="taxon:5066"
BASE COUNT 7 a 8 c 1 t
ORIGIN
Query Match 82.4%; Score 14; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
14 GTTGCTTCGGCGG 1

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RESULT 3
LOCUS AX402921/c 22 bp DNA linear PAT 07-JUN-2002
DEFINITION Sequence 405 from Patent WO0196612.
ACCESSION AX402921
VERSION AX402921.1 GI:21387912
KEYWORDS Aspergillus auricomus.
SOURCE Aspergillus auricomus.
ORGANISM Aspergillus auricomus.
REFERENCE
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 405 20-DEC-2001;
UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
FEATURES
SOURCE 1. .22
Location/Qualifiers

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BASE COUNT 7 a 8 c 6 g 1 t
/organism="Aspergillus auricomus"
/db_xref="taxon:138274"

Query Match 82.4%; Score 14; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGGG 14
14 GTTGCTTCGGCGGG 1

RESULT 4
AX402757 16 bp DNA linear PAT 07-JUN-2002
LOCUS Sequence 241 from Patent WO0196612.
ACCESSION AX402757
VERSION AX402757.1 GI:21387748
KEYWORDS
SOURCE Aspergillus flavipes.
ORGANISM Aspergillus flavipes.
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
TITLE Haugland, R. and Vesper, S.
JOURNAL Method of identifying and quantifying specific fungi and bacteria
PATENT: WO 0196612-A 241 20-DEC-2001;
UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
LOCATION/Qualifiers

FEATURES
source 1.16
/organism="Aspergillus flavipes"
/db_xref="taxon:41900"

BASE COUNT 0 a 6 c 6 g 4 t

Query Match 76.5%; Score 13; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGCTTCGGCGGG 14
1 TTGCTTCGGCGGG 13

RESULT 5
AX402760 16 bp DNA linear PAT 07-JUN-2002
LOCUS Sequence 244 from Patent WO0196612.
ACCESSION AX402760
VERSION AX402760.1 GI:21387751
KEYWORDS
SOURCE Fennellia nivea.
ORGANISM Fennellia nivea.
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
TITLE Haugland, R. and Vesper, S.
JOURNAL Method of identifying and quantifying specific fungi and bacteria
PATENT: WO 0196612-A 244 20-DEC-2001;
UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
LOCATION/Qualifiers

FEATURES
source 1.16
/organism="Fennellia nivea"
/db_xref="taxon:41281"

BASE COUNT 0 a 6 c 6 g 4 t

Query Match 76.5%; Score 13; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGCTTCGGCGGG 14
1 TTGCTTCGGCGGG 13

RESULT 6
AX402744 23 bp DNA linear PAT 07-JUN-2002
LOCUS Sequence 228 from Patent WO0196612.
ACCESSION AX402744
VERSION AX402744.1 GI:21387735
KEYWORDS
SOURCE Aspergillus caespitosus.
ORGANISM Aspergillus caespitosus.
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
TITLE Haugland, R. and Vesper, S.
JOURNAL Method of identifying and quantifying specific fungi and bacteria
PATENT: WO 0196612-A 228 20-DEC-2001;
UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
LOCATION/Qualifiers

FEATURES
source 1.23
/organism="Aspergillus caespitosus"
/db_xref="taxon:176165"

BASE COUNT 3 a 7 c 8 g 5 t

Query Match 75.3%; Score 12.8; DB 6; Length 23;
Best Local Similarity 87.5%; Pred. No. 2.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGGAA 16
5 GTTGCTTCGGCGGAGA 20

RESULT 7
AX402775 23 bp DNA linear PAT 07-JUN-2002
LOCUS Sequence 259 from Patent WO0196612.
ACCESSION AX402775
VERSION AX402775.1 GI:21387766
KEYWORDS
SOURCE Aspergillus unguis.
ORGANISM Aspergillus unguis.
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
TITLE Haugland, R. and Vesper, S.
JOURNAL Method of identifying and quantifying specific fungi and bacteria
PATENT: WO 0196612-A 259 20-DEC-2001;
UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
LOCATION/Qualifiers

FEATURES
source 1.23
/organism="Aspergillus unguis"
/db_xref="taxon:40381"

BASE COUNT 3 a 7 c 8 g 5 t

Query Match 75.3%; Score 12.8; DB 6; Length 23;
Best Local Similarity 87.5%; Pred. No. 2.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGGAA 16
5 GTTGCTTCGGCGGAGA 20

RESULT 8
AR210283 15 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 195 from patent US 6387652.

ACCESSION AR210283
VERSION AR210283.1 GI:21512474
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Haugland,R. and Vesper,S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: US 6387652-A 195 14-MAY-2002;
FEATURES Location/Qualifiers
1..15
source /organism="unknown"
BASE COUNT 1 a 4 c 6 g 4 t
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.9e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTGCTTCGGCGGGA 15
1 TTGCTTCGGCGGGA 14

RESULT 9
AX402711 15 bp DNA linear PAT 07-JUN-2002
LOCUS Sequence 195 from Patent WO0196612.
ACCESSION AX402711
VERSION AX402711.1 GI:21387702
KEYWORDS
SOURCE Trichoderma harzianum.
ORGANISM Trichoderma harzianum.
REFERENCE 1
AUTHORS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
TITLE Hypocreales; mitosporic Hypocreales; Trichoderma.
JOURNAL Haugland,R. and Vesper,S.
METHOD of identifying and quantifying specific fungi and bacteria
PATENT: WO 0196612-A 195 20-DEC-2001;
FEATURES UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
1..15
source Location/Qualifiers
/organism="Trichoderma harzianum"
/db_xref="taxon:5544"
BASE COUNT 1 a 4 c 6 g 4 t
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.9e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTGCTTCGGCGGGA 15
1 TTGCTTCGGCGGGA 14

RESULT 10
AX402941 16 bp DNA linear PAT 07-JUN-2002
LOCUS Sequence 425 from Patent WO0196612.
ACCESSION AX402941
VERSION AX402941.1 GI:21387932
KEYWORDS
SOURCE Penicillium expansum.
ORGANISM Penicillium expansum.
REFERENCE 1
AUTHORS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
TITLE Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
JOURNAL Haugland,R. and Vesper,S.
METHOD of identifying and quantifying specific fungi and bacteria
PATENT: WO 0196612-A 425 20-DEC-2001;
FEATURES UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)

FEATURES Location/Qualifiers
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source /organism="Penicillium expansum"
/db_xref="taxon:27334"
BASE COUNT 3 a 7 c 5 g 1 t
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 16;
Best Local Similarity 92.9%; Pred. No. 3.9e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 14
15 GTTGCTTCGGCGG 2

RESULT 11
AR210279 21 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 191 from patent US 6387652.
ACCESSION AR210279
VERSION AR210279.1 GI:21512469
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Haugland,R. and Vesper,S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: US 6387652-A 191 14-MAY-2002;
FEATURES Location/Qualifiers
1..21
source /organism="unknown"
BASE COUNT 3 a 7 c 7 g 4 t
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 21;
Best Local Similarity 92.9%; Pred. No. 4e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 14
8 GTTGCTTCGGCGG 21

RESULT 12
AR210282 21 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 194 from patent US 6387652.
ACCESSION AR210282
VERSION AR210282.1 GI:21512472
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Haugland,R. and Vesper,S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: US 6387652-A 194 14-MAY-2002;
FEATURES Location/Qualifiers
1..21
source /organism="unknown"
BASE COUNT 3 a 7 c 7 g 4 t
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 21;
Best Local Similarity 92.9%; Pred. No. 4e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 14
8 GTTGCTTCGGCGG 21

RESULT 13
LOCUS AR210291 21 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 203 from patent US 6387652.
ACCESSION AR210291.1 GI:21512484
VERSION AR210291.1 GI:21512484
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: US 6387652-A 203 14-MAY-2002;
FEATURES
source location/Qualifiers
1..21
/organism="unknown"
BASE COUNT 3 a 7 g 7 g 4 c
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 21;
Best Local Similarity 92.9%; Pred. No. 4e+04; 1; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTGCTTCGGCGGG 14
|||||
8 GTTGCTTCGGCGGG 21

Db 8 GTTGCTTCGGCGGG 21

RESULT 14
LOCUS AX402707 21 bp DNA linear PAT 07-JUN-2002
DEFINITION Sequence 191 from Patent WO0196612.
ACCESSION AX402707
VERSION AX402707.1 GI:21387698
KEYWORDS
SOURCE Trichoderma asperellum.
ORGANISM Trichoderma asperellum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; microsporitic Hypocreales; Trichoderma.
REFERENCE 1
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 191 20-DEC-2001;
FEATURES
source location/Qualifiers
1..21
/organism="Trichoderma asperellum"
/db_xref="taxon:101201"
BASE COUNT 3 a 7 c 7 g 4 c
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 21;
Best Local Similarity 92.9%; Pred. No. 4e+04; 1; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTGCTTCGGCGGG 14
|||||
8 GTTGCTTCGGCGGG 21

Db 8 GTTGCTTCGGCGGG 21

RESULT 15
LOCUS AX402710 21 bp DNA linear PAT 07-JUN-2002
DEFINITION Sequence 194 from Patent WO0196612.
ACCESSION AX402710
VERSION AX402710.1 GI:21387701
KEYWORDS
SOURCE Trichoderma asperellum.
ORGANISM Trichoderma asperellum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; microsporitic Hypocreales; Trichoderma.

REFERENCE 1
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 194 20-DEC-2001;
FEATURES
source location/Qualifiers
1..21
/organism="Trichoderma asperellum"
/db_xref="taxon:101201"
BASE COUNT 3 a 7 c 7 g 4 c
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 21;
Best Local Similarity 92.9%; Pred. No. 4e+04; 1; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTGCTTCGGCGGG 14
|||||
8 GTTGCTTCGGCGGG 21

Db 8 GTTGCTTCGGCGGG 21

RESULT 16
LOCUS AX402719 21 bp DNA linear PAT 07-JUN-2002
DEFINITION Sequence 203 from Patent WO0196612.
ACCESSION AX402719
VERSION AX402719.1 GI:21387710
KEYWORDS
SOURCE Trichoderma viride.
ORGANISM Trichoderma viride
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; microsporitic Hypocreales; Trichoderma.
REFERENCE 1
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 203 20-DEC-2001;
FEATURES
source location/Qualifiers
1..21
/organism="Trichoderma viride"
/db_xref="taxon:5547"
BASE COUNT 3 a 7 c 7 g 4 c
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 21;
Best Local Similarity 92.9%; Pred. No. 4e+04; 1; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTGCTTCGGCGGG 14
|||||
8 GTTGCTTCGGCGGG 21

Db 8 GTTGCTTCGGCGGG 21

RESULT 17
LOCUS AR210119 22 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 31 from Patent US 6387652.
ACCESSION AR210119
VERSION AR210119.1 GI:21512267
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: US 6387652-A 31 14-MAY-2002;
FEATURES
source location/Qualifiers
1..22
/organism="unknown"
BASE COUNT 2 a 8 c 6 g 6 c
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 22;
Best Local Similarity 92.9%; Pred. No. 4e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTGCTTCGGCGG 14
Db 6 GTTGCTTCGGCGG 19

RESULT 18
AX402547
LOCUS Sequence 31 from Patent WO0196612.
DEFINITION AX402547 22 bp DNA linear PAT 07-JUN-2002
ACCESSION AX402547 GI:21387538
VERSION
KEYWORDS
SOURCE Aspergillus ochraceus.
ORGANISM Aspergillus ochraceus
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
AUTHORS Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
TITLE Haugland, R. and Vesper, S.
JOURNAL Method of identifying and quantifying specific fungi and bacteria
Patent: WO 0196612-A 31 20-DEC-2001;
FEATURES UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
Source location/Qualifiers
1. .22
/organism="Aspergillus ochraceus"
/db_xref="taxon:40380"

BASE COUNT 2 a 8 c 6 g 6 t

Query Match 72.9%; Score 12.4; DB 6; Length 22;
Best Local Similarity 92.9%; Pred. No. 4e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTGCTTCGGCGG 14
Db 6 GTTGCTTCGGCGG 19

RESULT 19
AR043140
LOCUS AR043140 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 24 from patent US 5814453.
ACCESSION AR043140
VERSION AR043140.1 GI:5964148
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 20)
TITLE Beck, J. Joseph.
JOURNAL Detection of fungal pathogens using the polymerase chain reaction
Patent: US 5814453-A 24 29-SEP-1998;
FEATURES Location/Qualifiers
1. .20
/organism="unknown"

BASE COUNT 1 a 5 c 9 g 5 t

Query Match 71.8%; Score 12.2; DB 6; Length 20;
Best Local Similarity 82.4%; Pred. No. 5.2e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTTGCTTCGGCGGAC 17
Db 1 GTTGCTTCGGCGGCGAC 17

RESULT 20
AR074640
LOCUS AR074640 20 bp DNA linear PAT 28-AUG-2000

DEFINITION Sequence 24 from patent US 5955274.
ACCESSION AR074640
VERSION AR074640.1 GI:10001393
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 20)
TITLE Iijon, J.M. and Beck, J.J.
JOURNAL Detection of fungal pathogens using the polymerase chain reaction
Patent: US 5955274-A 24 21-SEP-1999;
FEATURES Location/Qualifiers
1. .20
/organism="unknown"

BASE COUNT 1 a 5 c 9 g 5 t

Query Match 71.8%; Score 12.2; DB 6; Length 20;
Best Local Similarity 82.4%; Pred. No. 5.2e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTTGCTTCGGCGGAC 17
Db 1 GTTGCTTCGGCGGCGAC 17

RESULT 21
I32080
LOCUS I32080 20 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 24 from patent US 5585238.
ACCESSION I32080
VERSION I32080.1 GI:1822871
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 20)
TITLE Iijon, J.M. and Beck, J.J.
JOURNAL Detection of fungal pathogens using the polymerase chain reaction
Patent: US 5585238-A 24 17-DEC-1996;
FEATURES Location/Qualifiers
1. .20
/organism="unknown"

BASE COUNT 1 a 5 c 9 g 5 t

Query Match 71.8%; Score 12.2; DB 6; Length 20;
Best Local Similarity 82.4%; Pred. No. 5.2e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTTGCTTCGGCGGAC 17
Db 1 GTTGCTTCGGCGGCGAC 17

RESULT 22
AX286541
LOCUS AX286541 24 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 15 from Patent WO0181423.
ACCESSION AX286541
VERSION AX286541.1 GI:17048644
KEYWORDS
SOURCE Synthetic construct.
ORGANISM Synthetic construct
REFERENCE Artificial sequences.
AUTHORS Terres, P., Kleist, C., Opelz, G., Wejschof, M., Arnold-Schild, D.,
TITLE Schild, H. and Rammensee, H.G.
JOURNAL Antibodies against native gp96, production and use thereof
Patent: WO 0181423-A 15 01-NOV-2001;
FEATURES Dr. Ferring Biomed GmbH (DB)
Source Location/Qualifiers
1. .24

/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Zufallssequenz, codiert für CDR3 einer schweren
Kette eines Antikorpers, Herstellung siehe Mission et al,
1994"

BASE COUNT 3 a 4 c 8 g 9 t
ORIGIN

Query Match 71.8%; Score 12.2; DB 6; Length 24;
Best Local Similarity 82.4%; Pred. No. 5.2e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTTGCTTCGGCGGAC 17
Db 6 GTTGCTTCGGCGGAC 22

RESULT 23
LOCUS AR210208 17 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 120 from patent US 6387652.
ACCESSION AR210208
VERSION AR210208.1 GI:21512380
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 17)
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: US 6387652-A 120 14-MAY-2002;
FEATURES
source 1.17
/organism="unknown"

BASE COUNT 1 a 5 c 5 g 6 t
ORIGIN

Query Match 70.6%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTGCTTCGGCG 12
Db 5 GTTGCTTCGGCG 16

RESULT 24
LOCUS AX402636 17 bp DNA linear PAT 07-JUN-2002
DEFINITION Sequence 120 from Patent WO0196612.
ACCESSION AX402636
VERSION AX402636.1 GI:21387627
KEYWORDS
SOURCE Penicillium brevicompactum.
ORGANISM Penicillium brevicompactum.
REFERENCE 1 (bases 1 to 17)
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 120 20-DEC-2001;
UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
FEATURES
source 1.17
/organism="Penicillium brevicompactum"
/db_xref="taxon:5074"

BASE COUNT 1 a 5 c 5 g 6 t
ORIGIN

Query Match 70.6%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTGCTTCGGCG 12
Db 5 GTTGCTTCGGCG 16

RESULT 25
LOCUS AX150222 19 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 18 from Patent WO0132919.
ACCESSION AX150222
VERSION AX150222.1 GI:14348242
KEYWORDS
SOURCE soybean.
ORGANISM Glycine max

REFERENCE 1 (bases 1 to 19)
AUTHORS Vollenhofer, S., Mansfeld, M. and Kroath, H.
TITLE Group of novel primer pairs for PCR amplification, primer pairs,
gene probes and method for detecting technically genetically
modified plant material
JOURNAL Patent: WO 0132919-A 18 10-MAY-2001;
Oesterreichisches Forschungszentrum Seibersdorf Ges.m.b.H (AT)
FEATURES
source 1.19
/organism="Glycine max"
/db_xref="taxon:3847"
/note="SojaLeitin-Gen Lb1"

BASE COUNT 3 a 5 c 5 g 6 t
ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 19;
Best Local Similarity 86.7%; Pred. No. 8.9e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGCTTCGGCGGAC 17
Db 1 TGCTTCGGCGGAC 15

RESULT 26
LOCUS AR125569 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 70 from patent US 6177273.
ACCESSION AR125569
VERSION AR125569.1 GI:14111631
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C. Frank. and Cowsett, L.M.
TITLE Antisense modulation of integrin-linked kinase expression
JOURNAL Patent: US 6177273-A 70 23-JAN-2001;
FEATURES
source 1.20
/organism="unknown"

BASE COUNT 6 a 8 c 3 g 3 t
ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 20;
Best Local Similarity 86.7%; Pred. No. 8.9e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGCTTCGGCGGAC 17
Db 18 TGCTTCGGCGGAC 4

RESULT 27
AX294487/c

LOCUS AX294487 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 6249 from Patent WO0179548.
ACCESSION AX294487
VERSION AX294487.1 GI:17056170
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Barany, F., Zivvi, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL Sequence differences using ligase detection reaction
Patent: WO 0179548-A 6249 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
source
1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"
BASE COUNT 7 a 6 c 5 g 2 t
ORIGIN
Query Match 69.4%; Score 11.8; DB 6; Length 20;
Best Local Similarity 86.7%; Pred. No. 8.9e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 TTGCTTCGGCGGAA 16
DB 20 TTGCTTCGGCGTCA 6
RESULT 26
LOCUS AX289854 24 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 1616 from Patent WO0179548.
ACCESSION AX289854
VERSION AX289854.1 GI:17051537
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Barany, F., Zivvi, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL Sequence differences using ligase detection reaction
Patent: WO 0179548-A 1616 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
source
1..24
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"
BASE COUNT 7 a 7 c 7 g 3 t
ORIGIN
Query Match 69.4%; Score 11.8; DB 6; Length 24;
Best Local Similarity 86.7%; Pred. No. 9e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 TTGCTTCGGCGGAA 16
DB 20 TTGCTTCGGCTCA 6
RESULT 29
LOCUS AX100490 25 bp DNA linear PAT 10-APR-2001
DEFINITION Sequence 4 from Patent WO0121783.
ACCESSION AX100490
VERSION AX100490.1 GI:13619504
KEYWORDS
SOURCE
ORGANISM
Zea mays.
Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 25)
AUTHORS Jiao, S., Habben, J.E. and Niu, X.
TITLE Seed-preferred promoter from maize.
JOURNAL Patent: WO 0121783-A 4 29-MAR-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source
1..25
/organism="Zea mays"
/db_xref="taxon:4577"
BASE COUNT 5 a 8 c 6 g 6 t
ORIGIN
Query Match 69.4%; Score 11.8; DB 6; Length 25;
Best Local Similarity 86.7%; Pred. No. 9e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 TTGCTTCGGCGGAA 16
DB 15 TTGCTTCGGCGCA 1
RESULT 30
LOCUS AR043173 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 57 from patent US 5814453.
ACCESSION AR043173
VERSION AR043173.1 GI:5964181
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 16)
AUTHORS Beck, J. Joseph.
TITLE Detection of fungal pathogens using the polymerase chain reaction
JOURNAL Patent: US 5814453-A 57 29-SEP-1998;
FEATURES
source
1..16
/organism="unknown"
BASE COUNT 1 a 4 c 6 g 5 t
ORIGIN
Query Match 67.1%; Score 11.4; DB 6; Length 16;
Best Local Similarity 92.3%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 GTTGCTTCGGCGG 13
DB 4 GTTGCTTCGGCGG 16
RESULT 31
LOCUS AR043180 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 64 from patent US 5814453.
ACCESSION AR043180
VERSION AR043180.1 GI:5964188
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 16)
AUTHORS Beck, J. Joseph.
TITLE Detection of fungal pathogens using the polymerase chain reaction
JOURNAL Patent: US 5814453-A 64 29-SEP-1998;
FEATURES
source
1..16
/organism="unknown"
BASE COUNT 1 a 5 c 6 g 4 t
ORIGIN

Query Match 67.1%; Score 11.4; DB 6; Length 16;
 Best Local Similarity 92.3%; Pred. No. 1.5e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 13
 |||||
 1 GTTGCTTCGGCGG 13

Db 1 GTTGCTTCGGCGG 13

RESULT 32
 LOCUS AR074673 16 bp DNA linear PAT 28-AUG-2000
 DEFINITION Sequence 57 from patent US 5955274.
 ACCESSION AR074673
 VERSION AR074673.1 GI:10001426
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Ijgon,J.M. and Beck,J.J.
 TITLE Detection of fungal pathogens using the polymerase chain reaction
 JOURNAL Patent: US 5955274-A 57 21-SEP-1999;
 FEATURES Location/Qualifiers
 1..16
 source /organism="unknown"

BASE COUNT 1 a 4 c 6 g 5 t

Query Match 67.1%; Score 11.4; DB 6; Length 16;
 Best Local Similarity 92.3%; Pred. No. 1.5e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 13
 |||||
 4 GTTGCTTCGGCGG 16

Db 4 GTTGCTTCGGCGG 16

RESULT 33
 LOCUS AR074680 16 bp DNA linear PAT 28-AUG-2000
 DEFINITION Sequence 64 from patent US 5955274.
 ACCESSION AR074680
 VERSION AR074680.1 GI:10001433
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Ijgon,J.M. and Beck,J.J.
 TITLE Detection of fungal pathogens using the polymerase chain reaction
 JOURNAL Patent: US 5955274-A 64 21-SEP-1999;
 FEATURES Location/Qualifiers
 1..16
 source /organism="unknown"

BASE COUNT 1 a 5 c 6 g 4 t

Query Match 67.1%; Score 11.4; DB 6; Length 16;
 Best Local Similarity 92.3%; Pred. No. 1.5e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 13
 |||||
 1 GTTGCTTCGGCGG 13

Db 1 GTTGCTTCGGCGG 13

RESULT 34
 LOCUS AR210286 16 bp DNA linear PAT 20-JUN-2002
 DEFINITION Sequence 198 from patent US 6387652.
 ACCESSION AR210286
 VERSION AR210286.1 GI:21512477

KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Haugland,R. and Vesper,S.
 TITLE Method of identifying and quantifying specific fungi and bacteria
 JOURNAL Patent: US 6387652-A 198 14-MAY-2002;
 FEATURES Location/Qualifiers
 1..16
 source /organism="unknown"

BASE COUNT 1 a 5 c 6 g 4 t

Query Match 67.1%; Score 11.4; DB 6; Length 16;
 Best Local Similarity 92.3%; Pred. No. 1.5e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGCTTCGGCGGA 15
 |||||
 1 TGCTTCGGCGGA 13

Db 1 TGCTTCGGCGGA 13

RESULT 35
 LOCUS AX402714 16 bp DNA linear PAT 07-JUN-2002
 DEFINITION Sequence 198 from Patent WO0196612.
 ACCESSION AX402714
 VERSION AX402714.1 GI:21387705
 KEYWORDS
 SOURCE Trichoderma longibrachiatum.
 ORGANISM Trichoderma longibrachiatum.
 REFERENCE 1
 AUTHORS Haugland,R. and Vesper,S.
 TITLE Method of identifying and quantifying specific fungi and bacteria
 JOURNAL Patent: WO 0196612-A 198 20-DEC-2001;
 UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
 FEATURES Location/Qualifiers
 1..16
 source /organism="Trichoderma longibrachiatum"
 /db_xref="taxon:5548"

BASE COUNT 1 a 5 c 6 g 4 t

Query Match 67.1%; Score 11.4; DB 6; Length 16;
 Best Local Similarity 92.3%; Pred. No. 1.5e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGCTTCGGCGGA 15
 |||||
 1 TGCTTCGGCGGA 13

Db 1 TGCTTCGGCGGA 13

RESULT 36
 LOCUS I62258 16 bp DNA linear PAT 07-OCT-1997
 DEFINITION Sequence 812 from patent US 5658780.
 ACCESSION I62258
 VERSION I62258.1 GI:2480206
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Stinchcomb,D.T., Draper,K.G. and McSwiggan,J.
 TITLE Rel a targeted ribozymes
 JOURNAL Patent: US 5658780-A 812 19-AUG-1997;
 FEATURES Location/Qualifiers
 1..16
 source /organism="unknown"

BASE COUNT 7 a 5 c 4 g 0 t

ORIGIN

Query Match 67.1%; Score 11.4; DB 6; Length 16;
Best Local Similarity 92.3%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTGCTTCGGCGG 13
Db 16 GTTGCTTCGGCGG 4

RESULT 37
LOCUS AR110539 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 19 from patent US 6114601.
ACCESSION AR110539
VERSION AR110539.1 GI:12826815
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kikuchi,Y., Kiyokawa,S., Shimada,Y., Ohbayashi,M., Shimada,R. and Okinaka,Y.
TITLE Plant genes encoding flavonoid-3', 5'-hydroxylase
JOURNAL Patent: US 6114601-A 19 05-SEP-2000;
FEATURES
source 1..18
/organism="unknown"

BASE COUNT 4 a 7 c 4 g 1 t 2 others
ORIGIN

Query Match 67.1%; Score 11.4; DB 6; Length 18;
Best Local Similarity 80.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TGGCTTCGGCGGAC 17
Db 18 TGGCTTCGGCGGATC 4

RESULT 38
LOCUS AR151759 18 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 19 from patent US 6232109.
ACCESSION AR151759
VERSION AR151759.1 GI:15117809
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kikuchi,Y., Kiyokawa,S., Shimada,Y., Ohbayashi,M., Shimada,R. and Okinaka,Y.
TITLE Plant genes
JOURNAL Patent: US 6232109-A 19 15-MAY-2001;
FEATURES
source 1..18
/organism="unknown"

BASE COUNT 4 a 7 c 4 g 1 t 2 others
ORIGIN

Query Match 67.1%; Score 11.4; DB 6; Length 18;
Best Local Similarity 80.0%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TGGCTTCGGCGGAC 17
Db 18 TGGCTTCGGCGGATC 4

RESULT 39
AR022121

LOCUS AR022121 21 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 1 from patent US 5792611.
ACCESSION AR022121
VERSION AR022121.1 GI:3976183
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Hamelin,R.C.
TITLE Detection of plant pathogenic fungi
JOURNAL Patent: US 5792611-A 11 11-AUG-1998;
FEATURES
source 1..21
/organism="unknown"

BASE COUNT 0 a 6 c 8 g 7 t
ORIGIN

Query Match 67.1%; Score 11.4; DB 6; Length 21;
Best Local Similarity 92.3%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTGCTTCGGCGG 13
Db 3 GTTGCTTCGGCGG 15

RESULT 40
LOCUS AX057972 21 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 32 from Patent W00075333.
ACCESSION AX057972
VERSION AX057972.1 GI:12310590
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Goshorn,S.C., Graves,S.S., Schultz,J.E., Lin,Y., Sanderson,J.A. and Reno,J.M.
TITLE Streptavidin expressed gene fusions and methods of use thereof
JOURNAL Patent: WO 0075333-A 32 14-DEC-2000;
FEATURES
source 1..21
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide primer"

BASE COUNT 2 a 6 c 9 g 4 t
ORIGIN

Query Match 67.1%; Score 11.4; DB 6; Length 21;
Best Local Similarity 92.3%; Pred. No. 1.5e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTGCTTCGGCGG 13
Db 7 GTTGCTTCGGCGG 19

Search completed: June 7, 2003, 08:50:45
Job time : 400.673 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 07:20:34 ; Search time 434.909 Seconds

(without alignments)
1338.340 Million cell updates/sec

Title: US-10-080-959A-2

Perfect score: 20

Sequence: 1 ttctgcgttcgcaccacagag 20

Scoring table: IDENTITY_NUC

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 521186

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

```

1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pac:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rtd:*
36: em_hcg_man:*
37: em_hcg_vrc:*
38: em_ey:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

```

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	15	75.0	25 6 AR210275	AR210275 Sequence
2	15	75.0	25 6 AX402703	AX402703 Sequence
3	14.4	72.0	24 6 AX164511	AX164511 Sequence
4	13.8	69.0	20 6 AR122463	AR122463 Sequence
5	13.4	67.0	17 6 BD000958	BD000958 Method an
6	13.4	67.0	17 6 BD001387	BD001387 Method an
7	12.8	64.0	24 6 AX288902	AX288902 Sequence
8	12.8	64.0	25 6 AX150973	AX150973 Sequence
9	12.6	63.0	20 6 AX353540	AX353540 Sequence
10	12.6	63.0	21 6 AX039884	AX039884 Sequence
11	12.2	61.0	17 6 AX217169	AX217169 Sequence
12	12.2	61.0	17 6 AX422057	AX422057 Sequence
13	12.2	61.0	22 4 DOGP41402	DOGP41402 Sequence
14	12.2	61.0	22 6 AR003705	AR003705 Sequence
15	12.2	61.0	24 6 AR210196	AR210196 Sequence
16	12.2	61.0	24 6 AX402624	AX402624 Sequence
17	12.2	60.0	17 6 AR040151	AR040151 Sequence
18	12	60.0	21 6 AR166679	AR166679 Sequence
19	12	60.0	23 6 AX268543	AX268543 Sequence
20	11.8	59.0	17 6 AX216558	AX216558 Sequence
21	11.8	59.0	20 6 AX059295	AX059295 Sequence
22	11.8	59.0	22 6 AX467734	AX467734 Sequence
23	11.8	59.0	24 6 AX291474	AX291474 Sequence
24	11.6	58.0	21 6 AR088260	AR088260 Sequence
25	11.6	58.0	21 6 I13019	I13019 Sequence 4
26	11.6	58.0	21 6 I34228	I34228 Sequence 4
27	11.6	58.0	21 12 AB068925	AB068925 Synthetic
28	11.6	58.0	24 6 AX445793	AX445793 Sequence
29	11.6	58.0	25 6 AX116728	AX116728 Sequence
30	11.4	57.0	21 6 AX001122	AX001122 Sequence
31	11.4	57.0	21 6 AX153966	AX153966 Sequence
32	11.4	57.0	24 6 AX32924	AX32924 Synthetic P
33	11.4	57.0	24 6 AX175376	AX175376 Sequence
34	11.4	57.0	25 6 AR090389	AR090389 Sequence
35	11.4	57.0	25 6 AR197424	AR197424 Sequence
36	11.4	57.0	25 6 BD006741	BD006741 Novel pol
37	11.2	56.0	17 6 AX215063	AX215063 Sequence
38	11.2	56.0	17 6 AX422987	AX422987 Sequence
39	11.2	56.0	19 6 AX119996	AX119996 Sequence
40	11.2	56.0	19 6 I25829	I25829 Sequence 9
41	11.2	56.0	19 6 I50992	I50992 Sequence 7
42	11.2	56.0	20 6 AX020042	AX020042 Sequence
43	11.2	56.0	20 6 AX020117	AX020117 Sequence
44	11.2	56.0	20 6 AX296539	AX296539 Sequence
45	11.2	56.0	21 6 I30543	I30543 Sequence 6
46	11.2	56.0	24 6 AX291906	AX291906 Sequence
47	11.2	56.0	25 6 AX150972	AX150972 Sequence
48	11	55.0	20 6 AX249751	AX249751 Sequence
49	11	55.0	20 6 AX250104	AX250104 Sequence
50	11	55.0	20 6 AX294335	AX294335 Sequence
51	11	55.0	20 6 AX406775	AX406775 Sequence
52	11	55.0	20 6 I50807	I50807 Sequence 1
53	11	55.0	20 12 AB068086	AB068086 Synthetic
54	11	55.0	21 6 AR129440	AR129440 Sequence
55	11	55.0	22 6 AR099850	AR099850 Sequence
56	11	55.0	22 6 AX402193	AX402193 Sequence
57	11	55.0	23 6 AR048502	AR048502 Sequence
58	11	55.0	23 6 AR088530	AR088530 Sequence
59	11	55.0	23 6 AX003422	AX003422 Sequence
60	11	55.0	23 6 BD011748	BD011748 795, a no
61	11	55.0	23 23 BD007700	BD007700 795, a no
62	11	55.0	24 6 AR000483	AR000483 Sequence
63	11	55.0	24 6 AX289702	AX289702 Sequence
64	11	55.0	25 6 AX043396	AX043396 Sequence
65	11	55.0	25 6 AX043429	AX043429 Sequence

66	10.8	54.0	15	6	AR055806	AR055806 Sequence	139	10.4	52.0	20	6	E64282	E64282 Polynucleo
67	10.8	54.0	15	6	AR113564	AR113564 Sequence	140	10.4	52.0	21	6	A11444	A11444 Nucleotide
68	10.8	54.0	17	6	AX215924	AX215924 Sequence	141	10.4	52.0	21	6	AR139867	AR139867 Sequence
69	10.8	54.0	17	6	AX422988	AX422988 Sequence	142	10.4	52.0	21	6	AR167511	AR167511 Sequence
70	10.8	54.0	20	6	AR061755	AR061755 Sequence	143	10.4	52.0	21	6	AX096854	AX096854 Sequence
71	10.8	54.0	20	6	AR061996	AR061996 Sequence	144	10.4	52.0	21	6	AX154083	AX154083 Sequence
72	10.8	54.0	20	6	AR067304	AR067304 Sequence	145	10.4	52.0	21	6	AX268953	AX268953 Sequence
73	10.8	54.0	20	6	AR203381	AR203381 Sequence	146	10.4	52.0	22	6	AR084023	AR084023 Sequence
74	10.8	54.0	20	6	AR206230	AR206230 Sequence	147	10.4	52.0	22	6	E15741	E15741 PCR primer
75	10.8	54.0	20	6	AX011279	AX011279 Sequence	148	10.4	52.0	23	6	A47958	A47958 Sequence 25
76	10.8	54.0	20	6	AX293191	AX293191 Sequence	149	10.4	52.0	23	6	AR177003	AR177003 Sequence
77	10.8	54.0	20	6	BD002116	BD002116 Method an	150	10.4	52.0	23	6	AR210193	AR210193 Sequence
78	10.8	54.0	20	6	BD002159	BD002159 Method an	151	10.4	52.0	23	6	AX190966	AX190966 Sequence
79	10.8	54.0	20	6	E39136	E39136 Improved PC	152	10.4	52.0	23	6	AX398144	AX398144 Sequence
80	10.8	54.0	20	12	AB069624	AB069624 Synthetic	153	10.4	52.0	23	8	AF501817	AF501817 Sequence
81	10.8	54.0	21	6	AX096504	AX096504 Sequence	154	10.4	52.0	24	6	A20329	A20329 oligonucleo
82	10.8	54.0	21	6	AX486782	AX486782 Sequence	155	10.4	52.0	24	6	A30124	A30124 Probe E. 7/
83	10.8	54.0	21	6	E31656	E31656 Method for	156	10.4	52.0	24	6	A61975	A61975 Sequence 5
84	10.8	54.0	22	6	E119934	E119934 Sequence 31	157	10.4	52.0	24	6	AX292827	AX292827 Sequence
85	10.8	54.0	22	6	A65306	A65306 Sequence 29	158	10.4	52.0	24	6	AX443648	AX443648 Sequence
86	10.8	54.0	23	6	AR150454	AR150454 Sequence	159	10.4	52.0	24	6	AX445030	AX445030 Sequence
87	10.8	54.0	23	6	AX027161	AX027161 Sequence	160	10.4	52.0	24	6	E37777	E37777 Process for
88	10.8	54.0	24	6	AX288558	AX288558 Sequence	161	10.4	52.0	24	6	A04036	A04036 Synthetic o
89	10.8	54.0	24	6	AX291090	AX291090 Sequence	162	10.4	52.0	25	6	A11445	A11445 Nucleotide
90	10.8	54.0	24	6	AX354440	AX354440 Sequence	163	10.4	52.0	25	6	AR073583	AR073583 Sequence
91	10.8	54.0	24	6	AX445927	AX445927 Sequence	164	10.4	52.0	25	6	AR073586	AR073586 Sequence
92	10.8	54.0	24	6	AR026643	AR026643 Sequence	165	10.4	52.0	25	6	AR173780	AR173780 Sequence
93	10.8	54.0	25	6	AR051187	AR051187 Sequence	166	10.4	52.0	25	6	AX042879	AX042879 Sequence
94	10.6	53.0	18	6	AR095853	AR095853 Sequence	167	10.4	52.0	25	6	AX042938	AX042938 Sequence
95	10.6	53.0	18	6	I25331	I25331 Sequence 11	168	10.4	52.0	25	6	AX043081	AX043081 Sequence
96	10.6	53.0	19	6	AX132156	AX132156 Sequence	169	10.4	52.0	25	6	AX043482	AX043482 Sequence
97	10.6	53.0	19	6	AR067020	AR067020 Sequence	170	10.4	52.0	25	6	AX043594	AX043594 Sequence
98	10.6	53.0	20	6	AR159419	AR159419 Sequence	171	10.4	52.0	25	6	AX043734	AX043734 Sequence
99	10.6	53.0	20	6	AR159419	AR159419 Sequence	172	10.4	52.0	25	6	AX116818	AX116818 Sequence
100	10.6	53.0	20	6	AR159421	AR159421 Sequence	173	10.4	52.0	25	6	AX147633	AX147633 Sequence
101	10.6	53.0	20	6	AR159422	AR159422 Sequence	174	10.4	52.0	25	6	A70258	A70258 Sequence 5
102	10.6	53.0	20	6	AR159422	AR159422 Sequence	175	10.4	52.0	25	6	I70261	I70261 Sequence 8
103	10.6	53.0	20	6	AR166671	AR166671 Sequence	176	10.4	52.0	25	6	AR098711	AR098711 Sequence
104	10.6	53.0	20	6	AX488335	AX488335 Sequence	177	10.2	51.0	15	6	AR204785	AR204785 Sequence
105	10.6	53.0	20	12	AB068206	AB068206 Synthetic	178	10.2	51.0	15	6	E17174	E17174 Pseudomonas
106	10.6	53.0	20	12	AB068529	AB068529 Synthetic	179	10.2	51.0	15	6	I30549	I30549 Sequence 12
107	10.6	53.0	21	6	AR067057	AR067057 Sequence	180	10.2	51.0	15	6	AR057662	AR057662 Sequence
108	10.6	53.0	21	6	AR136529	AR136529 Sequence	181	10.2	51.0	17	6	AR057792	AR057792 Sequence
109	10.6	53.0	21	6	AX095127	AX095127 Sequence	182	10.2	51.0	17	6	AR057800	AR057800 Sequence
110	10.6	53.0	21	6	AX096902	AX096902 Sequence	183	10.2	51.0	17	6	AR115520	AR115520 Sequence
111	10.6	53.0	21	6	AR109794	AR109794 Sequence	184	10.2	51.0	17	6	AR115528	AR115528 Sequence
112	10.6	53.0	24	6	AR109794	AR109794 Sequence	185	10.2	51.0	17	6	AR190535	AR190535 Sequence
113	10.6	53.0	24	6	AX291622	AX291622 Sequence	186	10.2	51.0	17	6	AR190536	AR190536 Sequence
114	10.6	53.0	24	6	AX444464	AX444464 Sequence	187	10.2	51.0	17	6	AR190537	AR190537 Sequence
115	10.6	53.0	24	6	AX445147	AX445147 Sequence	188	10.2	51.0	17	6	AR215062	AR215062 Sequence
116	10.6	53.0	25	6	AX117432	AX117432 Sequence	189	10.2	51.0	17	6	AX423203	AX423203 Sequence
117	10.6	52.0	15	6	AR055807	AR055807 Sequence	190	10.2	51.0	17	6	AR190537	AR190537 Sequence
118	10.4	52.0	15	6	AR113565	AR113565 Sequence	191	10.2	51.0	17	6	AR190537	AR190537 Sequence
119	10.4	52.0	18	6	AX139356	AX139356 Sequence	192	10.2	51.0	17	6	AR190537	AR190537 Sequence
120	10.4	52.0	18	6	AX175528	AX175528 Sequence	193	10.2	51.0	18	6	AR2021351	AR2021351 Sequence
121	10.4	52.0	18	6	I72023	I72023 Sequence 59	194	10.2	51.0	18	6	AX049304	AX049304 Sequence
122	10.4	52.0	19	6	AX130125	AX130125 Sequence	195	10.2	51.0	18	6	BD000638	BD000638 Formation
123	10.4	52.0	19	6	AX130125	AX130125 Sequence	196	10.2	51.0	19	6	AR139456	AR139456 Sequence
124	10.4	52.0	19	6	AX201282	AX201282 Sequence	197	10.2	51.0	19	6	AX119997	AX119997 Sequence
125	10.4	52.0	20	6	A48345	A48345 Sequence 3	198	10.2	51.0	19	6	AX130216	AX130216 Sequence
126	10.4	52.0	20	6	AR074834	AR074834 Sequence	199	10.2	51.0	19	6	AX130217	AX130217 Sequence
127	10.4	52.0	20	6	AR083479	AR083479 Sequence	200	10.2	51.0	19	6	AX132155	AX132155 Sequence
128	10.4	52.0	20	6	AR091960	AR091960 Sequence	201	10.2	51.0	19	6	AX235876	AX235876 Sequence
129	10.4	52.0	20	6	AR136237	AR136237 Sequence	202	10.2	51.0	19	6	AX319459	AX319459 Sequence
130	10.4	52.0	20	6	AR136262	AR136262 Sequence	203	10.2	51.0	19	6	I34832	I34832 Sequence 25
131	10.4	52.0	20	6	AR141373	AR141373 Sequence	204	10.2	51.0	20	6	A94714	A94714 oligonucleo
132	10.4	52.0	20	6	AR162396	AR162396 Sequence	205	10.2	51.0	20	6	AR021350	AR021350 Sequence
133	10.4	52.0	20	6	AX008434	AX008434 Sequence	206	10.2	51.0	20	6	AR036086	AR036086 Sequence
134	10.4	52.0	20	6	AX008469	AX008469 Sequence	207	10.2	51.0	20	6	AR054240	AR054240 Sequence
135	10.4	52.0	20	6	AX297460	AX297460 Sequence	208	10.2	51.0	20	6	AR062684	AR062684 Sequence
136	10.4	52.0	20	6	AX470207	AX470207 Sequence	209	10.2	51.0	20	6	AR100318	AR100318 Sequence
137	10.4	52.0	20	6	AX470241	AX470241 Sequence	210	10.2	51.0	20	6	AR104787	AR104787 Sequence
138	10.4	52.0	20	6	AX470275	AX470275 Sequence	211	10.2	51.0	20	6		

C 212	10.2	51.0	20	6	AR105609	AR105609 Sequence	285	10	50.0	18	6	E02993	E02993 DNA encodin
C 213	10.2	51.0	20	6	AR108791	AR108791 Sequence	C 286	10	50.0	18	12	AB069550	AB069550 Synthetic
C 214	10.2	51.0	20	6	AR120021	AR120021 Sequence	287	10	50.0	19	6	AB2118	AB2118 Sequence 38
C 215	10.2	51.0	20	6	AR120117	AR120117 Sequence	288	10	50.0	19	6	AX001189	AX001189 Sequence
C 216	10.2	51.0	20	6	AR123271	AR123271 Sequence	289	10	50.0	19	6	AX131404	AX131404 Sequence
C 217	10.2	51.0	20	6	AR124879	AR124879 Sequence	290	10	50.0	19	6	AX132366	AX132366 Sequence
C 218	10.2	51.0	20	6	AR124880	AR124880 Sequence	C 291	10	50.0	19	6	AX404210	AX404210 Sequence
C 219	10.2	51.0	20	6	AR141077	AR141077 Sequence	C 292	10	50.0	19	6	E07044	E07044 Partial seq
C 220	10.2	51.0	20	6	AR141973	AR141973 Sequence	293	10	50.0	19	6	E07068	E07068 Probe for H
C 221	10.2	51.0	20	6	AR153734	AR153734 Sequence	294	10	50.0	20	6	A48125	A48125 Sequence 19
C 222	10.2	51.0	20	6	AR164159	AR164159 Sequence	295	10	50.0	20	6	AR124981	AR124981 Sequence
C 223	10.2	51.0	20	6	AR164170	AR164170 Sequence	296	10	50.0	20	6	AR144312	AR144312 Sequence
C 224	10.2	51.0	20	6	AR165317	AR165317 Sequence	297	10	50.0	20	6	AR177170	AR177170 Sequence
C 225	10.2	51.0	20	6	AR165318	AR165318 Sequence	C 298	10	50.0	20	6	AR207157	AR207157 Sequence
C 226	10.2	51.0	20	6	AR179598	AR179598 Sequence	299	10	50.0	20	6	AX191133	AX191133 Sequence
C 227	10.2	51.0	20	6	AR179601	AR179601 Sequence	300	10	50.0	20	6	AX204816	AX204816 Sequence
C 228	10.2	51.0	20	6	AR179602	AR179602 Sequence	301	10	50.0	20	6	AX293511	AX293511 Sequence
C 229	10.2	51.0	20	6	AR179603	AR179603 Sequence	C 302	10	50.0	20	6	AX293842	AX293842 Sequence
C 230	10.2	51.0	20	6	AR179604	AR179604 Sequence	303	10	50.0	20	6	AX295479	AX295479 Sequence
C 231	10.2	51.0	20	6	AR179605	AR179605 Sequence	304	10	50.0	20	6	AX418782	AX418782 Sequence
C 232	10.2	51.0	20	6	AR179606	AR179606 Sequence	305	10	50.0	20	6	AX477121	AX477121 Sequence
C 233	10.2	51.0	20	6	AR179608	AR179608 Sequence	306	10	50.0	20	6	BD011112	BD011112 Human tel
C 234	10.2	51.0	20	6	AR179610	AR179610 Sequence	307	10	50.0	20	6	BD011113	BD011113 Human tel
C 235	10.2	51.0	20	6	AR202054	AR202054 Sequence	308	10	50.0	20	6	E36862	E36862 Human telom
C 236	10.2	51.0	20	6	AR203443	AR203443 Sequence	309	10	50.0	20	6	E36861	E36861 Human telom
C 237	10.2	51.0	20	6	AR212339	AR212339 Sequence	C 310	10	50.0	21	6	AX097110	AX097110 Sequence
C 238	10.2	51.0	20	6	AX164498	AX164498 Sequence	311	10	50.0	21	6	AX356931	AX356931 Sequence
C 239	10.2	51.0	20	6	AX295248	AX295248 Sequence	C 312	10	50.0	21	6	E14731	E14731 Japanese He
C 240	10.2	51.0	20	6	AX297028	AX297028 Sequence	C 313	10	50.0	22	6	AX443510	AX443510 Sequence
C 241	10.2	51.0	20	6	113817	113817 Sequence	C 314	10	50.0	23	6	E59870	E59870 Method for
C 242	10.2	51.0	20	6	120686	120686 Sequence	C 315	10	50.0	24	6	AR078736	AR078736 Sequence
C 243	10.2	51.0	20	6	127034	127034 Sequence	C 316	10	50.0	24	6	AR164356	AR164356 Sequence
C 244	10.2	51.0	20	6	133451	133451 Sequence	C 317	10	50.0	24	6	AR205899	AR205899 Sequence
C 245	10.2	51.0	21	6	AB6795	AB6795 Sequence	318	10	50.0	24	6	AX078711	AX078711 Sequence
C 246	10.2	51.0	21	6	AR094479	AR094479 Sequence	319	10	50.0	24	6	AX288878	AX288878 Sequence
C 247	10.2	51.0	21	6	AR139687	AR139687 Sequence	320	10	50.0	24	6	AX289205	AX289205 Sequence
C 248	10.2	51.0	21	6	AX000973	AX000973 Sequence	C 321	10	50.0	24	6	AX289209	AX289209 Sequence
C 249	10.2	51.0	21	6	AX063587	AX063587 Sequence	C 322	10	50.0	24	6	AX290403	AX290403 Sequence
C 250	10.2	51.0	21	6	AX092721	AX092721 Sequence	C 323	10	50.0	24	6	AX290680	AX290680 Sequence
C 251	10.2	51.0	21	6	E16121	E16121 PCR primer	324	10	50.0	24	6	AX290846	AX290846 Sequence
C 252	10.2	51.0	21	6	150989	150989 Sequence	325	10	50.0	25	6	AR000443	AR000443 Sequence
C 253	10.2	51.0	21	6	150990	150990 Sequence	C 326	10	50.0	25	6	AR164354	AR164354 Sequence
C 254	10.2	51.0	21	6	150991	150991 Sequence	C 327	10	50.0	25	6	AR205897	AR205897 Sequence
C 255	10.2	51.0	22	6	AB0977	AB0977 Sequence	328	10	50.0	25	6	AX043124	AX043124 Sequence
C 256	10.2	51.0	22	6	AB0977	AB0977 Sequence	329	10	50.0	25	6	AX043125	AX043125 Sequence
C 257	10.2	51.0	22	6	AB0977	AB0977 Sequence	C 330	10	50.0	25	6	AX104989	AX104989 Sequence
C 258	10.2	51.0	22	6	AR062627	AR062627 Sequence	C 331	10	50.0	25	6	AX197191	AX197191 Sequence
C 259	10.2	51.0	22	6	AR068108	AR068108 Sequence	332	10	50.0	25	6	AX300144	AX300144 Sequence
C 260	10.2	51.0	22	6	AR104730	AR104730 Sequence	333	10	50.0	25	6	112305	112305 Sequence 10
C 261	10.2	51.0	22	6	AR105552	AR105552 Sequence	334	10	50.0	25	6	115635	115635 Sequence 2
C 262	10.2	51.0	22	6	AR110392	AR110392 Sequence	C 335	10	50.0	25	6	117008	117008 Sequence 19
C 263	10.2	51.0	22	6	AR123214	AR123214 Sequence	336	10	50.0	25	6	126909	126909 Sequence 2
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C 266	10.2	51.0	22	6	133322	133322 Sequence	C 339	9.8	49.0	15	6	138981	138981 Sequence 19
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C 271	10.2	51.0	24	6	AX001467	AX001467 Sequence	C 344	9.8	49.0	17	6	AR158521	AR158521 Sequence
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C 275	10.2	51.0	24	6	AX292395	AX292395 Sequence	C 348	9.8	49.0	17	6	AX215925	AX215925 Sequence
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C 507	9.6	48.0	20	6	AX293220	Sequence	580	9.4	47.0	18	6	AX172305	Sequence
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C 564	9.6	48.0	25	6	AX148271	Sequence	637	9.4	47.0	21	6	A13513	Sequence
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C 571	9.4	47.0	17	6	AX215926	Sequence	644	9.4	47.0	21	6	AR103377	Sequence
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C 574	9.4	47.0	17	6	I52637	Sequence 37	647	9.4	47.0	21	6	AR208941	Sequence
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ALIGNMENTS

11linear PAT 20-JUN-2002

RESULT 1
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DEFINITION Sequence 187 from patent US 6387652
ACCESSION AR210275
VERSION AR210275.1 GI:21512464
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

25 bp DNA
US 6387652

Untranslated.
REFERENCE 1 (bases 1 to 25)
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: US 6387652-A 187 14-MAY-2002;
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location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 2.5e+03;
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QY 6 GTTGGCACTCAGAG 20
Db 1 GTTGGCACTCAGAG 15

RESULT 2
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DEFINITION Sequence 187 from Patent WO0196612.
ACCESSION AX402703
VERSION AX402703.1 GI:21387694
KEYWORDS
SOURCE
ORGANISM

Stachybotrys chartarum.
Stachybotrys chartarum.
Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Stachybotrys.

REFERENCE 1
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 187 20-DEC-2001;
UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)

FEATURES
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/organism="Stachybotrys chartarum"
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Db 1 GTTGGCACTCAGAG 15

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LOCUS AX164511
DEFINITION Sequence 341 from Patent WO0138564.
ACCESSION AX164511
VERSION AX164511.1 GI:14545445
KEYWORDS
SOURCE
ORGANISM

synthetic construct.
synthetic construct.
artificial sequences.

REFERENCE 1 (bases 1 to 24)
AUTHORS Rouleau, G. A., Latrenerie, R. G., Rochefort, D., Cossette, P. and
Ragdale, D.
TITLE Local for idiopathic generalized epilepsy, mutations thereof and
method using same to assess, diagnose, prognosis or treat epilepsy
JOURNAL Patent: WO 0138564-A 341 31-MAY-2001;
MCGill University (CA)
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Db 6 TTGGCTTTATTCACCTCAG 23

RESULT 4
ARI22463/c ARI22463 20 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 17 from patent US 6165728.
ACCESSION ARI22463
VERSION ARI22463.1 GI:14106780
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ward, D.T. and Cowser, L.M.
TITLE Antisense modulation of NCK-2 expression
JOURNAL Patent: US 6165728-A 17 26-DEC-2000;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 7 a 4 c 7 g 2 t
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Query Match 69.0%; Score 13.8; DB 6; Length 20;
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Db 19 TCTGCGTTTGCCAGTCA 3

RESULT 5
BD000958/c BD000958 17 bp RNA linear PAT 31-JAN-2002
LOCUS
DEFINITION Method and reagent for inhibiting viral replication.
ACCESSION BD000958
VERSION BD000958.1 GI:18625517
KEYWORDS UP 2000342285-A/118.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Draper, K.G., Dadykztz, L.W., Macswigen, J.A., Maysejak, D.G.,
Holessek, J.J., and Mamone, A.J.
TITLE Method and reagent for inhibiting viral replication
JOURNAL Patent: JP 2000342285-A 118 12-DEC-2000;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2000342285-A/118
PD 12-DEC-2000
PR 01-MAY-2000 JP 2000132616
PR 11-MAY-1992 US 07/882689, 14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713, 14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823, 14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882886, 14-MAY-1992 US 07/882888 PR
14-MAY-1992 US 07/882889, 14-MAY-1992 US 07/882922 PR
14-MAY-1992 US 07/882922, 14-MAY-1992 US 07/882923 PR
14-MAY-1992 US 07/883849, 14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074, 14-MAY-1992 US 07/884333 PR
14-MAY-1992 US 07/884422, 14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436, 14-MAY-1992 US 07/884521 PR
14-MAY-1992 US 07/923738, 26-AUG-1992 US 07/935855 PR
26-AUG-1992 US 07/936086, 18-SEP-1992 US 07/948359 PR

15-OCT-1992 US 07/963322, 07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130, 07-DEC-1992 US 07/987133 PI
KENNETH G DRAPER, LEC W DADYKZT, JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLESEK, ANTHONY J MAMONE
PC C12N15/09, C12N5/10, C12N7/00, C12N9/22// (C12N5/10, C12R1.91), PC
C12N15/00,
PC C12N5/00, (C12N5/00, C12R1.91)
CC
FH Key Location/Qualifiers
FT source 1..17
/organism="Artificial Sequence".
FEATURES
source 1..17
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 4 a 6 c 4 g 3 t
ORIGIN
Query Match 67.0%; Score 13.4; DB 6; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 GCGTTGCCACTCAG 18
Db 15 GAGTTTGCCACTCAG 1

RESULT 6
BD001387/c BD001387 17 bp RNA linear PAT 31-JAN-2002
LOCUS
DEFINITION Method and reagent for inhibiting viral replication.
ACCESSION BD001387
VERSION BD001387.1 GI:18625946
KEYWORDS UP 2000342286-A/118.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Draper, K.G., Dadykztz, L.W., Macswigen, J.A., Maysejak, D.G.,
Holessek, J.J., and Mamone, A.J.
TITLE Method and reagent for inhibiting viral replication
JOURNAL Patent: JP 2000342286-A 118 12-DEC-2000;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2000342286-A/118
PD 12-DEC-2000
PR 01-MAY-2000 JP 2000132651
PR 11-MAY-1992 US 07/882689, 14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713, 14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823, 14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882886, 14-MAY-1992 US 07/882888 PR
14-MAY-1992 US 07/882889, 14-MAY-1992 US 07/882921 PR
14-MAY-1992 US 07/882922, 14-MAY-1992 US 07/882923 PR
14-MAY-1992 US 07/883849, 14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074, 14-MAY-1992 US 07/884333 PR
14-MAY-1992 US 07/884422, 14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436, 14-MAY-1992 US 07/884521 PR
14-MAY-1992 US 07/923738, 26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086, 18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322, 07-DEC-1992 US 07/987129 PR
15-OCT-1992 US 07/987130, 07-DEC-1992 US 07/987133 PI
KENNETH G DRAPER, LEC W DADYKZT, JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLESEK, ANTHONY J MAMONE
PC C12N15/09, C12N5/10, C12N7/00//A61K38/43, A61K39/125, A61K39/13,
PC C12N15/09, C12N5/10, C12N7/00//A61K38/43, A61K39/125, A61K39/13,
PC A61K39/135, A61K39/21, A61K39/23, A61K39/245, A61K39/29, A61K48/00,
PC A61P1/16,
PC A61P1/14, A61P31/16, A61P31/18, A61P31/22, A61P35/02, C12Q1/68, PC
(C12N15/09, C12R1.93), C12N15/00, C12N5/00, A61K37/48, (C12N15/00, PC
C12R1.93)

PH Key Location/Qualifiers
FT source 1..17 /organism='Artificial Sequence'
ORIGIN

FEATURES
source
1..17
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT
4 a 6 c 4 g 3 t

Query Match
Best Local Similarity 93.3%; Score 13.4; DB 6; Length 17;
Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY
4 GCGTTGGCCACTCAG 18
15 GAGTTGCCACTCAG 1

RESULT 7
AX288902/c 24 bp DNA linear PAT 21-NOV-2001
LOCUS
DEFINITION
Sequence 664 from Patent WO0179548.
ACCESSION
AX288902
VERSION
AX288902.1 GI:17050585
KEYWORDS
synthetic construct.
synthetic construct.
artificial sequences.
ORGANISM

REFERENCE
1
AUTHORS
Barany, F., Zivri, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE
Method of designing addressable array for detection of nucleic acid
JOURNAL
Sequence differences using ligase detection reaction
Patent: WO 0179548-A 664 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)

FEATURES
source
Location/Qualifiers
1..24
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

BASE COUNT
3 a 9 c 6 g 6 t

ORIGIN

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 6; Length 24;
Pred. No. 4.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY
4 GCGTTGGCCACTCAGA 19
16 GGGATTGCCACTCAGA 1

RESULT 8
AX150973/c 25 bp DNA linear PAT 22-JUN-2001
LOCUS
DEFINITION
Sequence 3 from Patent WO0140471.
ACCESSION
AX150973
VERSION
AX150973.1 GI:14533204
KEYWORDS
Mycoplasma mycoides.
Mycoplasma mycoides.
Mycoplasma mycoides.
Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
Entomoplasmataceae.
1 (bases 1 to 25)
Prey, J.J., Nicolet, J.J. and Abdo, E.B.
TITLE
Antigenic protein lppg of Mycoplasma mycoides subsp. (mycoides)
JOURNAL
Patent: WO 0140471-A 3 07-JUN-2001;
Akzo Nobel N.V. (NL)

FEATURES
source
Location/Qualifiers
1..25
/organism="Mycoplasma mycoides"
/db_xref="taxon:2102"

primer_bind 1..25
BASE COUNT 15 a 3 c 5 g 2 t
ORIGIN

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 6; Length 25;
Pred. No. 4.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY
2 TTGGCTTGGCCACTCA 17
23 TTGTTTGGCCACTCA 8

RESULT 9
AX353540 20 bp DNA linear PAT 06-FEB-2002
LOCUS
DEFINITION
Sequence 72 from Patent WO0204636.
ACCESSION
AX353540
VERSION
AX353540.1 GI:18618615
KEYWORDS
synthetic construct.
synthetic construct.
artificial sequences.
ORGANISM

REFERENCE
1
AUTHORS
van Roy, F., Goossens, S., Janssens, B. and Vampoucke, G.
TITLE
Novel g(a) expressed in heart and testis
JOURNAL
Patent: WO 0204636-A 72 17-JAN-2002;
Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)

FEATURES
source
Location/Qualifiers
1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Lower primer FVR2536"

BASE COUNT
6 a 5 c 5 g 4 t

ORIGIN

Query Match
Best Local Similarity 63.0%; Score 12.6; DB 6; Length 20;
Pred. No. 5.2e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY
2 TTGGCTTGGCCACTCAG 20
1 TGGCACTTGACACTCAG 19

RESULT 10
AX039884 21 bp DNA linear PAT 18-NOV-2000
LOCUS
DEFINITION
Sequence 273 from Patent WO0063441.
ACCESSION
AX039884
VERSION
AX039884.1 GI:11229913
KEYWORDS
synthetic construct.
synthetic construct.
artificial sequences.
ORGANISM

REFERENCE
1 (bases 1 to 21)
Herrnstadt, C. and Davis, R.E.
TITLE
Single nucleotide polymorphisms in mitochondrial genes that segregate with Alzheimer's disease
JOURNAL
Patent: WO 0063441-A 273 26-OCT-2000;
MITOXOR (US)

FEATURES
source
Location/Qualifiers
1..21
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PCR primer"

BASE COUNT
5 a 2 c 6 g 8 t

ORIGIN

Query Match
Best Local Similarity 63.0%; Score 12.6; DB 6; Length 21;
Pred. No. 5.2e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;


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Qy 1 TTTGGCTTGCACCTCAGA 19
Db 1 TTTGAGTTTGCTAGGACAGA 19

RESULT 11
AX217169 17 bp mRNA linear PAT 07-SEP-2001
LOCUS Sequence 2611 from Patent WO0159103.
DEFINITION AX217169
ACCESSION AX217169.1 GI:15527230
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE artificial sequences.
AUTHORS 1 (bases 1 to 17)
TITLE Blatt, L., Meswigen, J. and Chowrita, B. M.
JOURNAL Method and reagent for the modulation and diagnosis of cd20 and
PATENT: WO 0159103-A 2611 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
Meswigen, James (US); Chowrita, Bharat M. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Nucleic Acid"

BASE COUNT 2 a 6 c 3 g 6 t
ORIGIN

Query Match 61.0%; Score 12.2; DB 6; Length 17;
Best Local Similarity 82.4%; Pred. No. 8.4e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTGGCTTGCACCTCA 17
Db 1 TCTGCTTGCACCTCA 17

RESULT 12
AX422057 17 bp mRNA linear PAT 18-JUN-2002
LOCUS Sequence 393 from Patent WO0188124.
DEFINITION AX422057
ACCESSION AX422057
VERSION AX422057.1 GI:21525439
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE Jarvis, T., von Carlwiltz, I., Meswigen, J. A., McLaughlin, F. G. and
JOURNAL Randi, A. M.
METHOD: Method and reagent for the inhibition of erg
PATENT: WO 0188124-A 393 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 3 a 5 c 5 g 4 t
ORIGIN

Query Match 61.0%; Score 12.2; DB 6; Length 17;
Best Local Similarity 82.4%; Pred. No. 8.4e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCGTTGCACCTCAGAG 20
Db 17 GCGTTGCACCTCAAG 1

RESULT 13

```

```

DOGPA41402
LOCUS DOGPA41402 20 bp DNA linear MAM 07-MAR-1996
DEFINITION Dog (Clone: CXK 414) primer for STS 414, 3' end.
ACCESSION L24303
VERSION L24303.1 GI:401997
KEYWORDS PCR identification; PCR primer; STS.
SEGMENT 2 of 2
SOURCE Canis familiaris (library: E. Osterander, in pbluescript+) adult
spliced DNA.
ORGANISM Canis familiaris
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
TITLE 1 (bases 1 to 20)
JOURNAL Osterander, E. A., Mapa, F. A., Yee, M. and Rhine, J.
PUBMED One hundred and one new simple sequence repeat-based markers for
the canine genome
Mamm. Genome 6 (3), 192-195 (1995)
95268214
7749226
COMMENT Submitted by:
Fred Hutchinson Cancer Research Center
Transplantation Biology Dept
1124 Columbia; Mailstop M318
Seattle, WA 98104, USA
e-mail: EOsterander@bl.gov
PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
PCR Profile: Denaturation: 94 degrees C for 1.00 minute
Annealing: 55 or 59 degrees C for 0.45 minutes
Polymerization: 74 degrees C for 1.00 minutes
PCR Cycles: 33
Final Extension: 74 degrees C for 5.00 minutes.
FEATURES
source Location/Qualifiers
1..20
/organism="Canis familiaris"
/db_xref="taxon:9615"
/tissue.type="spleen"
/dev stage="adult"
/tissue_lbp="E. Osterander, in pbluescript+"
complement(1..20)

BASE COUNT 4 a 5 c 5 g 6 t
ORIGIN

primer_bind
4 a 5 c 5 g 6 t

Query Match 61.0%; Score 12.2; DB 4; Length 20;
Best Local Similarity 82.4%; Pred. No. 8.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TTTGGCTTGCACCTCAG 18
Db 1 TTTGGCTTGCACCTCAG 17

RESULT 14
AR003705 22 bp DNA linear PAT 04-DEC-1998
LOCUS AR003705
DEFINITION Sequence 2 from patent US 5744368.
ACCESSION AR003705
VERSION AR003705.1 GI:3964964
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 22)
TITLE Goldgaber, D. Y., Schwartzman, A. L. and Eisenberg-Grunberg, M.
JOURNAL Methods for the detection of soluble amyloid beta-protein
PATENT: US 5744368-A 2 28-APR-1998;
FEATURES
source Location/Qualifiers
1..22
/organism="unknown"

BASE COUNT 8 a 2 c 10 g 2 t
ORIGIN

Query Match 61.0%; Score 12.2; DB 6; Length 22;

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Best Local Similarity 82.4%; Pred. No. 8.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTCGCTTGGCACTCA 17
19 TTCCCGTTGGCCCTCA 3

Db

RESULT 15
AR210196 24 bp DNA linear PAT 20-JUN-2002
LOCUS
DEFINITION Sequence 108 from patent US 6387652.
ACCESSION AR210196
VERSION AR210196.1 GI:21512365
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: US 6387652-A 108 14-MAY-2002;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"

BASE COUNT 9 a 4 c 6 g 5 t

ORIGIN

Query Match 61.0%; Score 12.2; DB 6; Length 24;
Best Local Similarity 82.4%; Pred. No. 8.7e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCGTTGGCACTCAG 20
1 GCTGTGCACTCAG 17

Db

RESULT 16
AX402624 24 bp DNA linear PAT 07-JUN-2002
LOCUS
DEFINITION Sequence 108 from Patent W00196612.
ACCESSION AX402624
VERSION AX402624.1 GI:21387615
KEYWORDS
SOURCE nematode egg-parasitic fungus.
ORGANISM Paecilomyces lilacinus
REFERENCE 1
AUTHORS Haugland, R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 108 20-DEC-2001;
FEATURES Location/Qualifiers
source 1..24
/organism="Paecilomyces lilacinus"
/db_xref="taxon:33203"

BASE COUNT 9 a 4 c 6 g 5 t

ORIGIN

Query Match 61.0%; Score 12.2; DB 6; Length 24;
Best Local Similarity 82.4%; Pred. No. 8.7e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCGTTGGCACTCAG 20
1 GCTGTGCACTCAG 17

Db

RESULT 17
AR040151 17 bp DNA linear PAT 29-SEP-1999
LOCUS

DEFINITION Sequence 999 from patent US 5807743.
ACCESSION AR040151
VERSION AR040151.1 GI:5959514
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb, D.T. and McSwigen, J.A.
TITLE Interleukin-2 receptor gamma-chain ribozymes
JOURNAL Patent: US 5807743-A 999 15-SEP-1998;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"

BASE COUNT 3 a 7 c 2 g 5 t

ORIGIN

Query Match 60.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTCCCACTCAGA 19
1 TTCCCACTCAGA 12

Db

RESULT 18
AR166679 21 bp DNA linear PAT 17-OCT-2001
LOCUS
DEFINITION Sequence 29 from patent US 6281346.
ACCESSION AR166679
VERSION AR166679.1 GI:16242091
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Hees, J.W., Caskey, C., Thome, L., Liu, Q. and Phillips, M. Sean.
TITLE Rat ob-receptors and nucleotides encoding them
JOURNAL Patent: US 6281346-A 29 28-AUG-2001;
FEATURES Location/Qualifiers
source 1..21
/organism="unknown"

BASE COUNT 5 a 3 c 7 g 6 t

ORIGIN

Query Match 60.0%; Score 12; DB 6; Length 21;
Best Local Similarity 75.0%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TTTCGCTTGGCACTCAG 20
2 TTTCGCTTGGCACTCAG 21

Db

RESULT 19
AX268543 23 bp DNA linear PAT 29-OCT-2001
LOCUS
DEFINITION Sequence 22 from Patent W00174903.
ACCESSION AX268543
VERSION AX268543.1 GI:16541697
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Welcher, A.A. and Calzone, F.J.
TITLE CD20/ige-receptor like molecules and uses thereof
JOURNAL Patent: WO 0174903-A 22 11-OCT-2001;
FEATURES Location/Qualifiers
source 1..23
/organism="synthetic construct"

BASE COUNT 7 a 7 c 4 g 5 t
 ORIGIN

Query Match 60.0%; Score 12; DB 6; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGGCCTGAG 20
 23 TGGCCTGAG 12

RESULT 20
 AX216558
 LOCUS AX216558 17 bp mRNA linear PAT 07-SEP-2001
 DEFINITION Sequence 2000 from Patent WO0159103.
 ACCESSION AX216558
 VERSION AX216558.1 GI:15526619
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE

1 (bases 1 to 17)
 Blatt, L., Meswigen, J. and Chowrira, B.M.
 Method and reagent for the modulation and diagnosis of cdc20 and
 nogo gene expression
 Patent: WO 0159103-A 2000 16-AUG-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
 Meswigen, James (US); Chowrira, Bharat M. (US)
 Location/Qualifiers

FEATURES
 source
 1. 17
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Nucleic Acid"
 BASE COUNT 3 a 6 c 3 g 5 t
 ORIGIN

Query Match 59.0%; Score 11.8; DB 6; Length 17;
 Best Local Similarity 86.7%; Pred. No. 1.4e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGGCTTGGCCTCA 17
 2 TGGCTTGGCCTCA 16

RESULT 21
 AX059295/c 20 bp DNA linear PAT 17-JAN-2001
 LOCUS AX059295
 DEFINITION Sequence 28 from Patent WO0055325.
 ACCESSION AX059295
 VERSION AX059295.1 GI:12311400
 KEYWORDS
 SOURCE
 ORGANISM

thale cress.
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 20)
 Preuss, D., Copenhaver, G. and Kelch, K.
 Plant chromosome compositions and methods
 Patent: WO 0055325-A 28 21-SEP-2000;
 The University of Chicago (US)
 Location/Qualifiers

FEATURES
 source

1. 20
 /organism="Arabidopsis thaliana"
 /db_xref="taxon:3702"
 BASE COUNT 9 a 4 c 5 g 2 t
 ORIGIN

Query Match 59.0%; Score 11.8; DB 6; Length 20;

Best Local Similarity 86.7%; Pred. No. 1.4e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTTCGTTGGCACT 15
 17 TTTCGTTGGCACT 3

RESULT 22
 AX467734 22 bp DNA linear PAT 16-JUL-2002
 LOCUS AX467734
 DEFINITION Sequence 14 from Patent WO0244332.
 ACCESSION AX467734
 VERSION AX467734.1 GI:21900906
 KEYWORDS
 SOURCE

human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 ORIGINE
 1 Sun, Z., Li, X. and Jay, G.
 Prostate polynucleotides and uses
 Patent: WO 0244332-A 14 06-JUN-2002;
 Origene Technologies Inc. (US)
 Location/Qualifiers

FEATURES
 source
 1. 22
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 6 a 8 c 2 g 5 t
 ORIGIN

Query Match 59.0%; Score 11.8; DB 6; Length 22;
 Best Local Similarity 86.7%; Pred. No. 1.4e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGGCTTGGCCTCA 17
 5 TGGCTTGGCCTCA 19

RESULT 23
 AX291474/c 24 bp DNA linear PAT 21-NOV-2001
 LOCUS AX291474
 DEFINITION Sequence 3236 from Patent WO0179548.
 ACCESSION AX291474
 VERSION AX291474.1 GI:17053157
 KEYWORDS
 SOURCE
 ORGANISM

synthetic construct.
 artificial sequences.
 1 Barany, F., Ziv, M., Gerry, N.P., Favis, R. and Kliman, R.
 Method of designing addressable array for detection of nucleic acid
 sequence differences using ligase detection reaction
 Patent: WO 0179548-A 3236 25-OCT-2001;
 CORNELL RESEARCH FOUNDATION, INC. (US)
 Location/Qualifiers

FEATURES
 source

1. 24
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Hypothetical Probe Sequence"
 BASE COUNT 4 a 7 c 7 g 6 t
 ORIGIN

Query Match 59.0%; Score 11.8; DB 6; Length 24;
 Best Local Similarity 86.7%; Pred. No. 1.4e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CGTTGGCACTGAG 19
 23 CGTTGGCACTGAG 9

TITLE Probes and decoder oligonucleotides
JOURNAL Patent: WO 0216649-A 2248 28-FEB-2002;
Illumina, Inc. (US)
FEATURES Location/Qualifiers
source 1..24
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."
BASE COUNT 8 a 5 c 7 g 4 t
ORIGIN

Query Match 58.0%; Score 11.6; DB 6; Length 24;
Best Local Similarity 77.8%; Pred. No. 1.9e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTGGGTTGGCACTCAG 18
|||
18 TTGGGTTGGCACTCAG 1

RESULT 29
LOCUS AX116728 25 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 1851 from Patent WO0129262.
ACCESSION AX116728
VERSION AX116728.1 GI:14033670
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE 1 (bases 1 to 25)
AUTHORS Picoult-Newburg, L. and Pohl, M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 1851 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES Location/Qualifiers
source 1..25
/organism="synthetic construct"
/db_xref="taxon:32630"
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BASE COUNT 6 a 8 c 4 g 7 t
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Query Match 58.0%; Score 11.6; DB 6; Length 25;
Best Local Similarity 77.8%; Pred. No. 1.9e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TTGGGTTGGCACTCAGA 19
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3 TTGGGTTGGCTCTCTCGA 20

RESULT 30
LOCUS AX001122 21 bp DNA linear PAT 10-MAR-2000
DEFINITION Sequence 1 from Patent WO9901563.
ACCESSION AX001122
VERSION AX001122.1 GI:7241321
KEYWORDS
SOURCE
ORGANISM
unidentified.
unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Goddijn, O. J. and Ohl, S. A.
TITLE PLASMIDS FOR PLANT TRANSFORMATION AND METHOD FOR USING THE SAME
JOURNAL Patent: WO 9901563-A 1 14-JAN-1999;
GODDIJN OSCAR JOHANNA MARIA (NL); OHL STEPHAN ANDREAS (NL)
FEATURES Location/Qualifiers
source 1..21
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 8 a 3 c 7 g 3 t
ORIGIN

Query Match 57.0%; Score 11.4; DB 6; Length 21;
Best Local Similarity 92.3%; Pred. No. 2.4e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGGTTGGCCA 13
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15 TTAGCGTTGGCCA 3

RESULT 31
LOCUS AX153966 21 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 64 from Patent WO0138576.
ACCESSION AX153966
VERSION AX153966.1 GI:14535580
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 21)
AUTHORS Cargill, M., Ireland, J. S. and Lander, E. S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0138576-A 64 31-MAY-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES Location/Qualifiers
source 1..21
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 3 a 2 c 5 g 10 t 1 others
ORIGIN

Query Match 57.0%; Score 11.4; DB 6; Length 21;
Best Local Similarity 80.0%; Pred. No. 2.4e+05;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCGTTGGCACTCAG 18
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3 GGTGTTGCATTCAG 17

RESULT 32
LOCUS A32924 24 bp DNA linear PAT 11-DEC-1996
DEFINITION Synthetic PCR primer FPCRFROR.
ACCESSION A32924
VERSION A32924.1 GI:1926573
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
FEATURES Location/Qualifiers
source 1..24
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 4 a 8 c 4 g 8 t
ORIGIN

Query Match 57.0%; Score 11.4; DB 6; Length 24;
Best Local Similarity 92.3%; Pred. No. 2.4e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGGTTGGCCA 13
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12 TTAGCGTTGGCCA 24

RESULT 33
LOCUS AX175376 24 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 53 from Patent WO0142308.
ACCESSION AX175376

VERSION AX175376.1 GI:14598736
 KEYWORDS
 SOURCE
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 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
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 /db_xref="taxon:32630"
 /note="9c primer"
 BASE COUNT 3 a 9 c 4 g 8 t
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 Best Local Similarity 92.3%; Pred. No. 2.4e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 TTGGCGTTGCCA 13
 Db 10 TTAGCGTTGCCA 22
 RESULT 34
 AR090389/c
 LOCUS AR090389 Sequence 509 from patent US 5994076. 25 bp DNA linear PAT 07-SEP-2000
 DEFINITION
 ACCESSION AR090389
 VERSION AR090389.1 GI:10017144
 KEYWORDS
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 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
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 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 8 TTGGCACTCAGAG 20
 Db 17 TTGCCACTCTGAG 5
 RESULT 35
 AR197424/c
 LOCUS AR197424 Sequence 509 from patent US 6352829. 25 bp DNA linear PAT 20-APR-2002
 DEFINITION
 ACCESSION AR197424
 VERSION AR197424.1 GI:20247273
 KEYWORDS
 SOURCE
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 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
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 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 Db 17 TTGCCACTCTGAG 5

BASE COUNT 7 a 7 c 8 g 3 t
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 Best Local Similarity 92.3%; Pred. No. 2.4e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 8 TTGGCACTCAGAG 20
 Db 17 TTGCCACTCTGAG 5
 RESULT 36
 BD006741/c
 LOCUS BD006741 Novel polypeptide. 25 bp DNA linear PAT 31-JAN-2002
 DEFINITION
 ACCESSION BD006741
 VERSION BD006741.1 GI:18635112
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 1 (bases 1 to 25)
 Ito, Y., Mogi, S., Tanaka, H., Okubo, S. and Ogi, K.
 Novel polypeptide
 Patent: JP 2001029090-A 44 06-FEB-2001;
 TAKEDA CHEMICAL INDUSTRIES LTD
 OS Artificial Sequence
 PN JP 2001029090-A/44
 PD 06-FEB-2001 JP 2000147530
 PF 19-MAY-2000 JP 2000147530
 PR
 PI YASUAKI ITO, SHINICHI MOGI, HIDEYUKI TANAKA, SHOICHI OKUBO, PI
 KAZUHIRO OGI
 PC C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61K45/00, A61K48/00,
 PC A61P1/00,
 PC A61P5/00, A61P9/00, A61P11/00, A61P25/00, A61P25/18, A61P31/00, PC
 A61P35/00,
 PC A61P37/00, C07K14/47, C07K16/18, C12P21/02, G01N33/15, G01N33/50,
 PC G01N33/566//
 PC C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/08, (C12P21/02, PC
 C12R1:91),
 PC (C12N5/10, C12R1:91), (C12P21/08, C12R1:91), C12N15/00, A61K37/02,
 PC C12N5/00,
 PC (C12N5/00, C12R1:91)
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 FT source 1..25
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 Best Local Similarity 92.3%; Pred. No. 2.4e+05;
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 Oy 2 TTGGGTTGCCAC 14
 Db 20 TTGCATTGCCAC 8
 RESULT 37
 AX215063
 LOCUS AX215063 Sequence 505 from Patent WO0159103. 17 bp mRNA linear PAT 07-SEP-2001
 DEFINITION
 ACCESSION AX215063
 VERSION AX215063.1 GI:15525106
 KEYWORDS

SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Blact, L., Mcswigen, J. and Chowira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNML Patent: WO 0159103-A 505 16-AUG-2001;
RHOZYME PHARMACEUTICALS, INC. (US); Blact, Lawrence (US);
Mcswigen, James (US); Chowira, Bharat M. (US)
FEATURES
source
1.17
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 1 a 6 c 3 g 7 t
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Best Local Similarity 81.2%; Pred. No. 3e+05; 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 TTGGCTTGGCCACTC 16
2 TCTGCTTGGCCACTC 17
Db 2 TCTGCTTGGCCACTC 17
RESULT 38
AX422987 17 bp mRNA linear PAT 18-JUN-2002
LOCUS AX422987/c
DEFINITION Sequence 1323 from Patent WO0188124.
ACCESSION AX422987
VERSION AX422987.1 GI:21526369
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis, T., von Carlwitz, I., Mcswigen, J.A., McLaughlin, F.G. and
Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNML Patent: WO 0188124-A 1323 22-NOV-2001.
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
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1.17
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 3 a 4 c 5 g 5 t
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Best Local Similarity 81.2%; Pred. No. 3e+05; 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 4 GCGTTGCCACTCAGA 19
16 GCGTTGCCACTCAGA 1
Db 16 GCGTTGCCACTCAGA 1
RESULT 39
AX119996 19 bp DNA linear PAT 11-MAY-2001
LOCUS AX119996
DEFINITION Sequence 18 from Patent WO0129217.
ACCESSION AX119996
VERSION AX119996.1 GI:114036730
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 19)
AUTHORS Prayaga, S.K., Taupier, R.J. and Bandaru, R.
TITLE Polypeptides and polynucleotides encoding same

JOURNML Patent: WO 0129217-A 18 26-APR-2001;
Curagen Corporation (US)
FEATURES
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1.19
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"
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ORIGIN
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Best Local Similarity 81.2%; Pred. No. 3e+05; 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3 TGCCTTGGCCACTCAG 18
4 TGCCTTGGCCACTCAG 19
Db 4 TGCCTTGGCCACTCAG 19
RESULT 40
I25829/c 19 bp DNA linear PAT 07-OCT-1996
LOCUS I25829
DEFINITION Sequence 9 from patent US 5552390.
ACCESSION I25829
VERSION I25829.1 GI:1605699
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Scholar, E.M. and Iversen, P.L.
TITLE Phosphorothioate inhibitors of metastatic breast cancer
JOURNML Patent: US 5552390-A 9 03-SEP-1996;
FEATURES
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/organism="Unknown"
BASE COUNT 4 a 3 c 9 g 3 t
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Best Local Similarity 81.2%; Pred. No. 3e+05; 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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19 TTGGCTTGGCCACTCA 4
Db 19 TTGGCTTGGCCACTCA 4
Search completed: June 7, 2003, 08:51:04
Job time : 453.909 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 08:19:34 ; Search time 35.8545 Seconds

(without alignments)
145,407 Million cell updates/sec

Title: US-10-080-959A-1

Perfect score: 17
Sequence: 1 gtcgctcggcggggaac 17

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 364338

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	12.4	72.9	15	4	US-09-593-012-195
2	12.4	72.9	21	4	US-09-593-012-191
3	12.4	72.9	21	4	US-09-593-012-194
4	12.4	72.9	21	4	US-09-593-012-203
5	12.4	72.9	22	4	US-09-593-012-31
6	12.2	71.8	20	1	US-08-233-608-24
7	12.2	71.8	20	1	US-08-887-480-24
8	12.2	71.8	20	2	US-08-723-187-24
9	12.2	71.8	20	5	PCT-US95-04712-24
10	12	70.6	17	4	US-09-593-012-120
11	11.8	69.4	20	4	US-09-428-219-70
12	11.4	67.1	16	1	US-08-291-932A-812
13	11.4	67.1	16	1	US-08-887-480-57
14	11.4	67.1	16	1	US-08-887-480-64
15	11.4	67.1	16	2	US-08-722-187-57
16	11.4	67.1	16	2	US-08-722-187-57
17	11.4	67.1	16	2	US-08-722-187-57
18	11.4	67.1	16	4	US-09-593-012-198
19	11.4	67.1	16	5	PCT-US95-04712-57
20	11.4	67.1	16	5	PCT-US95-04712-64
21	11.4	67.1	18	3	US-08-606-505B-19
22	11.4	67.1	18	4	US-09-616-990-19
23	11.4	67.1	21	1	US-08-652-127C-1
24	11.2	65.9	18	2	US-08-358-556A-1
25	11.2	65.9	20	3	US-08-281-203-6
26	11.2	65.9	20	4	US-09-326-186B-146
27	11.2	65.9	25	1	US-08-005-283-4
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98	11.2	65.9	25	1	US-08-005-283-6
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C 102	9.8	57.6	18	4	US-08-616-990-23	Sequence 25, Appl	C 175	9.4	55.3	21	1	US-08-410-779B-63	Sequence 63, Appl
C 103	9.8	57.6	18	4	US-09-679-645-1169	Sequence 1169, Ap	C 176	9.4	55.3	21	2	US-08-474-659-15	Sequence 15, Appl
C 104	9.8	57.6	18	4	US-09-808-126-26	Sequence 26, Appl	C 177	9.4	55.3	21	2	US-08-474-659-15	Sequence 15, Appl
C 105	9.8	57.6	18	4	US-09-803-951-26	Sequence 5, Appl	C 178	9.4	55.3	21	2	US-08-611-977-15	Sequence 15, Appl
C 106	9.8	57.6	19	2	US-08-655-220-5	Sequence 5, Appl	C 179	9.4	55.3	21	5	PCT-US95-04477-62	Sequence 62, Appl
C 107	9.8	57.6	19	2	US-08-618-408B-5	Sequence 9, Appl	C 180	9.4	55.3	21	5	US-08-231-990-44	Sequence 44, Appl
C 108	9.8	57.6	19	3	US-08-811-256A-9	Sequence 9, Appl	C 181	9.4	55.3	22	1	US-08-367-122-44	Sequence 44, Appl
C 109	9.8	57.6	19	3	US-09-931-692-5	Sequence 5, Appl	C 182	9.4	55.3	22	1	US-07-951-715A-86	Sequence 86, Appl
C 110	9.8	57.6	20	1	US-07-932-379A-52	Sequence 52, Appl	C 183	9.4	55.3	22	1	US-08-168-091A-18	Sequence 18, Appl
C 111	9.8	57.6	20	1	US-08-379-295-52	Sequence 52, Appl	C 184	9.4	55.3	22	1	US-08-459-446A-86	Sequence 86, Appl
C 112	9.8	57.6	20	1	US-08-379-296-52	Sequence 52, Appl	C 185	9.4	55.3	22	3	US-08-459-595A-86	Sequence 86, Appl
C 113	9.8	57.6	20	3	US-08-777-266A-65	Sequence 65, Appl	C 186	9.4	55.3	22	3	US-08-459-504B-86	Sequence 86, Appl
C 114	9.8	57.6	20	4	US-09-428-696-12	Sequence 12, Appl	C 187	9.4	55.3	22	3	US-08-912-272-60	Sequence 60, Appl
C 115	9.8	57.6	20	4	US-09-428-219-43	Sequence 43, Appl	C 188	9.4	55.3	22	3	US-08-459-444-86	Sequence 86, Appl
C 116	9.8	57.6	20	4	US-09-593-711A-192	Sequence 192, App	C 189	9.4	55.3	22	4	US-09-547-422-86	Sequence 86, Appl
C 117	9.8	57.6	20	4	US-09-326-186B-65	Sequence 65, Appl	C 190	9.4	55.3	22	4	US-09-547-422-86	Sequence 86, Appl
C 118	9.8	57.6	20	4	US-09-556-031-6	Sequence 6, Appl	C 191	9.4	55.3	22	4	US-09-026-030-60	Sequence 60, Appl
C 119	9.8	57.6	20	4	US-09-456-773-6	Sequence 6, Appl	C 192	9.4	55.3	22	6	5472855-26	Patent No. 5472855
C 120	9.8	57.6	20	5	PCT-US91-11908-4	Sequence 4, Appl	C 193	9.4	55.3	25	1	US-08-062-022-10	Sequence 10, Appl
C 121	9.8	57.6	21	4	US-09-245-248B-71	Sequence 71, Appl	C 194	9.4	55.3	25	1	US-08-495-743-10	Sequence 10, Appl
C 122	9.8	57.6	22	1	US-08-346-774-3	Sequence 3, Appl	C 195	9.4	55.3	25	1	US-08-182-961B-29	Sequence 29, Appl
C 123	9.8	57.6	22	1	US-08-209-172-1	Sequence 1, Appl	C 196	9.4	55.3	25	1	US-08-495-739-10	Sequence 10, Appl
C 124	9.8	57.6	22	1	US-08-717-526-25	Sequence 25, Appl	C 197	9.4	55.3	25	1	US-08-495-741-10	Sequence 10, Appl
C 125	9.8	57.6	22	1	US-08-462-577B-38	Sequence 38, Appl	C 198	9.4	55.3	25	4	US-08-062-023-10	Sequence 10, Appl
C 126	9.8	57.6	22	2	US-09-018-422-1	Sequence 1, Appl	C 199	9.4	55.3	25	4	US-09-493-352A-3	Sequence 3, Appl
C 127	9.8	57.6	22	2	US-08-288-508C-29	Sequence 29, Appl	C 200	9.4	55.3	25	4	US-08-845-739-9	Sequence 29, Appl
C 128	9.8	57.6	22	3	US-08-987-326-24	Sequence 24, Appl	C 201	9.4	55.3	25	4	US-09-007-678B-29	Sequence 29, Appl
C 129	9.8	57.6	22	3	US-09-064-964-13	Sequence 13, Appl	C 202	9.4	55.3	25	4	US-08-991-932A-116	Sequence 116, Appl
C 130	9.8	57.6	22	3	US-08-289-222E-42	Sequence 42, Appl	C 203	9.4	55.3	25	1	US-08-291-932A-35	Sequence 35, Appl
C 131	9.8	57.6	22	3	US-09-105-907-11	Sequence 11, Appl	C 204	9.4	55.3	25	1	US-08-495-741-10	Sequence 10, Appl
C 132	9.8	57.6	22	4	US-09-351-351-1	Sequence 1, Appl	C 205	9.4	55.3	25	1	US-08-291-932A-784	Sequence 784, Appl
C 133	9.8	57.6	22	4	US-09-218-176-21	Sequence 21, Appl	C 206	9.4	55.3	25	1	US-08-291-932A-817	Sequence 817, Appl
C 134	9.8	57.6	22	4	US-09-054-526B-42	Sequence 42, Appl	C 207	9.4	55.3	25	1	US-08-379-081B-274	Sequence 274, Appl
C 135	9.8	57.6	22	4	US-09-183-931-1	Sequence 1, Appl	C 208	9.4	55.3	25	1	US-08-379-078-274	Sequence 274, Appl
C 136	9.8	57.6	22	4	US-08-903-446A-28	Sequence 28, Appl	C 209	9.4	55.3	25	1	US-08-379-078-274	Sequence 274, Appl
C 137	9.8	57.6	22	4	US-09-578-378-11	Sequence 11, Appl	C 210	9.4	55.3	25	1	US-08-005-283-3	Sequence 3, Appl
C 138	9.8	57.6	22	4	US-09-705-160-1	Sequence 1, Appl	C 211	9.4	55.3	25	1	US-08-005-283-3	Sequence 3, Appl
C 139	9.8	57.6	22	4	US-08-863-639A-27	Sequence 27, Appl	C 212	9.4	55.3	25	1	US-08-435-628-1605	Sequence 1605, Appl
C 140	9.8	57.6	24	3	US-09-068-198-5	Sequence 89, Appl	C 213	9.4	55.3	25	1	US-08-951-130-9	Sequence 9, Appl
C 141	9.8	57.6	25	4	US-08-776-971-89	Sequence 89, Appl	C 214	9.4	55.3	25	1	US-08-584-040-1723	Sequence 1723, Appl
C 142	9.8	57.6	25	4	US-09-212-247C-17	Sequence 17, Appl	C 215	9.4	55.3	25	1	US-08-233-608-37	Sequence 37, Appl
C 143	9.8	57.6	25	4	US-09-517-467B-251	Sequence 251, App	C 216	9.4	55.3	25	1	US-08-887-480-37	Sequence 37, Appl
C 144	9.8	57.6	21	1	US-08-135-511-16	Sequence 16, Appl	C 217	9.4	55.3	25	1	US-08-722-187-37	Sequence 37, Appl
C 145	9.8	57.6	21	1	US-08-187-453-16	Sequence 16, Appl	C 218	9.4	55.3	25	1	US-08-722-187-37	Sequence 37, Appl
C 146	9.8	57.6	22	1	US-08-487-135B-10	Sequence 10, Appl	C 219	9.4	55.3	25	1	US-08-584-040-8325	Sequence 8325, Appl
C 147	9.8	57.6	22	2	US-08-915-972A-10	Sequence 10, Appl	C 220	9.4	55.3	25	1	PCT-US95-04713-37	Sequence 37, Appl
C 148	9.8	57.6	22	2	US-09-177-909-10	Sequence 10, Appl	C 221	9.4	55.3	25	1	US-07-722-798A-90	Sequence 90, Appl
C 149	9.8	57.6	22	2	US-08-582-257-11	Sequence 11, Appl	C 222	9.4	55.3	25	1	US-08-704-207-3	Sequence 207, Appl
C 150	9.8	57.6	24	2	US-08-529-190B-26	Sequence 11, Appl	C 223	9.4	55.3	25	1	US-08-500-860A-18	Sequence 18, Appl
C 151	9.8	57.6	24	2	US-08-582-258-11	Sequence 26, Appl	C 224	9.4	55.3	25	1	US-09-228-324A-45	Sequence 45, Appl
C 152	9.8	57.6	24	2	US-08-666-493-29	Sequence 29, Appl	C 225	9.4	55.3	25	1	US-07-722-798A-89	Sequence 89, Appl
C 153	9.8	57.6	24	4	US-09-284-033-9	Sequence 9, Appl	C 226	9.4	55.3	25	1	US-08-435-529-20	Sequence 20, Appl
C 154	9.8	57.6	24	4	US-09-284-033-15	Sequence 15, Appl	C 227	9.4	55.3	25	1	US-08-244-116B-33	Sequence 33, Appl
C 155	9.8	57.6	24	4	US-09-499-884-7	Sequence 7, Appl	C 228	9.4	55.3	25	1	US-08-947-965-44	Sequence 44, Appl
C 156	9.8	57.6	24	4	US-09-710-200-27	Sequence 27, Appl	C 229	9.4	55.3	25	1	US-08-688-376-6	Sequence 36, Appl
C 157	9.8	57.6	25	3	US-08-946-914-53	Sequence 53, Appl	C 230	9.4	55.3	25	1	US-08-379-452-16	Sequence 16, Appl
C 158	9.8	57.6	25	3	US-08-946-914-60	Sequence 60, Appl	C 231	9.4	55.3	25	1	US-08-409-610-36	Sequence 36, Appl
C 159	9.8	57.6	25	3	US-08-911-894-46	Sequence 46, Appl	C 232	9.4	55.3	25	1	US-09-488-671-12	Sequence 12, Appl
C 160	9.8	57.6	25	4	US-09-656-450-53	Sequence 53, Appl	C 233	9.4	55.3	25	1	US-09-110-517-15	Sequence 15, Appl
C 161	9.8	57.6	25	4	US-09-656-450-60	Sequence 60, Appl	C 234	9.4	55.3	25	1	US-09-561-497-77	Sequence 77, Appl
C 162	9.8	57.6	25	4	US-09-656-450-60	Sequence 60, Appl	C 235	9.4	55.3	25	1	US-09-844-634-133	Sequence 133, Appl
C 163	9.8	57.6	14	4	US-09-196-099-8	Sequence 8, Appl	C 236	9.4	55.3	25	1	US-09-844-634-133	Sequence 133, Appl
C 164	9.8	57.6	15	3	US-08-182-968A-307	Sequence 307, App	C 237	9.4	55.3	25	1	US-08-009-253C-69	Sequence 69, Appl
C 165	9.8	57.6	15	3	US-08-774-306A-307	Sequence 307, App	C 238	9.4	55.3	25	1	US-08-242-660-2	Sequence 2, Appl
C 166	9.8	57.6	17	1	US-08-742-023-40	Sequence 40, Appl	C 239	9.4	55.3	25	1	US-08-653-382A-2	Sequence 2, Appl
C 167	9.8	57.6	17	1	US-07-728-220C-13	Sequence 13, Appl	C 240	9.4	55.3	25	1	US-08-928-881-2	Sequence 2, Appl
C 168	9.8	57.6	17	3	US-08-968-505-40	Sequence 40, Appl	C 241	9.4	55.3	25	1	US-08-838-715B-69	Sequence 69, Appl
C 169	9.8	57.6	18	2	US-09-205-922-17	Sequence 17, Appl	C 242	9.4	55.3	25	1	US-09-543-921-2	Sequence 2, Appl
C 170	9.8	57.6	18	2	US-09-205-922-17	Sequence 17, Appl	C 243	9.4	55.3	25	1	US-09-064-935-9	Sequence 9, Appl
C 171	9.8	57.6	18	4	US-08-192-946-29	Sequence 29, Appl	C 244	9.4	55.3	25	1	US-09-266-014-7	Sequence 7, Appl
C 172	9.8	57.6	20	4	US-09-593-711A-193	Sequence 193, App	C 245	9.4	55.3	25	1	US-08-401-512-22	Sequence 22, Appl
C 173	9.4	55.3	20	4	US-09-295-593-28	Sequence 28, Appl	C 246	9.2	54.1	22	1	US-08-153-051B-15	Sequence 15, Appl

C 247	9.2	54.1	22	2	US-08-151-477A-15	Sequence 15, Appl	C 320	9	52.9	23	1	US-08-588-821-28	Sequence 28, Appl
C 248	9.2	54.1	22	4	US-09-014-241-2	Sequence 10, Appl	C 321	9	52.9	23	1	US-08-915-214-28	Sequence 28, Appl
C 249	9.2	54.1	22	4	US-09-226-012-10	Sequence 10, Appl	C 322	9	52.9	23	2	US-09-005-532-28	Sequence 28, Appl
C 250	9.2	54.1	22	4	US-09-226-012-72	Sequence 72, Appl	C 323	9	52.9	23	2	US-08-859-998-861	Sequence 861, App
C 251	9.2	54.1	23	1	US-08-293-086-22	Sequence 22, Appl	C 324	9	52.9	23	4	US-09-225-928-861	Sequence 861, App
C 252	9.2	54.1	23	3	US-08-500-860A-20	Sequence 20, Appl	C 325	9	52.9	23	4	US-09-632-098-24	Sequence 24, Appl
C 253	9.2	54.1	23	3	US-09-147-550-5	Sequence 5, Appl	C 326	9	52.9	24	1	US-08-010-099-3	Sequence 3, Appl
C 254	9.2	54.1	23	3	US-09-429-499-3	Sequence 3, Appl	C 327	9	52.9	24	1	US-08-010-099-7	Sequence 7, Appl
C 255	9.2	54.1	23	4	US-08-943-731-423	Sequence 423, App	C 328	9	52.9	24	1	US-08-010-099-10	Sequence 10, Appl
C 256	9.2	54.1	23	4	US-09-557-917-5	Sequence 5, Appl	C 329	9	52.9	24	1	US-08-010-099-13	Sequence 13, Appl
C 257	9.2	54.1	23	4	US-09-302-681-102	Sequence 102, App	C 330	9	52.9	24	1	US-08-010-099-19	Sequence 19, Appl
C 258	9.2	54.1	24	1	US-08-451-240-40	Sequence 40, App	C 331	9	52.9	24	1	US-08-448-716-3	Sequence 3, Appl
C 259	9.2	54.1	24	1	US-08-477-872B-23	Sequence 23, Appl	C 332	9	52.9	24	1	US-08-448-716-7	Sequence 7, Appl
C 260	9.2	54.1	24	1	US-08-538-875-50	Sequence 50, Appl	C 333	9	52.9	24	1	US-08-448-716-10	Sequence 10, Appl
C 261	9.2	54.1	24	1	US-08-472-81A-23	Sequence 23, Appl	C 334	9	52.9	24	1	US-08-448-716-13	Sequence 13, Appl
C 262	9.2	54.1	24	1	US-08-465-590-68	Sequence 68, Appl	C 335	9	52.9	24	1	US-08-448-716-19	Sequence 19, Appl
C 263	9.2	54.1	24	2	US-08-526-583-24	Sequence 24, Appl	C 336	9	52.9	24	2	US-08-690-734A-64	Sequence 64, Appl
C 264	9.2	54.1	24	2	US-08-470-846A-36	Sequence 36, Appl	C 337	9	52.9	24	3	US-08-859-998-11302	Sequence 1302, Ap
C 265	9.2	54.1	24	2	US-08-477-989B-23	Sequence 23, Appl	C 338	9	52.9	24	3	US-08-742-185-64	Sequence 64, Appl
C 266	9.2	54.1	24	4	US-09-150-900-38	Sequence 38, Appl	C 339	9	52.9	24	4	US-08-974-549A-472	Sequence 472, App
C 267	9.2	54.1	24	4	US-08-711-417C-68	Sequence 68, Appl	C 340	9	52.9	24	4	US-09-304-186-3	Sequence 3, Appl
C 268	9.2	54.1	24	5	PCT-US93-08743-68	Sequence 68, Appl	C 341	9	52.9	24	4	US-09-304-186-7	Sequence 7, Appl
C 269	9.2	54.1	24	5	PCT-US94-12591-40	Sequence 40, Appl	C 342	9	52.9	24	4	US-09-304-186-10	Sequence 10, Appl
C 270	9.2	54.1	25	1	US-07-901-707-32	Sequence 32, Appl	C 343	9	52.9	24	4	US-09-304-186-13	Sequence 13, Appl
C 271	9.2	54.1	25	1	US-07-988-430-32	Sequence 32, Appl	C 344	9	52.9	24	4	US-09-304-186-19	Sequence 19, Appl
C 272	9.2	54.1	25	1	US-08-425-336-32	Sequence 32, Appl	C 345	9	52.9	24	4	US-08-672-213-44	Sequence 44, Appl
C 273	9.2	54.1	25	1	US-08-468-113B-32	Sequence 32, Appl	C 346	9	52.9	24	4	US-09-521-617-1	Sequence 1, Appl
C 274	9.2	54.1	25	1	US-08-477-848B-32	Sequence 32, Appl	C 347	9	52.9	24	4	US-09-521-617-1	Sequence 1, Appl
C 275	9.2	54.1	25	2	US-08-646-360-32	Sequence 32, Appl	C 348	9	52.9	24	4	US-09-325-928-1302	Sequence 1302, Ap
C 276	9.2	54.1	25	2	US-08-117-952-566	Sequence 566, App	C 349	9	52.9	25	2	US-08-260-546-12	Sequence 12, Appl
C 277	9.2	54.1	25	3	US-09-038-741-3	Sequence 3, Appl	C 350	9	52.9	25	2	US-08-324-003A-3	Sequence 3, Appl
C 278	9.2	54.1	25	3	US-08-839-765-32	Sequence 32, Appl	C 351	9	52.9	25	2	US-08-810-856-11	Sequence 11, Appl
C 279	9.2	54.1	25	3	US-09-136-389-32	Sequence 32, Appl	C 352	9	52.9	25	3	US-08-859-998-777	Sequence 777, App
C 280	9.2	54.1	25	4	US-08-943-731-379	Sequence 379, App	C 353	9	52.9	25	3	US-08-913-374-5	Sequence 5, Appl
C 281	9.2	54.1	25	4	US-09-537-696-3	Sequence 3, Appl	C 354	9	52.9	25	3	US-09-124-758-22	Sequence 22, Appl
C 282	9.2	54.1	25	4	US-09-537-696-4	Sequence 4, Appl	C 355	9	52.9	25	4	US-09-225-928-777	Sequence 777, App
C 283	9.2	54.1	25	4	US-09-610-838-32	Sequence 32, Appl	C 356	9	52.9	25	4	US-09-438-068B-10	Sequence 10, Appl
C 284	9.2	54.1	25	5	US-09-569-572C-2	Sequence 2, Appl	C 357	9	52.9	25	4	US-09-538-709-324	Sequence 324, App
C 285	9.2	54.1	25	5	PCT-US92-09487-32	Sequence 32, Appl	C 358	9	52.9	25	4	US-09-538-709-456	Sequence 456, App
C 286	9.2	54.1	16	2	US-08-282-197C-4	Sequence 4, Appl	C 359	8.8	51.8	14	2	US-08-687-551-14	Sequence 14, Appl
C 287	9	52.9	17	1	US-08-373-124A-1387	Sequence 1387, Ap	C 360	8.8	51.8	15	1	US-08-333-030-27	Sequence 27, Appl
C 288	9	52.9	18	3	US-09-071-710-21	Sequence 21, Appl	C 361	8.8	51.8	15	1	US-09-063-667-18	Sequence 18, Appl
C 289	9	52.9	18	4	US-09-825-397-21	Sequence 21, Appl	C 362	8.8	51.8	15	1	US-08-241-372-10	Sequence 10, Appl
C 290	9	52.9	18	4	US-08-651-155B-2	Sequence 2, Appl	C 363	8.8	51.8	15	1	US-08-291-932A-190	Sequence 190, Appl
C 291	9	52.9	18	4	US-09-545-686-32	Sequence 32, Appl	C 364	8.8	51.8	15	1	US-08-110-294A-4	Sequence 4, Appl
C 292	9	52.9	19	1	US-08-717-526-38	Sequence 38, Appl	C 365	8.8	51.8	15	2	US-08-585-684B-2259	Sequence 2259, Ap
C 293	9	52.9	19	2	US-08-671-978A-22	Sequence 22, Appl	C 366	8.8	51.8	15	2	US-09-038-073-2259	Sequence 2259, Ap
C 294	9	52.9	19	2	US-08-671-978A-24	Sequence 24, Appl	C 367	8.8	51.8	15	4	US-09-180-437-146	Sequence 146, App
C 295	9	52.9	20	1	US-08-525-697-12	Sequence 12, Appl	C 368	8.8	51.8	15	4	US-09-081-646-415	Sequence 415, App
C 296	9	52.9	20	2	US-08-743-637B-229	Sequence 229, App	C 369	8.8	51.8	15	4	PCT-US95-05420-10	Sequence 10, Appl
C 297	9	52.9	20	3	US-09-287-796-105	Sequence 105, App	C 370	8.8	51.8	17	1	US-08-286-856C-14	Sequence 14, Appl
C 298	9	52.9	20	3	US-09-288-461-27	Sequence 27, Appl	C 371	8.8	51.8	18	1	US-08-717-526-45	Sequence 45, Appl
C 299	9	52.9	20	4	US-09-130-616-105	Sequence 105, App	C 372	8.8	51.8	18	1	US-08-742-023-28	Sequence 28, Appl
C 300	9	52.9	20	4	US-09-489-869-34	Sequence 34, Appl	C 373	8.8	51.8	18	2	US-08-533-306A-13	Sequence 13, Appl
C 301	9	52.9	20	4	US-09-488-295-17	Sequence 17, Appl	C 374	8.8	51.8	18	2	US-08-742-923A-13	Sequence 22, Appl
C 302	9	52.9	20	4	US-09-705-299-71	Sequence 71, Appl	C 375	8.8	51.8	18	2	US-08-912-129B-42	Sequence 42, Appl
C 303	9	52.9	21	1	US-07-718-274A-48	Sequence 48, Appl	C 376	8.8	51.8	18	2	US-09-256-496-79	Sequence 79, Appl
C 304	9	52.9	21	1	US-08-149-106-48	Sequence 48, Appl	C 377	8.8	51.8	18	2	US-09-144-579-11	Sequence 11, Appl
C 305	9	52.9	21	1	US-08-280-757B-9	Sequence 9, Appl	C 378	8.8	51.8	18	3	US-08-968-505-28	Sequence 28, Appl
C 306	9	52.9	21	1	US-08-280-757B-9	Sequence 9, Appl	C 379	8.8	51.8	18	3	US-09-387-341-209	Sequence 209, App
C 307	9	52.9	21	2	US-07-662-764D-5	Sequence 5, Appl	C 380	8.8	51.8	18	3	US-08-102-863-5	Sequence 5, Appl
C 308	9	52.9	21	2	US-08-101-624-9	Sequence 9, Appl	C 381	8.8	51.8	18	4	US-09-387-341-213	Sequence 213, App
C 309	9	52.9	21	3	US-08-479-744A-9	Sequence 9, Appl	C 382	8.8	51.8	20	1	US-08-448-716-3	Sequence 3, Appl
C 310	9	52.9	21	3	US-08-280-757B-9	Sequence 9, Appl	C 383	8.8	51.8	20	1	US-08-448-716-7	Sequence 7, Appl
C 311	9	52.9	21	3	US-08-611-587-28	Sequence 28, Appl	C 384	8.8	51.8	20	1	US-08-448-716-10	Sequence 10, Appl
C 312	9	52.9	21	4	US-09-168-406A-39	Sequence 39, Appl	C 385	8.8	51.8	20	1	US-08-448-716-13	Sequence 13, Appl
C 313	9	52.9	21	4	US-09-471-016-11	Sequence 11, Appl	C 386	8.8	51.8	20	1	US-08-448-716-19	Sequence 19, Appl
C 314	9	52.9	21	4	US-09-249-697A-13	Sequence 13, Appl	C 387	8.8	51.8	20	1	US-08-448-716-19	Sequence 19, Appl
C 315	9	52.9	21	4	US-09-363-316B-13	Sequence 13, Appl	C 388	8.8	51.8	20	1	US-08-448-716-19	Sequence 19, Appl
C 316	9	52.9	22	1	US-08-233-030-50	Sequence 50, Appl	C 389	8.8	51.8	20	1	US-08-448-716-19	Sequence 19, Appl
C 317	9	52.9	22	4	US-09-302-812-35	Sequence 35, Appl	C 390	8.8	51.8	20	1	US-08-448-716-19	Sequence 19, Appl
C 318	9	52.9	22	4	US-09-511-477-35	Sequence 35, Appl	C 391	8.8	51.8	20	1	US-08-448-716-19	Sequence 19, Appl
C 319	9	52.9	22	4	US-09-511-507-35	Sequence 35, Appl	C 392	8.8	51.8	20	1	US-08-531-556-113	Sequence 113, App

C 393	8.8	51.8	20	2	US-08-448-386A-13	Sequence 13, Appl
C 394	8.8	51.8	20	2	US-08-117-952-417	Sequence 417, Appl
C 395	8.8	51.8	20	2	US-08-690-734A-5	Sequence 5, Appl1
C 396	8.8	51.8	20	2	US-08-690-734A-76	Sequence 76, Appl
C 397	8.8	51.8	20	2	US-08-483-528B-77	Sequence 77, Appl
C 398	8.8	51.8	20	2	US-08-483-528B-78	Sequence 78, Appl
C 399	8.8	51.8	20	2	US-08-483-528B-78	Sequence 78, Appl
C 400	8.8	51.8	20	2	US-08-566-806A-18	Sequence 23, Appl
C 401	8.8	51.8	20	2	US-08-031-538-23	Sequence 45, Appl
C 402	8.8	51.8	20	3	US-08-589-939-45	Sequence 5, Appl1
C 403	8.8	51.8	20	3	US-08-742-185-5	Sequence 76, Appl
C 404	8.8	51.8	20	3	US-08-816-426-13	Sequence 13, Appl
C 405	8.8	51.8	20	3	US-08-673-799C-77	Sequence 77, Appl
C 406	8.8	51.8	20	3	US-08-673-799C-78	Sequence 78, Appl
C 407	8.8	51.8	20	3	US-09-143-214-18	Sequence 18, Appl
C 408	8.8	51.8	20	3	US-09-418-640-67	Sequence 67, Appl
C 409	8.8	51.8	20	4	US-09-433-699-24	Sequence 24, Appl
C 410	8.8	51.8	20	4	US-09-488-857B-16	Sequence 16, Appl
C 411	8.8	51.8	20	4	US-09-593-711A-158	Sequence 158, Appl
C 412	8.8	51.8	20	4	US-09-484-617-99	Sequence 99, Appl
C 413	8.8	51.8	20	4	US-09-393-529-17	Sequence 17, Appl
C 414	8.8	51.8	20	4	US-09-506-073-18	Sequence 18, Appl
C 415	8.8	51.8	20	4	US-09-393-385B-77	Sequence 77, Appl
C 416	8.8	51.8	20	4	US-09-393-385B-78	Sequence 78, Appl
C 417	8.8	51.8	20	4	US-09-658-679A-25	Sequence 25, Appl
C 418	8.8	51.8	20	4	US-09-853-768-50	Sequence 50, Appl
C 419	8.8	51.8	20	5	PCT-US92-10885-5	Sequence 5, Appl1
C 420	8.8	51.8	20	5	PCT-US93-12161-13	Sequence 13, Appl
C 421	8.8	51.8	20	5	PCT-US95-07111A-18	Sequence 18, Appl
C 422	8.8	51.8	21	1	US-08-663-325-119	Sequence 119, Appl
C 423	8.8	51.8	21	1	US-08-653-740-22	Sequence 22, Appl
C 424	8.8	51.8	21	2	US-09-073-594-22	Sequence 22, Appl
C 425	8.8	51.8	21	3	US-09-975-925-22	Sequence 22, Appl
C 426	8.8	51.8	21	3	US-08-881-037-104	Sequence 104, Appl
C 427	8.8	51.8	21	3	US-09-358-685-3	Sequence 3, Appl1
C 428	8.8	51.8	21	4	US-09-338-308-3	Sequence 3, Appl1
C 429	8.8	51.8	21	4	US-07-974-409C-350	Sequence 350, Appl
C 430	8.8	51.8	21	4	US-09-553-331-27	Sequence 27, Appl
C 431	8.8	51.8	22	1	US-08-242-680-5	Sequence 5, Appl1
C 432	8.8	51.8	22	1	US-07-977-284A-152	Sequence 152, Appl
C 433	8.8	51.8	22	1	US-08-717-526-21	Sequence 21, Appl
C 434	8.8	51.8	22	1	US-08-482-577B-33	Sequence 33, Appl
C 435	8.8	51.8	22	2	US-08-482-577B-37	Sequence 37, Appl
C 436	8.8	51.8	22	2	US-08-653-382A-5	Sequence 5, Appl1
C 437	8.8	51.8	22	2	US-08-256-426B-152	Sequence 152, Appl
C 438	8.8	51.8	22	2	US-08-751-305-29	Sequence 29, Appl
C 439	8.8	51.8	22	2	US-08-288-508C-24	Sequence 24, Appl
C 440	8.8	51.8	22	2	US-08-288-508C-28	Sequence 28, Appl
C 441	8.8	51.8	22	3	US-08-289-222E-37	Sequence 37, Appl
C 442	8.8	51.8	22	3	US-08-289-222E-41	Sequence 41, Appl
C 443	8.8	51.8	22	4	US-09-218-176-16	Sequence 16, Appl
C 444	8.8	51.8	22	4	US-09-218-176-20	Sequence 20, Appl
C 445	8.8	51.8	22	4	US-09-054-526B-37	Sequence 37, Appl
C 446	8.8	51.8	22	4	US-09-054-526B-41	Sequence 41, Appl
C 447	8.8	51.8	22	4	US-09-269-136B-12	Sequence 12, Appl
C 448	8.8	51.8	22	4	US-08-903-446A-17	Sequence 17, Appl
C 449	8.8	51.8	23	3	US-08-881-784-33	Sequence 33, Appl
C 450	8.8	51.8	23	3	US-09-292-768-34	Sequence 34, Appl
C 451	8.8	51.8	24	1	US-08-464-148-7	Sequence 7, Appl1
C 452	8.8	51.8	24	1	US-08-385-500-7	Sequence 7, Appl1
C 453	8.8	51.8	24	1	US-08-846-784-7	Sequence 7, Appl1
C 454	8.8	51.8	24	3	US-08-569-221A-3	Sequence 47, Appl
C 455	8.8	51.8	24	3	US-09-245-041-47	Sequence 47, Appl
C 456	8.8	51.8	24	5	PCT-US93-07603-10	Sequence 10, Appl
C 457	8.8	51.8	25	1	US-08-279-625A-2	Sequence 2, Appl1
C 458	8.8	51.8	25	1	US-08-321-071A-2	Sequence 2, Appl1
C 459	8.8	51.8	25	1	US-08-465-590-46	Sequence 46, Appl
C 460	8.8	51.8	25	4	US-08-954-395A-21	Sequence 21, Appl
C 461	8.8	51.8	25	4	US-08-711-417C-46	Sequence 46, Appl
C 462	8.8	51.8	25	4	US-08-853-774-19	Sequence 19, Appl
C 463	8.8	51.8	25	4	US-08-934-386-40	Sequence 40, Appl
C 464	8.8	51.8	25	4	US-09-538-709-147	Sequence 147, Appl
C 465	8.8	51.8	25	4	US-09-538-709-148	Sequence 148, Appl
C 466	8.8	51.8	25	5	PCT-US93-08743-46	Sequence 46, Appl
C 467	8.8	51.8	15	1	US-08-311-486C-267	Sequence 267, Appl
C 468	8.8	50.6	16	1	US-09-102-528-15	Sequence 15, Appl
C 469	8.8	50.6	17	2	US-08-308-818-10	Sequence 10, Appl
C 470	8.8	50.6	17	4	US-09-383-630-10	Sequence 10, Appl
C 471	8.8	50.6	17	4	US-08-584-040-2463	Sequence 2463, Appl
C 472	8.8	50.6	17	4	US-08-584-040-2464	Sequence 2464, Appl
C 473	8.8	50.6	17	4	US-08-679-645-727	Sequence 727, Appl
C 474	8.8	50.6	17	4	US-08-679-645-728	Sequence 728, Appl
C 475	8.8	50.6	17	4	US-09-457-066-7	Sequence 7, Appl1
C 476	8.8	50.6	18	2	US-08-505-317-13	Sequence 13, Appl
C 477	8.8	50.6	18	2	US-09-197-318-29	Sequence 29, Appl
C 478	8.8	50.6	18	3	US-09-205-921-9	Sequence 9, Appl1
C 479	8.8	50.6	18	3	US-08-798-269-13	Sequence 13, Appl
C 480	8.8	50.6	18	3	US-09-213-719-88	Sequence 88, Appl
C 481	8.8	50.6	18	4	US-09-102-528-17	Sequence 17, Appl
C 482	8.8	50.6	18	4	US-09-230-637-12	Sequence 12, Appl
C 483	8.8	50.6	18	4	US-09-496-694B-99	Sequence 99, Appl
C 484	8.8	50.6	18	4	US-09-055-210-13	Sequence 13, Appl
C 485	8.8	50.6	19	1	US-08-438-500-4	Sequence 4, Appl1
C 486	8.8	50.6	19	1	US-08-477-442-4	Sequence 4, Appl1
C 487	8.8	50.6	19	3	US-08-945-086-27	Sequence 27, Appl
C 488	8.8	50.6	19	4	US-09-258-967-11	Sequence 11, Appl
C 489	8.8	50.6	19	4	US-09-110-517-31	Sequence 31, Appl
C 490	8.8	50.6	19	5	PCT-US94-05910-4	Sequence 4, Appl1
C 491	8.8	50.6	20	1	US-08-129-719-13	Sequence 13, Appl
C 492	8.8	50.6	20	1	US-08-306-871-13	Sequence 13, Appl
C 493	8.8	50.6	20	1	US-08-569-959-13	Sequence 13, Appl
C 494	8.8	50.6	20	1	US-08-484-192-73	Sequence 73, Appl
C 495	8.8	50.6	20	1	US-08-484-192-128	Sequence 128, Appl
C 496	8.8	50.6	20	2	US-08-470-426B-9	Sequence 9, Appl1
C 497	8.8	50.6	20	2	US-08-775-009-27	Sequence 27, Appl
C 498	8.8	50.6	20	3	US-09-058-489-63	Sequence 63, Appl
C 499	8.8	50.6	20	3	US-08-855-588A-28	Sequence 28, Appl
C 500	8.8	50.6	20	4	US-09-444-051-70	Sequence 55, Appl
C 501	8.8	50.6	20	4	US-09-147-933-55	Sequence 55, Appl
C 502	8.8	50.6	20	4	US-09-258-967-10	Sequence 10, Appl
C 503	8.8	50.6	20	4	US-09-619-444-28	Sequence 28, Appl
C 504	8.8	50.6	20	4	US-09-657-042A-23	Sequence 23, Appl
C 505	8.8	50.6	20	4	US-09-462-606-23	Sequence 23, Appl
C 506	8.8	50.6	20	4	US-09-470-443-112	Sequence 112, Appl
C 507	8.8	50.6	21	1	US-08-433-126A-441	Sequence 441, Appl
C 508	8.8	50.6	21	1	US-08-477-877B-10	Sequence 10, Appl
C 509	8.8	50.6	21	1	US-08-433-124A-241	Sequence 241, Appl
C 510	8.8	50.6	21	1	US-08-410-779B-62	Sequence 62, Appl
C 511	8.8	50.6	21	1	US-08-410-779B-63	Sequence 63, Appl
C 512	8.8	50.6	21	1	US-08-410-779B-80	Sequence 80, Appl
C 513	8.8	50.6	21	1	US-08-410-779B-81	Sequence 81, Appl
C 514	8.8	50.6	21	1	US-08-410-779B-89	Sequence 89, Appl
C 515	8.8	50.6	21	1	US-08-410-779B-104	Sequence 104, Appl
C 516	8.8	50.6	21	1	US-08-472-281A-10	Sequence 10, Appl
C 517	8.8	50.6	21	1	US-08-488-470A-71	Sequence 71, Appl
C 518	8.8	50.6	21	1	US-08-484-552A-71	Sequence 71, Appl
C 519	8.8	50.6	21	1	US-08-484-552A-127	Sequence 127, Appl
C 520	8.8	50.6	21	1	US-08-410-779B-134	Sequence 134, Appl
C 521	8.8	50.6	21	1	US-08-410-779B-135	Sequence 135, Appl
C 522	8.8	50.6	21	2	US-08-472-281A-10	Sequence 10, Appl
C 523	8.8	50.6	21	2	US-08-488-470A-71	Sequence 71, Appl
C 524	8.8	50.6	21	2	US-08-484-552A-71	Sequence 71, Appl
C 525	8.8	50.6	21	2	US-08-477-989B-10	Sequence 10, Appl
C 526	8.8	50.6	21	2	US-09-009-913-47	Sequence 47, Appl
C 527	8.8	50.6	21	3	US-08-855-583A-7	Sequence 7, Appl1
C 528	8.8	50.6	21	3	US-08-976-413A-241	Sequence 241, Appl
C 529	8.8	50.6	21	4	US-09-619-915-2	Sequence 2, Appl1
C 530	8.8	50.6	21	4	US-09-359-915-2	Sequence 2, Appl1
C 531	8.8	50.6	21	4	US-09-702-330-7	Sequence 7, Appl1
C 532	8.8	50.6	21	4	US-09-702-330-7	Sequence 7, Appl1
C 533	8.8	50.6	21	5	PCT-US94-05085A-39	Sequence 39, Appl
C 534	8.8	50.6	21	5	PCT-US94-05085A-39	Sequence 39, Appl
C 535	8.8	50.6	21	5	PCT-US95-04477-62	Sequence 62, Appl
C 536	8.8	50.6	21	5	PCT-US95-04477-63	Sequence 63, Appl
C 537	8.8	50.6	21	5	PCT-US95-04477-63	Sequence 63, Appl
C 538	8.8	50.6	21	5	PCT-US95-04477-80	Sequence 80, Appl

C 539	8.6	50.6	21	5	PCT-US95-04477-81	Sequence 81, Appl	C 612	8.4	49.4	12	5	PCT-US95-04712-55	Sequence 55, Appl
C 540	8.6	50.6	21	5	PCT-US95-04477-88	Sequence 88, Appl	C 613	8.4	49.4	13	3	US-09-289-750-7	Sequence 7, Appl
C 541	8.6	50.6	21	5	PCT-US95-04477-89	Sequence 89, Appl	C 614	8.4	49.4	13	4	US-09-503-859-7	Sequence 7, Appl
C 542	8.6	50.6	21	5	PCT-US95-04477-104	Sequence 104, Appl	C 615	8.4	49.4	14	4	US-09-177-917-2	Sequence 2, Appl
C 543	8.6	50.6	21	5	PCT-US95-04477-105	Sequence 105, Appl	C 616	8.4	49.4	14	4	US-08-535-249-41	Sequence 41, Appl
C 544	8.6	50.6	21	5	PCT-US95-04477-126	Sequence 126, Appl	C 617	8.4	49.4	15	1	US-08-311-486C-265	Sequence 265, Appl
C 545	8.6	50.6	21	5	PCT-US95-04477-127	Sequence 127, Appl	C 618	8.4	49.4	15	1	US-08-311-486C-266	Sequence 266, Appl
C 546	8.6	50.6	21	5	PCT-US95-04477-134	Sequence 134, Appl	C 619	8.4	49.4	15	1	US-08-887-480-73	Sequence 73, Appl
C 547	8.6	50.6	21	5	PCT-US95-04477-135	Sequence 135, Appl	C 620	8.4	49.4	15	2	US-08-585-684B-1915	Sequence 1815, Ap
C 548	8.6	50.6	21	5	PCT-US96-06059-241	Sequence 241, Appl	C 621	8.4	49.4	15	2	US-08-585-684B-2135	Sequence 2135, Ap
C 549	8.6	50.6	21	5	PCT-US96-09472-71	Sequence 71, Appl	C 622	8.4	49.4	15	3	US-08-721-187-73	Sequence 73, Appl
C 550	8.6	50.6	22	1	US-08-105-761-6	Sequence 6, Appl	C 623	8.4	49.4	15	3	US-08-781-891-65	Sequence 65, Appl
C 551	8.6	50.6	22	1	US-07-722-798A-110	Sequence 110, Appl	C 624	8.4	49.4	15	4	US-09-038-073-1815	Sequence 1815, Ap
C 552	8.6	50.6	22	1	US-08-379-081B-113	Sequence 113, Appl	C 625	8.4	49.4	15	4	US-09-038-073-2135	Sequence 2135, Ap
C 553	8.6	50.6	22	1	US-08-379-081B-114	Sequence 114, Appl	C 626	8.4	49.4	15	5	PCT-US95-04712-73	Sequence 73, Appl
C 554	8.6	50.6	22	1	US-08-379-081B-115	Sequence 115, Appl	C 627	8.4	49.4	16	1	US-08-402-964-11	Sequence 11, Appl
C 555	8.6	50.6	22	1	US-08-379-078-314	Sequence 314, Appl	C 628	8.4	49.4	16	1	US-08-402-964-15	Sequence 15, Appl
C 556	8.6	50.6	22	1	US-08-486-408-15	Sequence 15, Appl	C 629	8.4	49.4	17	4	US-09-356-118A-10	Sequence 10, Appl
C 557	8.6	50.6	22	1	US-08-371-001-3	Sequence 365, Appl	C 630	8.4	49.4	17	4	US-09-324-867-54	Sequence 54, Appl
C 558	8.6	50.6	22	2	US-08-173-489C-365	Sequence 15, Appl	C 631	8.4	49.4	17	4	US-08-679-645-80	Sequence 70, Appl
C 559	8.6	50.6	22	2	US-08-975-570-15	Sequence 15, Appl	C 632	8.4	49.4	17	4	US-08-679-645-80	Sequence 80, Appl
C 560	8.6	50.6	22	2	US-08-837-302-1	Sequence 1, Appl	C 633	8.4	49.4	17	4	US-08-679-645-82	Sequence 82, Appl
C 561	8.6	50.6	22	3	US-08-798-668-1	Sequence 1, Appl	C 634	8.4	49.4	17	4	US-08-679-645-84	Sequence 84, Appl
C 562	8.6	50.6	22	3	US-08-765-332-60	Sequence 60, Appl	C 635	8.4	49.4	18	1	US-09-549-804C-3	Sequence 3, Appl
C 563	8.6	50.6	22	4	US-08-855-825-1	Sequence 1, Appl	C 636	8.4	49.4	18	1	US-08-585-684B-2683	Sequence 14, Appl
C 564	8.6	50.6	22	4	US-09-448-894-60	Sequence 60, Appl	C 637	8.4	49.4	18	2	US-09-183-212-42	Sequence 42, Appl
C 565	8.6	50.6	22	4	US-09-608-285A-18	Sequence 18, Appl	C 638	8.4	49.4	18	3	US-09-183-212-42	Sequence 42, Appl
C 566	8.6	50.6	22	4	US-09-395-345-28	Sequence 28, Appl	C 639	8.4	49.4	18	3	US-09-183-212-42	Sequence 42, Appl
C 567	8.6	50.6	22	4	US-09-350-836B-18	Sequence 18, Appl	C 640	8.4	49.4	18	3	US-09-280-409-53	Sequence 53, Appl
C 568	8.6	50.6	22	4	US-09-462-569B-3	Sequence 3, Appl	C 641	8.4	49.4	18	4	US-09-038-073-2683	Sequence 2683, Ap
C 569	8.6	50.6	22	4	US-09-370-265-18	Sequence 18, Appl	C 642	8.4	49.4	18	4	US-09-071-433-72	Sequence 72, Appl
C 570	8.6	50.6	22	5	PCT-US92-11076-6	Sequence 6, Appl	C 643	8.4	49.4	18	4	US-09-632-580A-12	Sequence 12, Appl
C 571	8.6	50.6	22	5	PCT-US96-00331-3	Sequence 3, Appl	C 644	8.4	49.4	18	4	US-09-187-946-11	Sequence 11, Appl
C 572	8.6	50.6	23	1	US-08-105-761-12	Sequence 12, Appl	C 645	8.4	49.4	18	4	US-09-215-221-47	Sequence 47, Appl
C 573	8.6	50.6	23	1	US-08-466-033-120	Sequence 120, Appl	C 646	8.4	49.4	18	4	US-09-393-529-18	Sequence 18, Appl
C 574	8.6	50.6	23	1	US-08-444-733-120	Sequence 120, Appl	C 647	8.4	49.4	18	4	US-08-679-645-565	Sequence 565, Appl
C 575	8.6	50.6	23	2	US-08-464-134-120	Sequence 120, Appl	C 648	8.4	49.4	18	4	US-08-679-645-1167	Sequence 1167, Ap
C 576	8.6	50.6	23	2	US-08-461-361-120	Sequence 120, Appl	C 649	8.4	49.4	18	4	PCT-US93-05240-11	Sequence 40, Appl
C 577	8.6	50.6	23	2	US-08-485-910-120	Sequence 120, Appl	C 650	8.4	49.4	18	5	US-09-150-999-9	Sequence 9, Appl
C 578	8.6	50.6	23	2	US-08-825-426-8	Sequence 8, Appl	C 651	8.4	49.4	19	4	US-07-841-652-4	Sequence 4, Appl
C 579	8.6	50.6	23	4	US-08-943-731-600	Sequence 600, Appl	C 652	8.4	49.4	20	1	US-07-992-723A-28	Sequence 28, Appl
C 580	8.6	50.6	23	4	US-09-538-709-23	Sequence 23, Appl	C 653	8.4	49.4	20	1	US-07-992-728C-28	Sequence 28, Appl
C 581	8.6	50.6	23	5	PCT-US92-11076-12	Sequence 12, Appl	C 654	8.4	49.4	20	1	US-07-799-828C-28	Sequence 28, Appl
C 582	8.6	50.6	24	1	US-07-722-798A-109	Sequence 109, Appl	C 655	8.4	49.4	20	1	US-07-722-798A-98	Sequence 98, Appl
C 583	8.6	50.6	24	1	US-08-703-809-7	Sequence 7, Appl	C 656	8.4	49.4	20	1	US-07-681-1703B-28	Sequence 28, Appl
C 584	8.6	50.6	24	1	US-08-703-809-7	Sequence 7, Appl	C 657	8.4	49.4	20	1	US-08-031-147A-4	Sequence 4, Appl
C 585	8.6	50.6	24	1	US-08-545-562A-27	Sequence 27, Appl	C 658	8.4	49.4	20	1	US-08-255-892-55	Sequence 55, Appl
C 586	8.6	50.6	24	2	US-08-703-807-7	Sequence 7, Appl	C 659	8.4	49.4	20	1	US-08-293-237-1	Sequence 1, Appl
C 587	8.6	50.6	24	2	US-08-747-108A-7	Sequence 7, Appl	C 660	8.4	49.4	20	1	US-08-525-697-8	Sequence 8, Appl
C 588	8.6	50.6	24	3	US-09-211-631-7	Sequence 7, Appl	C 661	8.4	49.4	20	1	US-08-715-142-11	Sequence 11, Appl
C 589	8.6	50.6	24	3	US-09-265-628-7	Sequence 7, Appl	C 662	8.4	49.4	20	2	US-08-651-692-1	Sequence 1, Appl
C 590	8.6	50.6	24	4	US-09-518-386B-16	Sequence 16, Appl	C 663	8.4	49.4	20	2	US-07-952-277A-28	Sequence 28, Appl
C 591	8.6	50.6	24	4	US-09-673-018-6	Sequence 6, Appl	C 664	8.4	49.4	20	2	US-08-468-819-25	Sequence 25, Appl
C 592	8.6	50.6	25	2	US-08-902-623-21	Sequence 21, Appl	C 665	8.4	49.4	20	2	US-08-468-819-29	Sequence 29, Appl
C 593	8.6	50.6	25	2	US-08-983-108-14	Sequence 14, Appl	C 666	8.4	49.4	20	2	US-08-610-629A-13	Sequence 13, Appl
C 594	8.6	50.6	25	4	US-09-230-288-15	Sequence 15, Appl	C 667	8.4	49.4	20	2	US-08-845-998-10	Sequence 10, Appl
C 595	8.6	50.6	25	4	US-09-147-751-11	Sequence 11, Appl	C 668	8.4	49.4	20	2	US-07-965-285-17	Sequence 17, Appl
C 596	8.6	50.6	25	4	US-09-177-650-50	Sequence 50, Appl	C 669	8.4	49.4	20	2	US-08-474-450A-40	Sequence 40, Appl
C 597	8.6	50.6	25	4	US-09-350-969-65	Sequence 65, Appl	C 670	8.4	49.4	20	2	US-08-363-124A-7	Sequence 7, Appl
C 598	8.6	50.6	25	4	US-09-538-709-391	Sequence 391, Appl	C 671	8.4	49.4	20	2	US-08-487-231-17	Sequence 17, Appl
C 599	8.6	50.6	25	4	US-09-538-709-492	Sequence 492, Appl	C 672	8.4	49.4	20	2	US-08-911-434A-11	Sequence 11, Appl
C 600	8.6	49.4	12	1	US-08-441-887A-41	Sequence 41, Appl	C 673	8.4	49.4	20	2	US-08-487-231-17	Sequence 17, Appl
C 601	8.4	49.4	12	1	US-08-887-480-55	Sequence 55, Appl	C 674	8.4	49.4	20	2	US-08-487-231-17	Sequence 17, Appl
C 602	8.4	49.4	12	2	US-08-547-214-47	Sequence 47, Appl	C 675	8.4	49.4	20	2	US-08-487-231-17	Sequence 17, Appl
C 603	8.4	49.4	12	2	US-08-722-187-55	Sequence 55, Appl	C 676	8.4	49.4	20	2	US-08-487-231-17	Sequence 17, Appl
C 604	8.4	49.4	12	3	US-08-663-823B-47	Sequence 47, Appl	C 677	8.4	49.4	20	3	US-08-665-259-66	Sequence 66, Appl
C 605	8.4	49.4	12	3	US-08-942-406-47	Sequence 47, Appl	C 678	8.4	49.4	20	3	US-08-827-036A-11	Sequence 11, Appl
C 606	8.4	49.4	12	4	US-09-322-617-47	Sequence 47, Appl	C 679	8.4	49.4	20	3	US-09-249-730-148	Sequence 148, Appl
C 607	8.4	49.4	12	4	US-09-281-418-119	Sequence 119, Appl	C 680	8.4	49.4	20	3	US-09-249-730-148	Sequence 148, Appl
C 608	8.4	49.4	12	4	US-09-203-231B-51	Sequence 51, Appl	C 681	8.4	49.4	20	3	US-09-418-641-15	Sequence 15, Appl
C 609	8.4	49.4	12	4	US-09-751-561-47	Sequence 47, Appl	C 682	8.4	49.4	20	3	US-09-206-537-10	Sequence 10, Appl
C 610	8.4	49.4	12	4	US-09-724-385-47	Sequence 47, Appl	C 683	8.4	49.4	20	3	US-09-287-796-13	Sequence 13, Appl
C 611	8.4	49.4	12	4	US-09-757-528-47	Sequence 47, Appl	C 684	8.4	49.4	20	3		

C 685	8.4	49.4	20	3	US-09-429-323-32	Sequence 32, Appl	C 758	8.4	49.4	24	4	US-09-043-303-16	Sequence 16, Appl
C 686	8.4	49.4	20	3	US-08-481-341-12	Sequence 12, Appl	759	8.4	49.4	24	4	US-09-349-677-14	Sequence 14, Appl
C 687	8.4	49.4	20	4	US-09-490-692-17	Sequence 17, Appl	C 760	8.4	49.4	24	4	US-09-430-503-11	Sequence 11, Appl
C 688	8.4	49.4	20	4	US-08-983-466-71	Sequence 71, Appl	761	8.4	49.4	24	4	US-09-455-960-17	Sequence 17, Appl
C 689	8.4	49.4	20	4	US-09-201-912-17	Sequence 17, Appl	C 762	8.4	49.4	24	5	PCT-US95-12624-3	Sequence 3, Appl
C 690	8.4	49.4	20	4	US-09-103-875-117	Sequence 117, Appl	763	8.4	49.4	25	1	US-08-261-206A-11	Sequence 7, Appl
C 691	8.4	49.4	20	4	US-09-130-616-13	Sequence 13, Appl	764	8.4	49.4	25	1	US-08-147-000B-7	Sequence 7, Appl
C 692	8.4	49.4	20	4	US-09-487-445-42	Sequence 42, Appl	C 765	8.4	49.4	25	2	US-08-338-530A-9	Sequence 9, Appl
C 693	8.4	49.4	20	4	US-08-797-358B-4	Sequence 4, Appl	766	8.4	49.4	25	3	US-08-737-607-14	Sequence 28, Appl
C 694	8.4	49.4	20	4	US-09-430-854-10	Sequence 10, Appl	C 767	8.4	49.4	25	3	US-08-589-028-33	Sequence 33, Appl
C 695	8.4	49.4	20	4	US-09-031-006-12	Sequence 12, Appl	C 768	8.4	49.4	25	3	US-08-784-582-33	Sequence 6, Appl
C 696	8.4	49.4	20	4	US-09-031-017-8	Sequence 8, Appl	C 769	8.4	49.4	25	4	US-09-077-205-6	Sequence 9, Appl
C 697	8.4	49.4	20	4	US-09-593-589-19	Sequence 19, Appl	770	8.4	49.4	25	4	US-09-267-384-9	Sequence 21, Appl
C 698	8.4	49.4	20	4	US-09-593-589-20	Sequence 20, Appl	C 771	8.4	49.4	25	4	US-08-785-271-33	Sequence 33, Appl
C 699	8.4	49.4	20	4	US-09-593-589-21	Sequence 21, Appl	772	8.4	49.4	25	4	US-08-943-731-410	Sequence 410, Appl
C 700	8.4	49.4	20	4	US-09-982-649B-74	Sequence 74, Appl	C 773	8.4	49.4	25	4	US-09-538-709-459	Sequence 459, Appl
C 701	8.4	49.4	20	4	US-09-082-649B-78	Sequence 84, Appl	C 774	8.4	49.4	25	5	PCT-US93-10106-19	Sequence 19, Appl
C 702	8.4	49.4	20	4	US-09-657-474-84	Sequence 84, Appl	C 775	8.4	49.4	25	5	US-08-259-148A-47	Sequence 47, Appl
C 703	8.4	49.4	20	4	US-09-792-594-43	Sequence 43, Appl	776	8.2	48.2	14	2	US-07-876-941A-63	Sequence 63, Appl
C 704	8.4	49.4	20	4	US-09-517-467B-29	Sequence 29, Appl	777	8.2	48.2	15	1	US-08-182-968A-333	Sequence 33, Appl
C 705	8.4	49.4	20	4	US-09-300-008B-39	Sequence 39, Appl	778	8.2	48.2	15	1	US-08-183-968A-382	Sequence 20, Appl
C 706	8.4	49.4	20	4	PCT-US94-00265-12	Sequence 12, Appl	779	8.2	48.2	15	1	US-08-795-788-20	Sequence 414, Appl
C 707	8.4	49.4	20	5	PCT-US94-02471-4	Sequence 4, Appl	780	8.2	48.2	15	2	US-08-292-620A-114	Sequence 332, Appl
C 708	8.4	49.4	21	1	US-07-697-421-4	Sequence 4, Appl	C 781	8.2	48.2	15	2	US-08-774-306A-382	Sequence 1746, Appl
C 709	8.4	49.4	21	1	US-07-714-687-45	Sequence 45, Appl	782	8.2	48.2	15	2	US-08-053-451B-132	Sequence 132, Appl
C 710	8.4	49.4	21	1	US-08-283-203-4	Sequence 4, Appl	C 783	8.2	48.2	15	2	US-08-585-684B-1746	Sequence 1746, Appl
C 711	8.4	49.4	21	1	US-08-224-391-45	Sequence 45, Appl	C 784	8.2	48.2	15	2	US-08-053-451B-132	Sequence 132, Appl
C 712	8.4	49.4	21	1	US-08-484-304-45	Sequence 45, Appl	C 785	8.2	48.2	15	3	US-08-271-882B-30	Sequence 30, Appl
C 713	8.4	49.4	21	1	US-08-351-413-5	Sequence 5, Appl	786	8.2	48.2	15	3	US-08-147-592A-29	Sequence 29, Appl
C 714	8.4	49.4	21	1	US-08-606-322-2	Sequence 2, Appl	C 787	8.2	48.2	15	3	US-08-147-592A-32	Sequence 32, Appl
C 715	8.4	49.4	21	1	US-08-624-545-21	Sequence 21, Appl	788	8.2	48.2	15	3	US-09-064-156A-333	Sequence 333, Appl
C 716	8.4	49.4	21	2	US-09-025-583-5	Sequence 5, Appl	C 789	8.2	48.2	15	3	US-09-064-156A-333	Sequence 333, Appl
C 717	8.4	49.4	21	2	US-08-804-439A-54	Sequence 54, Appl	790	8.2	48.2	15	3	US-09-071-845-414	Sequence 414, Appl
C 718	8.4	49.4	21	3	US-08-720-329-54	Sequence 54, Appl	C 791	8.2	48.2	15	3	US-09-038-077-1746	Sequence 1746, Appl
C 719	8.4	49.4	21	3	US-08-390-353A-16	Sequence 16, Appl	C 792	8.2	48.2	15	4	US-08-292-694A-29	Sequence 29, Appl
C 720	8.4	49.4	21	3	US-08-640-906-15	Sequence 15, Appl	C 793	8.2	48.2	15	4	US-08-292-694A-32	Sequence 32, Appl
C 721	8.4	49.4	21	3	US-09-407-818-37	Sequence 37, Appl	794	8.2	48.2	15	4	PCT-US93-93242-70	Sequence 70, Appl
C 722	8.4	49.4	21	4	US-09-462-975-7	Sequence 7, Appl	C 795	8.2	48.2	15	5	US-08-291-932A-779	Sequence 779, Appl
C 723	8.4	49.4	21	4	US-09-395-936-15	Sequence 15, Appl	C 796	8.2	48.2	16	1	US-08-412-376-6	Sequence 6, Appl
C 724	8.4	49.4	21	4	US-09-338-174A-73	Sequence 73, Appl	C 797	8.2	48.2	16	2	US-08-641-291A-70	Sequence 70, Appl
C 725	8.4	49.4	21	6	5219727-36	Patent No. 5219727	C 798	8.2	48.2	16	3	US-08-641-291A-70	Sequence 26, Appl
C 726	8.4	49.4	22	1	US-07-722-798A-97	Sequence 126, Appl	C 799	8.2	48.2	16	3	US-09-050-159-45	Sequence 45, Appl
C 727	8.4	49.4	22	1	US-08-105-483-126	Sequence 3, Appl	C 800	8.2	48.2	16	4	US-09-481-810-26	Sequence 26, Appl
C 728	8.4	49.4	22	1	US-07-714-687-39	Sequence 39, Appl	C 801	8.2	48.2	16	4	US-09-290-577-30	Sequence 30, Appl
C 729	8.4	49.4	22	1	US-08-224-391-39	Sequence 39, Appl	C 802	8.2	48.2	16	4	US-09-290-577-30	Sequence 30, Appl
C 730	8.4	49.4	22	1	US-08-484-304-39	Sequence 126, Appl	C 803	8.2	48.2	16	4	US-08-435-628-1603	Sequence 1603, Appl
C 731	8.4	49.4	22	1	US-08-709-209-126	Sequence 126, Appl	C 804	8.2	48.2	17	1	US-08-373-124A-1603	Sequence 1603, Appl
C 732	8.4	49.4	22	1	US-08-458-101-126	Sequence 14, Appl	C 805	8.2	48.2	17	1	US-08-663-927-28	Sequence 28, Appl
C 733	8.4	49.4	22	2	US-09-028-361A-14	Sequence 14, Appl	C 806	8.2	48.2	17	3	US-09-050-159-45	Sequence 45, Appl
C 734	8.4	49.4	22	2	US-09-357-072-4	Sequence 4, Appl	C 807	8.2	48.2	17	4	US-09-050-159-45	Sequence 28, Appl
C 735	8.4	49.4	22	3	US-08-538-666-14	Sequence 14, Appl	C 808	8.2	48.2	17	4	US-09-481-810-28	Sequence 28, Appl
C 736	8.4	49.4	22	3	US-08-538-666-20	Sequence 20, Appl	C 809	8.2	48.2	17	4	US-08-246-489-25	Sequence 25, Appl
C 737	8.4	49.4	22	3	US-09-193-562D-36	Sequence 36, Appl	C 810	8.2	48.2	17	4	US-09-268-140-22	Sequence 22, Appl
C 738	8.4	49.4	22	4	US-09-593-012-37	Sequence 37, Appl	C 811	8.2	48.2	17	4	US-08-584-040-2465	Sequence 2465, Appl
C 739	8.4	49.4	22	4	US-08-278-089A-10	Sequence 10, Appl	C 812	8.2	48.2	17	4	US-08-584-040-2465	Sequence 1722, Appl
C 740	8.4	49.4	23	1	US-08-668-753-26	Sequence 26, Appl	C 813	8.2	48.2	17	4	US-09-593-012-57	Sequence 57, Appl
C 741	8.4	49.4	23	2	US-08-859-998-1163	Sequence 1163, Appl	C 814	8.2	48.2	17	4	US-09-593-012-57	Sequence 60, Appl
C 742	8.4	49.4	23	2	US-08-859-998-1163	Sequence 16, Appl	C 815	8.2	48.2	17	4	US-08-313-185-5	Sequence 185, Appl
C 743	8.4	49.4	23	2	US-08-838-957A-10	Sequence 10, Appl	C 816	8.2	48.2	17	4	US-08-313-185-5	Sequence 1133, Appl
C 744	8.4	49.4	23	3	US-08-938-548B-16	Sequence 16, Appl	C 817	8.2	48.2	17	6	5486454-17	Patent No. 5486454
C 745	8.4	49.4	23	3	US-08-781-891-148	Sequence 148, Appl	C 818	8.2	48.2	18	1	US-08-221-285-15	Sequence 15, Appl
C 746	8.4	49.4	23	3	US-08-810-712-21	Sequence 21, Appl	C 819	8.2	48.2	18	1	US-08-376-157B-14	Sequence 14, Appl
C 747	8.4	49.4	23	3	US-08-810-712-21	Sequence 21, Appl	C 820	8.2	48.2	18	1	US-08-380-038-34	Sequence 34, Appl
C 748	8.4	49.4	23	4	US-09-282-147-23	Sequence 23, Appl	C 821	8.2	48.2	18	1	US-08-380-038-34	Sequence 1133, Appl
C 749	8.4	49.4	23	4	US-08-939-093A-16	Sequence 16, Appl	C 822	8.2	48.2	18	1	US-08-313-185-5	Sequence 5, Appl
C 750	8.4	49.4	23	4	US-09-268-347-41	Sequence 41, Appl	C 823	8.2	48.2	18	2	US-08-627-254C-12	Sequence 12, Appl
C 751	8.4	49.4	23	4	US-09-225-928-1163	Sequence 1163, Appl	C 824	8.2	48.2	18	2	US-08-385-335A-28	Sequence 28, Appl
C 752	8.4	49.4	24	2	US-08-890-980-42	Sequence 42, Appl	C 825	8.2	48.2	18	2	US-09-161-015-28	Sequence 28, Appl
C 753	8.4	49.4	24	3	US-08-890-979-42	Sequence 42, Appl	C 826	8.2	48.2	18	2	US-09-205-860-11	Sequence 11, Appl
C 754	8.4	49.4	24	3	US-08-483-316-3	Sequence 3, Appl	C 827	8.2	48.2	18	2	US-09-205-860-13	Sequence 13, Appl
C 755	8.4	49.4	24	3	US-09-023-894-42	Sequence 42, Appl	C 828	8.2	48.2	18	2	US-08-466-860-55	Sequence 55, Appl
C 756	8.4	49.4	24	4	US-09-067-800-14	Sequence 14, Appl	C 829	8.2	48.2	18	2	US-08-466-860-55	Sequence 7, Appl
C 757	8.4	49.4	24	4	US-09-031-626-42	Sequence 42, Appl	C 830	8.2	48.2	18	3	US-08-811-177A-7	Sequence 7, Appl

C 831	8.2	48.2	18	3	US-09-344-520-44	Sequence 44, Appl
C 832	8.2	48.2	18	3	US-09-344-579-20	Sequence 20, Appl
C 833	8.2	48.2	18	3	US-08-867-881A-7	Sequence 7, Appl1
C 834	8.2	48.2	18	3	US-09-443-212-25	Sequence 25, Appl
C 835	8.2	48.2	18	3	US-09-143-212-45	Sequence 45, Appl
C 836	8.2	48.2	18	3	US-08-472-040A-55	Sequence 55, Appl
C 837	8.2	48.2	18	3	US-09-280-409-31	Sequence 31, Appl
C 838	8.2	48.2	18	3	US-08-606-505B-20	Sequence 20, Appl
C 839	8.2	48.2	18	3	US-08-606-505B-22	Sequence 22, Appl
C 840	8.2	48.2	18	3	US-08-606-505B-24	Sequence 24, Appl
C 841	8.2	48.2	18	3	US-08-606-505B-29	Sequence 29, Appl
C 842	8.2	48.2	18	3	US-09-082-614A-5	Sequence 5, Appl1
C 843	8.2	48.2	18	3	US-08-894-736-10	Sequence 10, Appl
C 844	8.2	48.2	18	3	US-08-894-736-21	Sequence 21, Appl
C 845	8.2	48.2	18	4	US-08-276-776-55	Sequence 55, Appl
C 846	8.2	48.2	18	4	US-08-471-209-55	Sequence 55, Appl
C 847	8.2	48.2	18	4	US-09-616-990-20	Sequence 20, Appl
C 848	8.2	48.2	18	4	US-09-616-990-22	Sequence 22, Appl
C 849	8.2	48.2	18	4	US-09-616-990-24	Sequence 24, Appl
C 850	8.2	48.2	18	4	US-09-616-990-29	Sequence 29, Appl
C 851	8.2	48.2	18	4	US-08-678-750-4	Sequence 4, Appl1
C 852	8.2	48.2	18	4	US-08-428-596A-15	Sequence 15, Appl
C 853	8.2	48.2	18	4	US-08-537-732A-22	Sequence 22, Appl
C 854	8.2	48.2	18	4	US-09-521-144-7	Sequence 7, Appl1
C 855	8.2	48.2	18	4	US-08-584-040-8307	Sequence 8307, Ap
C 856	8.2	48.2	18	4	US-09-387-341-171	Sequence 171, App
C 857	8.2	48.2	18	4	US-09-375-318-23	Sequence 23, Appl
C 858	8.2	48.2	18	5	PCT-US96-00845-14	Sequence 14, Appl
C 859	8.2	48.2	19	1	US-08-116-388-1	Sequence 1, Appl1
C 860	8.2	48.2	19	1	US-08-474-542A-78	Sequence 78, Appl
C 861	8.2	48.2	19	1	US-08-502-185-48	Sequence 48, Appl
C 862	8.2	48.2	19	1	US-08-457-648-78	Sequence 78, Appl
C 863	8.2	48.2	19	1	US-08-398-945-48	Sequence 48, Appl
C 864	8.2	48.2	19	1	US-08-569-826-18	Sequence 18, Appl
C 865	8.2	48.2	19	1	US-08-501-779-48	Sequence 48, Appl
C 866	8.2	48.2	19	1	US-08-440-103-13	Sequence 13, Appl
C 867	8.2	48.2	19	1	US-08-440-542-13	Sequence 13, Appl
C 868	8.2	48.2	19	1	US-08-501-713-48	Sequence 48, Appl
C 869	8.2	48.2	19	1	US-08-510-032A-7	Sequence 7, Appl1
C 870	8.2	48.2	19	1	US-08-378-860-48	Sequence 48, Appl
C 871	8.2	48.2	19	1	US-08-211-368-13	Sequence 13, Appl
C 872	8.2	48.2	19	1	US-08-440-210-13	Sequence 13, Appl
C 873	8.2	48.2	19	1	US-08-742-023-34	Sequence 34, Appl
C 874	8.2	48.2	19	1	US-08-501-626-48	Sequence 48, Appl
C 875	8.2	48.2	19	1	US-08-501-356-48	Sequence 48, Appl
C 876	8.2	48.2	19	1	US-08-110-294A-44	Sequence 44, Appl
C 877	8.2	48.2	19	2	US-08-359-705B-21	Sequence 21, Appl
C 878	8.2	48.2	19	2	US-08-117-952-151	Sequence 151, App
C 879	8.2	48.2	19	2	US-08-389-926-44	Sequence 44, Appl
C 880	8.2	48.2	19	2	US-08-386-846A-21	Sequence 21, Appl
C 881	8.2	48.2	19	3	US-08-457-880A-21	Sequence 21, Appl
C 882	8.2	48.2	19	3	US-08-688-514-7	Sequence 7, Appl1
C 883	8.2	48.2	19	3	US-08-444-622A-21	Sequence 21, Appl
C 884	8.2	48.2	19	3	US-08-942-562-21	Sequence 21, Appl
C 885	8.2	48.2	19	3	US-09-344-579-2	Sequence 2, Appl1
C 886	8.2	48.2	19	3	US-09-199-859-3	Sequence 3, Appl1
C 887	8.2	48.2	19	3	US-08-968-505-34	Sequence 34, Appl
C 888	8.2	48.2	19	3	US-08-912-572-65	Sequence 65, Appl
C 889	8.2	48.2	19	3	US-09-156-923-21	Sequence 21, Appl
C 890	8.2	48.2	19	4	US-08-938-669A-6	Sequence 6, Appl1
C 891	8.2	48.2	19	4	US-09-050-159-18	Sequence 18, Appl
C 892	8.2	48.2	19	4	US-09-050-159-19	Sequence 19, Appl
C 893	8.2	48.2	19	4	US-09-338-907-442	Sequence 442, App
C 894	8.2	48.2	19	4	US-09-177-349-11	Sequence 11, Appl
C 895	8.2	48.2	19	4	US-09-046-604-13	Sequence 13, Appl
C 896	8.2	48.2	19	4	US-08-761-708-18	Sequence 18, Appl
C 897	8.2	48.2	19	4	US-09-026-039-65	Sequence 65, Appl
C 898	8.2	48.2	19	4	US-09-218-207-442	Sequence 442, App
C 899	8.2	48.2	19	4	US-09-342-681C-48	Sequence 48, Appl
C 900	8.2	48.2	19	4	US-08-970-166-6	Sequence 6, Appl1
C 901	8.2	48.2	19	4	US-09-320-911-18	Sequence 18, Appl
C 902	8.2	48.2	19	4	US-08-098-942C-3	Sequence 3, Appl1
C 903	8.2	48.2	19	4	US-09-091-952A-131	Sequence 131, App

C 904	8.2	48.2	19	4	US-09-178-098A-6	Sequence 6, Appl1
C 905	8.2	48.2	19	5	PCT-US94-09318-1	Sequence 1, Appl1
C 906	8.2	48.2	19	6	US-07-613-083B-5	Patent No. 5168062
C 907	8.2	48.2	20	1	US-07-063-217-5	Sequence 5, Appl1
C 908	8.2	48.2	20	1	US-08-036-217-5	Sequence 5, Appl1
C 909	8.2	48.2	20	1	US-08-105-483-5	Sequence 5, Appl1
C 910	8.2	48.2	20	1	US-08-073-962-21	Sequence 21, Appl
C 911	8.2	48.2	20	1	US-07-714-687-5	Sequence 28, Appl1
C 912	8.2	48.2	20	1	US-08-220-151-28	Sequence 28, Appl
C 913	8.2	48.2	20	1	US-07-977-284A-163	Sequence 163, App
C 914	8.2	48.2	20	1	US-08-435-529-18	Sequence 18, Appl
C 915	8.2	48.2	20	1	US-08-188-434A-9	Sequence 9, Appl1
C 916	8.2	48.2	20	1	US-08-233-030-24	Sequence 24, Appl
C 917	8.2	48.2	20	1	US-08-043-390-9	Sequence 28, Appl
C 918	8.2	48.2	20	1	US-08-413-118-28	Sequence 28, Appl
C 919	8.2	48.2	20	1	US-08-530-492-86	Sequence 86, Appl
C 920	8.2	48.2	20	1	US-08-131-625B-3	Sequence 3, Appl1
C 921	8.2	48.2	20	1	US-08-535-230A-9	Sequence 9, Appl1
C 922	8.2	48.2	20	1	US-08-411-020-16	Sequence 16, Appl
C 923	8.2	48.2	20	1	US-08-411-020-17	Sequence 17, Appl
C 924	8.2	48.2	20	1	US-08-224-391-5	Sequence 5, Appl1
C 925	8.2	48.2	20	1	US-08-484-304-5	Sequence 5, Appl1
C 926	8.2	48.2	20	1	US-08-224-657-5	Sequence 5, Appl1
C 927	8.2	48.2	20	1	US-08-475-063-5	Sequence 5, Appl1
C 928	8.2	48.2	20	1	US-08-207-792-5	Sequence 5, Appl1
C 929	8.2	48.2	20	1	US-08-487-412-21	Sequence 21, Appl
C 930	8.2	48.2	20	1	US-08-709-209-5	Sequence 5, Appl1
C 931	8.2	48.2	20	1	US-08-257-073-1	Sequence 1, Appl1
C 932	8.2	48.2	20	1	US-08-303-275-5	Sequence 5, Appl1
C 933	8.2	48.2	20	1	US-08-458-101-5	Sequence 5, Appl1
C 934	8.2	48.2	20	1	US-08-343-281A-2	Sequence 2, Appl1
C 935	8.2	48.2	20	1	US-08-715-142-23	Sequence 23, Appl
C 936	8.2	48.2	20	1	US-08-410-779B-70	Sequence 70, Appl
C 937	8.2	48.2	20	1	US-08-410-779B-71	Sequence 71, Appl
C 938	8.2	48.2	20	1	US-08-913-050A-4	Sequence 4, Appl1
C 939	8.2	48.2	20	2	US-08-184-009-5	Sequence 5, Appl1
C 940	8.2	48.2	20	2	US-08-486-969-5	Sequence 5, Appl1
C 941	8.2	48.2	20	2	US-08-412-376-11	Sequence 11, Appl
C 942	8.2	48.2	20	2	US-08-457-273B-16	Sequence 16, Appl
C 943	8.2	48.2	20	2	US-07-963-538B-13	Sequence 13, Appl
C 944	8.2	48.2	20	2	US-08-417-210A-5	Sequence 5, Appl1
C 945	8.2	48.2	20	2	US-08-876-766-9	Sequence 9, Appl1
C 946	8.2	48.2	20	2	US-08-478-178A-71	Sequence 71, Appl
C 947	8.2	48.2	20	2	US-08-488-177-71	Sequence 71, Appl
C 948	8.2	48.2	20	2	US-08-481-072A-71	Sequence 71, Appl
C 949	8.2	48.2	20	2	US-08-664-336-71	Sequence 71, Appl
C 950	8.2	48.2	20	2	US-08-458-336-5	Sequence 5, Appl1
C 951	8.2	48.2	20	2	US-08-256-426B-163	Sequence 163, App
C 952	8.2	48.2	20	2	US-08-481-066A-71	Sequence 71, Appl
C 953	8.2	48.2	20	2	US-08-637-201C-4	Sequence 4, Appl1
C 954	8.2	48.2	20	2	US-08-471-025-5	Sequence 5, Appl1
C 955	8.2	48.2	20	2	US-08-658-665-5	Sequence 5, Appl1
C 956	8.2	48.2	20	2	US-08-904-901-59	Sequence 59, Appl
C 957	8.2	48.2	20	3	US-08-947-965-15	Sequence 15, Appl1
C 958	8.2	48.2	20	3	US-08-975-698A-13	Sequence 13, Appl
C 959	8.2	48.2	20	3	US-08-473-446-28	Sequence 28, Appl
C 960	8.2	48.2	20	3	US-09-366-257-37	Sequence 37, Appl
C 961	8.2	48.2	20	3	US-09-357-073-34	Sequence 34, Appl
C 962	8.2	48.2	20	3	US-09-289-267-58	Sequence 58, Appl1
C 963	8.2	48.2	20	3	US-08-882-501-8	Sequence 8, Appl1
C 964	8.2	48.2	20	3	US-09-166-186-128	Sequence 128, App
C 965	8.2	48.2	20	3	US-07-933-035A-3	Sequence 3, Appl1
C 966	8.2	48.2	20	3	US-08-353-901-4	Sequence 4, Appl1
C 967	8.2	48.2	20	3	US-08-855-531D-3	Sequence 3, Appl1
C 968	8.2	48.2	20	3	US-09-449-730-59	Sequence 59, Appl
C 969	8.2	48.2	20	3	US-09-286-904-10	Sequence 10, Appl
C 970	8.2	48.2	20	3	US-09-277-016-32	Sequence 32, Appl
C 971	8.2	48.2	20	3	US-09-277-016-33	Sequence 33, Appl
C 972	8.2	48.2	20	3	US-09-288-461-4	Sequence 4, Appl1
C 973	8.2	48.2	20	3	US-09-288-461-5	Sequence 5, Appl1
C 974	8.2	48.2	20	4	US-09-428-696-13	Sequence 13, Appl
C 975	8.2	48.2	20	4	US-09-428-696-59	Sequence 59, Appl
C 976	8.2	48.2	20	4	US-09-433-694-35	Sequence 35, Appl

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C 977      8.2  48.2  20  4  US-09-435-296-48      Sequence 48, Appl
C 978      8.2  48.2  20  4  US-09-428-219-11      Sequence 11, Appl
C 979      8.2  48.2  20  4  US-09-490-692-59      Sequence 59, Appl
C 980      8.2  48.2  20  4  US-08-906-517-86      Sequence 86, Appl
C 981      8.2  48.2  20  4  US-09-280-805-34      Sequence 34, Appl
C 982      8.2  48.2  20  4  US-09-280-805-51      Sequence 51, Appl
C 983      8.2  48.2  20  4  US-09-050-159-30      Sequence 30, Appl
C 984      8.2  48.2  20  4  US-09-101-8868-15      Sequence 15, Appl
C 985      8.2  48.2  20  4  US-09-290-640-27      Sequence 27, Appl
C 986      8.2  48.2  20  4  US-08-983-466-20      Sequence 20, Appl
C 987      8.2  48.2  20  4  US-09-417-090-13      Sequence 13, Appl
C 988      8.2  48.2  20  4  US-09-067-400-15      Sequence 15, Appl
C 989      8.2  48.2  20  4  US-09-313-932-128      Sequence 128, Appl
C 990      8.2  48.2  20  4  US-09-313-930-11      Sequence 11, Appl
C 991      8.2  48.2  20  4  US-09-313-930-19      Sequence 19, Appl
C 992      8.2  48.2  20  4  US-09-467-082-10      Sequence 10, Appl
C 993      8.2  48.2  20  4  US-08-478-316-88      Sequence 88, Appl
C 994      8.2  48.2  20  4  US-08-855-5268-3      Sequence 3, Appl
C 995      8.2  48.2  20  4  US-09-487-445-83      Sequence 83, Appl
C 996      8.2  48.2  20  4  US-09-117-927-11      Sequence 1, Appl
C 997      8.2  48.2  20  4  US-09-117-927-11      Sequence 11, Appl
C 998      8.2  48.2  20  4  US-08-460-736-5      Sequence 5, Appl
C 999      8.2  48.2  20  4  US-09-085-273-5      Sequence 5, Appl
1000      8.2  48.2  20  4  US-09-593-711A-162      Sequence 162, Appl
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ALIGNMENTS

RESULT 1
US-09-593-012-195
Sequence 195, Application US/09593012

```
Patent No. 6387652
GENERAL INFORMATION:
APPLICANT: HAUGLAND, Richard
APPLICANT: VESPER, Stephen
TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
FILE REFERENCE: HAUGLAND=1A
CURRENT APPLICATION NUMBER: US/09/593, 012
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 09/290, 990
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 60/081, 773
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 225
SOFTWARE: Patentin version 3.0
SEQ ID NO 195
LENGTH: 15
TYPE: DNA
ORGANISM: Trichoderma harzianum
US-09-593-012-195
```

Query Match 72.9%; Score 12.4; DB 4; Length 15;
Best Local Similarity 92.9%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTTGCTCGCGCGG 15
Db 1 TTGCTCGCGCGG 14

RESULT 2
US-09-593-012-191

```
Sequence 191, Application US/09593012
Patent No. 6387652
GENERAL INFORMATION:
APPLICANT: HAUGLAND, Richard
APPLICANT: VESPER, Stephen
TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
FILE REFERENCE: HAUGLAND=1A
CURRENT APPLICATION NUMBER: US/09/593, 012
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 09/290, 990
```

```
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 60/081, 773
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 225
SOFTWARE: Patentin version 3.0
SEQ ID NO 191
LENGTH: 21
TYPE: DNA
ORGANISM: Trichoderma asperellum/hamatum
US-09-593-012-191
```

Query Match 72.9%; Score 12.4; DB 4; Length 21;
Best Local Similarity 92.9%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTGCTCGCGCGG 14
Db 8 GTTGCTCGCGCGG 21

RESULT 3
US-09-593-012-194
Sequence 194, Application US/09593012

```
Patent No. 6387652
GENERAL INFORMATION:
APPLICANT: HAUGLAND, Richard
APPLICANT: VESPER, Stephen
TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
FILE REFERENCE: HAUGLAND=1A
CURRENT APPLICATION NUMBER: US/09/593, 012
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 09/290, 990
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 60/081, 773
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 225
SOFTWARE: Patentin version 3.0
SEQ ID NO 194
LENGTH: 21
TYPE: DNA
ORGANISM: Trichoderma asperellum/hamatum/viride
US-09-593-012-194
```

Query Match 72.9%; Score 12.4; DB 4; Length 21;
Best Local Similarity 92.9%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTGCTCGCGCGG 14
Db 8 GTTGCTCGCGCGG 21

RESULT 4
US-09-593-012-203
Sequence 203, Application US/09593012

```
Patent No. 6387652
GENERAL INFORMATION:
APPLICANT: HAUGLAND, Richard
APPLICANT: VESPER, Stephen
TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
FILE REFERENCE: HAUGLAND=1A
CURRENT APPLICATION NUMBER: US/09/593, 012
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 09/290, 990
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 60/081, 773
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 225
SOFTWARE: Patentin version 3.0
SEQ ID NO 203
LENGTH: 21
TYPE: DNA
ORGANISM: Trichoderma viride/atroviride/koningii
```

US-09-593-012-203

Query Match 72.9%; Score 12.4; DB 4; Length 21;
Best Local Similarity 92.9%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGGG 14
|||||
DB 8 GTTGCTTCGGCGGG 21

RESULT 5

US-09-593-012-31
Sequence 31, Application US/09593012
Patent No. 6387652

GENERAL INFORMATION:
APPLICANT: HAUGLAND, Richard
APPLICANT: VESPER, Stephen
TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
FILE REFERENCE: HAUGLAND=1A
CURRENT APPLICATION NUMBER: US/09/593,012
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 09/290,990
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 60/081,773
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 225
SOFTWARE: Patentin version 3.0
SEQ ID NO 31
LENGTH: 22
TYPE: DNA
ORGANISM: Aspergillus ochraceus/ostianus/auricomus
US-09-593-012-31

Query Match: 72.9%; Score 12.4; DB 4; Length 22;
Best Local Similarity 92.9%; Pred. No. 4.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGGG 14
|||||
DB 6 GTTGCTTCGGCGGG 19

RESULT 6

US-08-233-608-24
Sequence 24, Application US/08233608
Patent No. 5585238

GENERAL INFORMATION:
APPLICANT: Ligou, James M
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
NUMBER OF SEQUENCES: 49
TITLE OF INVENTION: Polymerase Chain Reaction
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,608
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Spullin, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: CGC 1739

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8615
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid
DESCRIPTION: Oligonucleotide primer JB548
HYPOTHETICAL: NO
ANTI-SENSE: NO

US-08-233-608-24

Query Match 71.8%; Score 12.2; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. No. 5.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGGGAC 17
|||||
DB 1 GTTGCTTCGGCGGGAC 17

RESULT 7

US-08-887-480-24
Sequence 24, Application US/08887480
Patent No. 5814453

GENERAL INFORMATION:
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
NUMBER OF SEQUENCES: 96
TITLE OF INVENTION: Polymerase Chain Reaction
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5814453artis Corporation
STREET: 520 White Plains Road
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,480
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722,187
FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP

TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: Oligonucleotide primer JB548
HYPOTHETICAL: NO
ANTI-SENSE: NO

US-08-887-480-24

Query Match 71.8%; Score 12.2; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. No. 5.4e+02;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGGGAAC 17
|||||||
Db 1 GTTGCTTCGGCGGCGAC 17

RESULT 8

US-08-722-187-24
; Sequence 24, Application US/08722187
; Patent No. 5955274
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,187
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/233,608
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Walsh, Andrea C.
; REGISTRATION NUMBER: 34,988
; REFERENCE/DOCKET NUMBER: CGC 1739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8666
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: Oligonucleotide primer JB548
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-722-187-24

Query Match 71.8%; Score 12.2; DB 2; Length 20;
Best Local Similarity 82.4%; Pred. No. 5.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGGGAAC 17
|||||||
Db 1 GTTGCTTCGGCGGCGAC 17

RESULT 9

PCT-US95-04712-24
; Sequence 24, Application PC/TUS9504712
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04712
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: Oligonucleotide primer JB548
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US95-04712-24

Query Match 71.8%; Score 12.2; DB 5; Length 20;
Best Local Similarity 82.4%; Pred. No. 5.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGGGAAC 17
|||||||
Db 1 GTTGCTTCGGCGGCGAC 17

RESULT 10

US-09-593-012-120
; Sequence 120, Application US/09593012
; Patent No. 6387652
; GENERAL INFORMATION:
; APPLICANT: HAUGLAND, Richard
; APPLICANT: VESPER, Stephen
; TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTER.
; FILE REFERENCE: HAUGLAND-1A
; CURRENT APPLICATION NUMBER: US/09/593,012
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 09/290,990
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 60/081,773
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 225
; SOFTWARE: Patent version 3.0
; SEQ ID NO 120
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Penicillium brevicompactum/alberechii
US-09-593-012-120

Query Match 70.6%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGCTTGGCG 12
|||||
Db 5 GTTGCTTGGCG 16

RESULT 11

US-09-428-219-70/c
Sequence 70, Application US/09428219
Patent No. 6177273
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN-LINKED KINASE EXPRESSION
FILE REFERENCE: RTS-0101
CURRENT APPLICATION NUMBER: US/09/428,219
CURRENT FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 70
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-428-219-70

Query Match 69.4%; Score 11.8; DB 4; Length 20;
Best Local Similarity 86.7%; Pred. No. 8.9e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGCTTGGCGGAC 17
|||||
Db 18 TGCTTGTGGGAC 4

RESULT 12

US-08-291-932A-812/c
Sequence 812, Application US/08291932A
Patent No. 5658780
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth G.
APPLICANT: McSwigen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: NF-KB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992

Two

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 812:

SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-291-932A-812

Query Match 67.1%; Score 11.4; DB 1; Length 16;
Best Local Similarity 92.3%; Pred. No. 1.4e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTGGCG 13
|||||
Db 16 GTTGCTGGCTG 4

RESULT 13

US-08-887-480-57
Sequence 57, Application US/08887480
Patent No. 5814453
GENERAL INFORMATION:
APPLICANT: Beck, James J.
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 5814453artis Corporation
STREET: 520 White Plains Road
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,480
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722,187
FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide primer
DESCRIPTION: JB570"
HYPOTHETICAL: NO
US-08-887-480-57

Query Match 67.1%; Score 11.4; DB 1; Length 16;

Best Local Similarity 92.3%; Pred. No. 1.4e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 13
|||||
Db 4 GTTGCTTCGGCGG 16

RESULT 14

US-08-887-480-64
Sequence 64, Application US/08887480
Patent No. 5814453
GENERAL INFORMATION:
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5814453artis Corporation
STREET: 520 White Plains Road
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,480
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722,187
FILING DATE: 15-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide primer
DESCRIPTION: JB577"
HYPOTHETICAL: NO
US-08-887-480-64

Query Match 67.1%; Score 11.4; DB 1; Length 16;
Best Local Similarity 92.3%; Pred. No. 1.4e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 13
|||||
Db 1 GTTGCTTCGGCGG 13

RESULT 15
US-08-722-187-57
Sequence 57, Application US/08722187
Patent No. 5955274
GENERAL INFORMATION:
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction

NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,187
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea G.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide primer
DESCRIPTION: JB570"
HYPOTHETICAL: NO
US-08-722-187-57

Query Match 67.1%; Score 11.4; DB 2; Length 16;
Best Local Similarity 92.3%; Pred. No. 1.4e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 13
|||||
Db 4 GTTGCTTCGGCGG 16

RESULT 16

US-08-722-187-64
Sequence 64, Application US/08722187
Patent No. 5955274
GENERAL INFORMATION:
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,187
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide primer"
DESCRIPTION: J8577"
HYPOTHEICAL: NO
US-08-722-187-64

Query Match 67.1%; Score 11.4; DB 2; Length 16;
Best Local Similarity 92.3%; Pred. No. 1.4e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 13
DB 1 GTTGCTTCGGCGG 13

RESULT 17
US-09-593-012-198
Sequence 198; Application US/09593012
Patent No. 6387652
GENERAL INFORMATION:
APPLICANT: HAUGLAND, Richard
TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
FILE REFERENCE: HAUGLAND-1A
CURRENT APPLICATION NUMBER: US/09/593,012
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 09/290,990
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 60/081,773
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 198
LENGTH: 16
TYPE: DNA
ORGANISM: Trichoderma longibrachiatum/citreoviride
US-09-593-012-198

Query Match 67.1%; Score 11.4; DB 4; Length 16;
Best Local Similarity 92.3%; Pred. No. 1.4e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGCTTCGGCGGGA 15
DB 1 TGCTTCGGCGGGA 13

RESULT 18
PCT-US95-04712-57
Sequence 57; Application PC/TUS9504712
GENERAL INFORMATION:
APPLICANT: Ligon, James M
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
APPLICATION NUMBER: PCT/US95/04712
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04712
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide primer"
DESCRIPTION: J8570"
HYPOTHEICAL: NO
PCT-US95-04712-57

Query Match 67.1%; Score 11.4; DB 5; Length 16;
Best Local Similarity 92.3%; Pred. No. 1.4e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 13
DB 4 GTTGCTTCGGCGG 16

RESULT 19
PCT-US95-04712-64
Sequence 64; Application PC/TUS9504712
GENERAL INFORMATION:
APPLICANT: Ligon, James M
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
FILE REFERENCE: Beck, James J
CURRENT APPLICATION NUMBER: 86
CURRENT FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 60/081,773
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 198
LENGTH: 16
TYPE: DNA
ORGANISM: Trichoderma longibrachiatum/citreoviride
US-09-593-012-198

QY 3 TGCTTCGGCGGGA 15
DB 1 TGCTTCGGCGGGA 13

RESULT 18
PCT-US95-04712-57
Sequence 57; Application PC/TUS9504712
GENERAL INFORMATION:
APPLICANT: Ligon, James M
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
APPLICATION NUMBER: PCT/US95/04712
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
NUMBER OF SEQUENCES: 86

APPLICATION NUMBER: US 08/233,606
FILING DATE: 04-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: WALSH, ANDREA C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide primer"
DESCRIPTION: JB577"
HYPOTHETICAL: NO
PCT-US95-04712-64

BEST AVAILABLE COPY

Query Match 67.1%; Score 11.4; DB 5; Length 16;
Best Local Similarity 92.3%; Pred. No. 1.4e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTGGCGG 13
DB 1 GTTGCTGGCGG 13

RESULT 20
US-08-606-505B-19/C
Sequence 19, Application US/08606505B
Patent No. 6114601
GENERAL INFORMATION:
APPLICANT: KIKUCHI, Yasuhiro
APPLICANT: KIYOKAWA, Shigeto
APPLICANT: SHIMADA, Yukihisa
APPLICANT: OHBAYASHI, Masaya
APPLICANT: SHIMADA, Ritsuko
APPLICANT: OKINAKA, Yasushi
TITLE OF INVENTION: NOVEL PLANT GENES
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: FITZPATRICK, CELLA, HARPER & SCINTO
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112-3801
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage.
COMPUTER: IBM PS/4
OPERATING SYSTEM: MS-DOS Ver3.30
SOFTWARE: PATENT AID Ver1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,505B
FILING DATE: 23-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP44963/92
FILING DATE: 02-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: PERRY, Lawrence S.
REGISTRATION NUMBER: 31865
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-218-2100
TELEFAX: 212-218-2200
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid
DESCRIPTION: Synthetic RNA
US-09-616-990-19

Query Match 67.1%; Score 11.4; DB 3; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGCTGGCGGGAAC 17
DB 18 TGCTTGGGCGGATC 4

RESULT 21
US-09-616-990-19/C
Sequence 19, Application US/09616990
Patent No. 6232109
GENERAL INFORMATION:
APPLICANT: KIKUCHI, Yasuhiro
APPLICANT: KIYOKAWA, Shigeto
APPLICANT: SHIMADA, Yukihisa
APPLICANT: OHBAYASHI, Masaya
APPLICANT: SHIMADA, Ritsuko
APPLICANT: OKINAKA, Yasushi
TITLE OF INVENTION: NOVEL PLANT GENES
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: FITZPATRICK, CELLA, HARPER & SCINTO
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112-3801
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage.
COMPUTER: IBM PS/4
OPERATING SYSTEM: MS-DOS Ver3.30
SOFTWARE: PATENT AID Ver1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/616,990
FILING DATE: 14-JUL-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP44963/92
FILING DATE: 02-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: PERRY, Lawrence S.
REGISTRATION NUMBER: 31865
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-218-2100
TELEFAX: 212-218-2200
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: Synthetic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 19
US-09-616-990-19

Query Match 67.1%; Score 11.4; DB 4; Length 18;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGCTGGCGGGAAC 17
DB 18 TGCTTGGGCGGATC 4

RESULT 22
US-08-652-127C-1
Sequence 1, Application US/08652127C

Patent No. 5792611
GENERAL INFORMATION:
APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF PLANT
TITLE OF INVENTION: PATHOGEN FUNGI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: George A. Seaby
STREET: 880 Wellington Street, Suite 708
CITY: Ottawa
COUNTRY: Canada
ZIP: K1R 6K7
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652.127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-652-127C-1

Query Match 67.1%; Score 11.4; DB 1; Length 21;
Best Local Similarity 92.3%; Pred. No. 1.5e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 13
||| ||| ||| |||
Db 3 GTTGCTTCGGCGG 15

RESULT 23
US-08-358-556A-1
Sequence 1, Application US/08358556A
Patent No. 5869643
GENERAL INFORMATION:
APPLICANT: Chatelet, Francois
APPLICANT: Kumarev, Viktor
TITLE OF INVENTION: Process for Preparing Polynucleotides on
TITLE OF INVENTION: a Solid Support and Apparatus Permitting its
TITLE OF INVENTION: Implementation
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358.556A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 9315164
FILING DATE: 16-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
TELEX: RCH 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: CDS
LOCATION: 1..18
US-08-358-556A-1

Query Match 65.9%; Score 11.2; DB 2; Length 18;
Best Local Similarity 81.2%; Pred. No. 1.8e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGGAA 16
||| ||| ||| ||| |||
Db 3 GTTGCTTCGGCGGAA 18

RESULT 24
US-08-281-203-6
Sequence 6, Application US/08281203
Patent No. 6033909
GENERAL INFORMATION:
APPLICANT: Uhlmann, Eugen
APPLICANT: Peyman, Anuschirvan
APPLICANT: O'Malley, Gerard
APPLICANT: Halseberg, Matthias
APPLICANT: Winkler, Irvin
TITLE OF INVENTION: Oligonucleotide Analogs, Their
TITLE OF INVENTION: Preparation and Use
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/281.203
FILING DATE: 27-JULY-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/003,972
FILING DATE: 19-JAN-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Elnaui, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 02481.1269-01000
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-281-203-6

Query Match 65.9%; Score 11.2; DB 3; Length 20;
Best Local Similarity 81.2%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCTTCGGCGGGA 16
DB 4 GTTCTTCGGCGGGA 19

RESULT 25
US-09-326-186B-146
Sequence 146, Application US/09326186B
Patent No. 6319806
GENERAL INFORMATION:
APPLICANT: Bennett, Clarence Frank
APPLICANT: Vickers, Timothy A.
TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
FILE REFERENCE: ISPH-0376
CURRENT APPLICATION NUMBER: US/09/326,186B
PRIOR FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 08/777,266
NUMBER OF SEQ ID NOS: 226
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 146
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-326-186B-146

Query Match 65.9%; Score 11.2; DB 4; Length 20;
Best Local Similarity 81.2%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTGCTTCGGCGGGA 17
DB 3 TTGCTTCGGCGGGA 18

RESULT 26
US-08-005-283-4/C
Sequence 4, Application US/08005283
Patent No. 5646261
GENERAL INFORMATION:
APPLICANT: Uhlmann, Eugen
APPLICANT: Peyman, Anuschirwan
APPLICANT: O'Malley, Gerard
APPLICANT: Helberg, Matthias
APPLICANT: Winkler, Irvin
TITLE OF INVENTION: 3'-Derivatized Oligonucleotide Analogs
TITLE OF INVENTION: 3'-Derivatized Oligonucleotide Groupings, Their Preparation and
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSER: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA

ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/005,283
FILING DATE: 19-JAN-1993
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4201663.0
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hammond, Alan W.
REGISTRATION NUMBER: 35,178
REFERENCE/DOCKET NUMBER: 02481.1270-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-005-283-4

Query Match 65.9%; Score 11.2; DB 1; Length 25;
Best Local Similarity 81.2%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCTTCGGCGGGA 16
DB 19 GTTCTTCGGCGGGA 4

RESULT 27
US-08-005-283-6/C
Sequence 6, Application US/08005283
Patent No. 5646261
GENERAL INFORMATION:
APPLICANT: Uhlmann, Eugen
APPLICANT: Peyman, Anuschirwan
APPLICANT: O'Malley, Gerard
APPLICANT: Helberg, Matthias
APPLICANT: Winkler, Irvin
TITLE OF INVENTION: 3'-Derivatized Oligonucleotide Analogs
TITLE OF INVENTION: 3'-Derivatized Oligonucleotide Groupings, Their Preparation and
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSER: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/005,283
FILING DATE: 19-JAN-1993
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4201663.0
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hammond, Alan W.

REGISTRATION NUMBER: 35,178
REFERENCE/DOCKET NUMBER: 02481.1270-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-005-283-6

Query Match 65.9%; Score 11.2; DB 1; Length 25;
Best Local Similarity 81.2%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTGCTCGCGGGA 16
DB 19 GTTGCTCGCGGGA 4

RESULT 28
US-09-593-012-48/c
Sequence 48, Application US/09593012
Patent No. 6387652
GENERAL INFORMATION:
APPLICANT: HAUGLAND, Richard
APPLICANT: VESPER, Stephen
TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
FILE REFERENCE: HAUGLAND=1A
CURRENT APPLICATION NUMBER: US/09/593,012
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 09/290,990
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 60/081,773
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 48
LENGTH: 18
TYPE: DNA
ORGANISM: Aspergillus ustus
US-09-593-012-48

Query Match 64.7%; Score 11; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGCTCGGC 11
DB 11 GTTGCTCGGC 1

RESULT 29
US-08-472-255A-56
Sequence 56, Application US/08472255A
Patent No. 5766853
GENERAL INFORMATION:
APPLICANT: PARMA, DAVID
APPLICANT: GOLD, LARRY
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: TO SELECTINS (AS AMENDED)
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,255A
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/114,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All C's are 2'-NH2 cytosine
OTHER INFORMATION: All U's are 2'-NH2 uracil
US-08-472-255A-56

Query Match 64.7%; Score 11; DB 1; Length 20;
Best Local Similarity 90.9%; Pred. No. 2.4e+03;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGCGCGGAC 17
DB 6 TCGCGCGGAC 16

RESULT 30
US-08-479-724A-56
Sequence 56, Application US/08479724A
Patent No. 5780228
GENERAL INFORMATION:
APPLICANT: PARMA, DAVID
APPLICANT: GOLD, LARRY
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: TO LECTINS
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,724A
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/714,111
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1991
PRIOR APPLICATION DATA: 07/964,624
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All C's are 2'-NH2 cytosine
FEATURE:
OTHER INFORMATION: All U's are 2'-NH2 uracil
US-08-479-724A-56

Query Match 64.7%; Score 11; DB 1; Length 20;
Best Local Similarity 90.9%; Pred. No. 2.4e+0; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 0;

QY 7 TCGGCGGGAAC 17
Db 6 UCGCGGGAAC 16

RESULT 31
US-08-472-256B-56
Sequence 56, Application US/08472256B
Patent No. 6001988
GENERAL INFORMATION:
APPLICANT: PARMA, DAVID
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: TO LECTINS
NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,256B
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All C's are 2'-NH2 cytosine
FEATURE:
OTHER INFORMATION: All U's are 2'-NH2 uracil
US-08-472-256B-56

Query Match 64.7%; Score 11; DB 3; Length 20;
Best Local Similarity 90.9%; Pred. No. 2.4e+03; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 0;

QY 7 TCGGCGGGAAC 17
Db 6 UCGCGGGAAC 16

RESULT 32
US-08-952-793-56
Sequence 56, Application US/08952793
Patent No. 6280932
GENERAL INFORMATION:
APPLICANT: PARMA, et al.
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: TO LECTINS
NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,793
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09455
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40C/PCT
TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All C's are 2'-NH2 cytosine
OTHER INFORMATION: All U's are 2'-NH2 uracil
US-08-952-793-56

Query Match 64.7% Score 11; DB 4; Length 20;
Best Local Similarity 90.9%; Pred. No. 2.4e+03;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGGCGGGAAC 17
Db 6 UCGCGGGAAC 16

RESULT 33

PCT-US96-09455A-56

Sequence 56, Application PC/TUS9609455A

GENERAL INFORMATION:

APPLICANT: PARMA, et al.

TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID

NUMBER OF SEQUENCES: 390

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson & Bratschun, L.L.C.

STREET: 8400 E. Prentice Avenue, Suite 200

CITY: Englewood

STATE: Colorado

COUNTRY: USA

ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB

COMPUTER: IBM PC compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/09455A

FILING DATE: 05 JUNE 1996

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/479,724

FILING DATE: 07-JUNE-1995

APPLICATION NUMBER: 08/472,256

FILING DATE: 07-JUNE-1995

APPLICATION NUMBER: 08/472,255

FILING DATE: 07-JUNE-1995

APPLICATION NUMBER: 08/477,829

FILING DATE: 07-JUNE-1995

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215

REFERENCE/DOCKET NUMBER: NEX40C/PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333

TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 56:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All C's are 2'-NH2 cytosine
FEATURE:
OTHER INFORMATION: All U's are 2'-NH2 uracil
PCT-US96-09455A-56

Query Match 64.7% Score 11; DB 5; Length 20;
Best Local Similarity 90.9%; Pred. No. 2.4e+03;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCGGCGGGAAC 17
Db 6 UCGCGGGAAC 16

RESULT 34
US-08-679-645-539/c

Sequence 539, Application US/08679645

Patent No. 6350934

GENERAL INFORMATION:

APPLICANT: Zwick, Michael G.

APPLICANT: Edington, Brent E.

APPLICANT: McSwiggen, James A.

APPLICANT: Merlo, Patricia Ann Owens

APPLICANT: Guo, Lining

APPLICANT: Skokut, Thomas A.

APPLICANT: Young, Scott A.

APPLICANT: Folkerts, Otto

TITLE OF INVENTION: COMPOSITION AND METHODS FOR

TITLE OF INVENTION: MODULATION OF GENE EXPRESSION

NUMBER OF SEQUENCES: 1263

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/679,645

FILING DATE: July 12, 1996

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/001,135

FILING DATE: July 13, 1995

APPLICATION NUMBER: 08/300,726

FILING DATE: September 2, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 219/247

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 539:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-679-645-539

LOCATION: 822..803
OTHER INFORMATION: Antisense primer hts-6b for PCR amplification of part
OTHER INFORMATION: of 890 base pair fragment of human TS gene
OTHER INFORMATION: from nucleotide 50 to the C-terminus
US-09-367-007C-14

Query Match 63.5%; Score 10.8; DB 4; Length 20;
Best Local Similarity 85.7%; Pred. No. 3.1e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCTTGGCGGCGAAC 17
DB 19 GCTTCAGCGAGAAC 6

RESULT 39
PCT-US95-09069-2/C
Sequence 2, Application PC/TUS9509069

GENERAL INFORMATION:
APPLICANT: Wilson, David B.
APPLICANT: Walker, Larry P.
APPLICANT: Zhang, Sheng
TITLE OF INVENTION: Thermostable Cellulase From A Thermomonospora Gene
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
SOFTWARE: Wordperfect for Windows 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09069
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial No. 08/265,429
FILING DATE: 24/06/94

ATTORNEY/AGENT INFORMATION:

NAME: Nelson, M. Bud

REGISTRATION NUMBER: 35,300

REFERENCE/DOCKET NUMBER: 18617.0008

TELECOMMUNICATION INFORMATION:

TELEPHONE: (716)856-4000

TELEFAX: 716-849-0349

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single-stranded

MOLECULE TYPE: DNA

IMMEDIATE SOURCE: synthesized

ORIGINAL SOURCE: Thermomonospora fusca

STRAIN: YX36

CELL TYPE: bacterium

PCT-US95-09069-2

Query Match 63.5%; Score 10.8; DB 5; Length 20;
Best Local Similarity 85.7%; Pred. No. 3.1e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGCTTCGGCGGCGAA 16
DB 20 TGCAATGGCGGCGAA 7

RESULT 40
US-08-974-549A-510
Sequence 510, Application US/08974549A
Patent No. 6166178

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

APPLICANT: Lingner, Joachim

APPLICANT: Nakamura, Toru

APPLICANT: Chapman, Karen B.

APPLICANT: Morin, Gregg B.

APPLICANT: Hatley, Calvin B.

APPLICANT: Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A

FILING DATE: 19-NOV-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 510:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 08:05:49 ; Search time 973.327 Seconds
(without alignments)
282.868 Million cell updates/sec

Title: US-10-080-959a-1

Perfect score: 17

Sequence: 1 gttctctcggcgggaac 17

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 18144

Minimum DB seq length: 0
Maximum DB seq length: 25
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estlin:*
- 4: em_estmlu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hnc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hnc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estcom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vit:*
- 22: em_gss_fun:*
- 23: em_gss_man:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11.2	65.9	25	13	BI094828 EST-CD34N
2	10.4	61.2	25	17	TA352B06Q
3	10	58.8	21	17	AZ307451 IM0009B09
4	9.8	57.6	25	9	AI421881 tefsh03.x
5	9.6	56.5	22	17	TA114G12Q
6	9.4	55.3	24	17	AZ786547

7	9.2	54.1	18	13	BM398017
8	9.2	54.1	19	17	AZ781461
9	9.2	54.1	20	17	AZ432681
10	9.2	54.1	24	17	TA75A030
11	9.2	54.1	25	9	AI594892
12	9.2	54.1	25	9	BM854200
13	9.2	54.1	20	17	AZ659612
14	9.2	54.1	21	17	AZ663981
15	9.2	54.1	25	13	BM399936
16	9.2	54.1	25	17	AZ478429
17	9.2	54.1	23	17	AZ339811
18	9.2	54.1	23	17	TA106C010
19	9.2	54.1	23	17	TA266D03P
20	9.2	54.1	20	17	AZ345583
21	9.2	54.1	22	17	AW247820
22	9.2	54.1	23	17	AZ780543
23	9.2	54.1	25	9	AA034350
24	9.2	54.1	25	9	AI091780
25	9.2	54.1	25	13	BM397307
26	9.2	54.1	25	17	TA307A07Q
27	9.2	54.1	22	9	AA991484
28	9.2	54.1	22	9	AI352536
29	9.2	54.1	22	9	AU006620
30	9.2	54.1	22	9	AU006633
31	9.2	54.1	22	17	AZ476310
32	9.2	54.1	22	17	TA219C09P
33	9.2	54.1	20	17	AZ475852
34	9.2	54.1	20	17	AZ511616
35	9.2	54.1	20	17	AZ789409
36	9.2	54.1	21	17	AZ555490
37	9.2	54.1	22	9	AA908627
38	9.2	54.1	22	9	AI721471
39	9.2	54.1	22	17	TA174D06Q
40	9.2	54.1	23	9	AZ785027
41	9.2	54.1	25	13	BM401196
42	9.2	54.1	25	17	TA237D08Q
43	9.2	54.1	19	17	AZ499442
44	9.2	54.1	20	9	AU060353
45	9.2	54.1	22	17	AZ821049
46	9.2	54.1	22	17	TA28D01Q
47	9.2	54.1	22	17	TA28D02Q
48	9.2	54.1	23	17	AZ387178
49	9.2	54.1	23	17	AZ785889
50	9.2	54.1	23	17	AZ840388
51	9.2	54.1	23	17	AZ840388
52	9.2	54.1	23	17	BM848405
53	9.2	54.1	24	17	AZ405843
54	9.2	54.1	24	17	AZ584313
55	9.2	54.1	24	17	AZ595059
56	9.2	54.1	24	17	AZ809979
57	9.2	54.1	25	9	AA903841
58	9.2	54.1	25	17	TA72B02P
59	9.2	54.1	19	9	AI017937
60	9.2	54.1	19	17	AZ345964
61	9.2	54.1	19	17	AZ969805
62	9.2	54.1	20	9	AU257181
63	9.2	54.1	20	17	AZ592635
64	9.2	54.1	21	17	AZ318273
65	9.2	54.1	21	17	AZ581103
66	9.2	54.1	22	17	AM059920
67	9.2	54.1	22	14	DI8746
68	9.2	54.1	22	17	AZ644887
69	9.2	54.1	23	17	AZ308507
70	9.2	54.1	24	17	AZ316848
71	9.2	54.1	24	17	AZ492823
72	9.2	54.1	24	17	AZ792764
73	9.2	54.1	25	9	AA980269
74	9.2	54.1	25	9	AA993070
75	9.2	54.1	25	14	Z20702
76	9.2	54.1	25	17	AQ025268
77	9.2	54.1	25	17	AZ308557
78	9.2	54.1	25	17	AZ393511
79	9.2	54.1	25	17	AZ807246

C 375	10.2	51.0	21	18	AA780605	Antisense oligonuc	448	10	50.0	13	23	ABC30246	Oligonucleotide SE
C 376	10.2	51.0	21	18	AA780606	Antisense oligonuc	449	10	50.0	13	23	ABC30247	Oligonucleotide SE
C 377	10.2	51.0	21	19	AA726112	Human polymorphic	450	10	50.0	13	23	ABC47702	Oligonucleotide SE
C 378	10.2	51.0	21	19	AAV67343	Nucleotide fragmen	451	10	50.0	13	23	ABC47703	Oligonucleotide SE
C 379	10.2	51.0	21	19	AAV30757	Human endothelial	452	10	50.0	13	23	ABC80672	Oligonucleotide SE
C 380	10.2	51.0	21	20	AAV39277	Human AUR2 inhibi	453	10	50.0	13	23	ABC80673	Oligonucleotide SE
C 381	10.2	51.0	21	20	AAV35672	Human endogenous r	454	10	50.0	13	23	ABC82078	Oligonucleotide SE
C 382	10.2	51.0	21	21	AAV69338	Human ABC1 gene ex	455	10	50.0	13	23	ABC83914	Oligonucleotide SE
C 383	10.2	51.0	21	21	AAV288915	Human wolfram ex	456	10	50.0	13	23	ABC83915	Oligonucleotide SE
C 384	10.2	51.0	21	21	AAV240348	PCR primer for cap	457	10	50.0	13	23	ABF04484	Oligonucleotide SE
C 385	10.2	51.0	21	22	AAH62163	Kalitrein B plasm	458	10	50.0	13	23	ABF04485	Oligonucleotide SE
C 386	10.2	51.0	21	22	AAH62163	Polymorphic sequen	459	10	50.0	13	23	ABF17826	Oligonucleotide SE
C 387	10.2	51.0	21	22	AAH69357	T-DNA right border	460	10	50.0	13	23	ABF17827	Oligonucleotide SE
C 388	10.2	51.0	21	22	AAH69357	Human ADP-ribosyl	461	10	50.0	13	23	ABF29756	Oligonucleotide SE
C 389	10.2	51.0	21	22	AAH69357	AAV antisense prim	462	10	50.0	13	23	ABF29757	Oligonucleotide SE
C 390	10.2	51.0	21	24	AAH69357	Human single nucle	463	10	50.0	13	23	ABF30616	Oligonucleotide SE
C 391	10.2	51.0	22	13	AAH69357	Antisense oligonuc	464	10	50.0	13	23	ABF30617	Oligonucleotide SE
C 392	10.2	51.0	22	15	AAH69357	Antisense oligonuc	465	10	50.0	13	23	ABF40670	Oligonucleotide SE
C 393	10.2	51.0	22	16	AAH69357	ICAM antisense oli	466	10	50.0	13	23	ABF40671	Oligonucleotide SE
C 394	10.2	51.0	22	16	AAH69357	Peptide nucleic ac	467	10	50.0	13	23	ABF49644	Oligonucleotide SE
C 395	10.2	51.0	22	16	AAH69357	Peptide nucleic ac	468	10	50.0	13	23	ABF49645	Oligonucleotide SE
C 396	10.2	51.0	22	17	AAH69357	Antisense oligonuc	469	10	50.0	13	23	ABF50342	Oligonucleotide SE
C 397	10.2	51.0	22	18	AAH69357	ICAM inhibiting an	470	10	50.0	13	23	ABF50343	Oligonucleotide SE
C 398	10.2	51.0	22	18	AAH69357	PCR primer hmgp-74	471	10	50.0	13	23	ABF55570	Oligonucleotide SE
C 399	10.2	51.0	22	19	AAH69357	Human ICAM-1, B-se	472	10	50.0	13	23	ABF55571	Oligonucleotide SE
C 400	10.2	51.0	22	20	AAH69357	Human XIS gene fr	473	10	50.0	13	23	ABF71648	Oligonucleotide SE
C 401	10.2	51.0	22	20	AAH69357	Antisense thiol-de	474	10	50.0	13	23	ABF71649	Oligonucleotide SE
C 402	10.2	51.0	22	21	AAH69357	Protein production	475	10	50.0	13	23	ABF81342	Oligonucleotide SE
C 403	10.2	51.0	22	21	AAH69357	Human ICAM-1 antis	476	10	50.0	13	23	ABH18788	Oligonucleotide SE
C 404	10.2	51.0	22	22	AAH69357	Antisense oligo fo	477	10	50.0	13	23	ABH18789	Oligonucleotide SE
C 405	10.2	51.0	22	24	AAH69357	Human GPCR forwar	478	10	50.0	13	23	ABH18790	Oligonucleotide SE
C 406	10.2	51.0	22	24	AAH69357	Chromosomal locus	479	10	50.0	13	23	ABH18791	Oligonucleotide SE
C 407	10.2	51.0	23	18	AAH69357	Primer DBS349 for	480	10	50.0	15	22	AAH69357	Oligonucleotide SE
C 408	10.2	51.0	23	18	AAH69357	Mouse HYPLIP1 locu	481	10	50.0	15	22	AAH69357	Oligonucleotide SE
C 409	10.2	51.0	23	24	AAH69357	Mouse capniz spec	482	10	50.0	17	21	AAH69357	Oligonucleotide SE
C 410	10.2	51.0	23	24	AAH69357	Mouse capniz spec	483	10	50.0	17	21	AAH69357	Oligonucleotide SE
C 411	10.2	51.0	23	24	AAH69357	Helix-turn-helix d	484	10	50.0	17	21	AAH69357	Oligonucleotide SE
C 412	10.2	51.0	24	20	AAH69357	Human shear stress	485	10	50.0	18	20	AAH69357	Oligonucleotide SE
C 413	10.2	51.0	24	22	AAH69357	Oligonucleotide ad	486	10	50.0	18	20	AAH69357	Oligonucleotide SE
C 414	10.2	51.0	24	24	AAH69357	Oligonucleotide ad	487	10	50.0	18	22	AAH69357	Oligonucleotide SE
C 415	10.2	51.0	24	24	AAH69357	Oligonucleotide ad	488	10	50.0	18	24	AAH69357	Oligonucleotide SE
C 416	10.2	51.0	24	24	AAH69357	Oligonucleotide ad	489	10	50.0	19	15	AAH69357	Oligonucleotide SE
C 417	10.2	51.0	24	24	AAH69357	Oligonucleotide ad	490	10	50.0	19	15	AAH69357	Oligonucleotide SE
C 418	10.2	51.0	24	24	AAH69357	Oligonucleotide ad	491	10	50.0	19	20	AAH69357	Oligonucleotide SE
C 419	10.2	51.0	24	24	AAH69357	Oligonucleotide ad	492	10	50.0	19	21	AAH69357	Oligonucleotide SE
C 420	10.2	51.0	24	24	AAH69357	Capture oligonucle	493	10	50.0	19	21	AAH69357	Oligonucleotide SE
C 421	10.2	51.0	24	24	AAH69357	Capture oligonucle	494	10	50.0	19	21	AAH69357	Oligonucleotide SE
C 422	10.2	51.0	24	24	AAH69357	Capture oligonucle	495	10	50.0	19	21	AAH69357	Oligonucleotide SE
C 423	10.2	51.0	24	24	AAH69357	Capture oligonucle	496	10	50.0	19	21	AAH69357	Oligonucleotide SE
C 424	10.2	51.0	24	24	AAH69357	Capture oligonucle	497	10	50.0	19	21	AAH69357	Oligonucleotide SE
C 425	10.2	51.0	24	24	AAH69357	Capture oligonucle	498	10	50.0	19	22	AAH69357	Oligonucleotide SE
C 426	10.2	51.0	24	24	AAH69357	Capture oligonucle	499	10	50.0	19	22	AAH69357	Oligonucleotide SE
C 427	10.2	51.0	24	24	AAH69357	Capture oligonucle	500	10	50.0	19	24	AAH69357	Oligonucleotide SE
C 428	10.2	51.0	25	12	AAH69357	Probe RP based on	501	10	50.0	19	24	AAH69357	Oligonucleotide SE
C 429	10.2	51.0	25	12	AAH69357	PCR primer VR109 u	502	10	50.0	19	24	AAH69357	Oligonucleotide SE
C 430	10.2	51.0	25	21	AAH69357	Human growth hormo	503	10	50.0	20	17	AAH69357	Oligonucleotide SE
C 431	10.2	51.0	25	24	AAH69357	Human aquaporin 5	504	10	50.0	20	18	AAH69357	Oligonucleotide SE
C 432	10.2	51.0	25	24	AAH69357	P. patens Na+/H+ a	505	10	50.0	20	19	AAH69357	Oligonucleotide SE
C 433	10.2	51.0	25	24	AAH69357	Oligonucleotide ad	506	10	50.0	20	19	AAH69357	Oligonucleotide SE
C 434	10.2	51.0	25	24	AAH69357	Oligonucleotide ad	507	10	50.0	20	19	AAH69357	Oligonucleotide SE
C 435	10.2	51.0	25	24	AAH69357	Oligonucleotide ad	508	10	50.0	20	20	AAH69357	Oligonucleotide SE
C 436	10.2	51.0	25	24	AAH69357	Oligonucleotide ad	509	10	50.0	20	20	AAH69357	Oligonucleotide SE
C 437	10.2	51.0	25	24	AAH69357	Oligonucleotide ad	510	10	50.0	20	20	AAH69357	Oligonucleotide SE
C 438	10.2	51.0	25	24	AAH69357	Human interleukin	511	10	50.0	20	21	AAH69357	Oligonucleotide SE
C 439	10.2	51.0	25	24	AAH69357	Oligonucleotide pr	512	10	50.0	20	21	AAH69357	Oligonucleotide SE
C 440	10.2	51.0	25	24	AAH69357	Oligonucleotide pr	513	10	50.0	20	21	AAH69357	Oligonucleotide SE
C 441	10.2	51.0	25	24	AAH69357	Oligonucleotide pr	514	10	50.0	20	22	AAH69357	Oligonucleotide SE
C 442	10.2	51.0	25	24	AAH69357	Oligonucleotide pr	515	10	50.0	20	22	AAH69357	Oligonucleotide SE
C 443	10.2	51.0	25	24	AAH69357	Oligonucleotide pr	516	10	50.0	20	22	AAH69357	Oligonucleotide SE
C 444	10.2	51.0	25	24	AAH69357	Oligonucleotide pr	517	10	50.0	20	22	AAH69357	Oligonucleotide SE
C 445	10.2	51.0	25	24	AAH69357	Oligonucleotide SE	518	10	50.0	20	22	AAH69357	Oligonucleotide SE
C 446	10.2	51.0	25	24	AAH69357	Oligonucleotide SE	519	10	50.0	20	22	AAH69357	Oligonucleotide SE
C 447	10.2	51.0	25	24	AAH69357	Oligonucleotide SE	520	10	50.0	20	24	AAH69357	Oligonucleotide SE

C 518	6.4	37.6	20	17	AZ465809	AZ465809	1M0276112	C 591	6.4	37.6	22	17	TA140A04P	AL466405 T. brucei
C 519	6.4	37.6	20	17	AZ466238	AZ466238	1M0276116	C 592	6.4	37.6	22	17	TA272E02Q	AL487827 T. brucei
C 520	6.4	37.6	20	17	AZ465923	AZ465923	1M0407B18	C 593	6.4	37.6	22	17	TA272H06Q	AL487850 T. brucei
C 521	6.4	37.6	20	17	AZ603553	AZ603553	1M0422P21	C 594	6.4	37.6	22	17	TA338G08Q	AL491807 T. brucei
C 522	6.4	37.6	20	17	AZ615402	AZ615402	1M0444A16	C 595	6.4	37.6	22	17	TA346E12P	AL496439 T. brucei
C 523	6.4	37.6	20	17	AZ654725	AZ654725	1M0529003	C 596	6.4	37.6	22	17	TA372G12P	AL496638 T. brucei
C 524	6.4	37.6	20	17	AZ785547	AZ785547	2M0029A05	C 597	6.4	37.6	22	17	TA7H01P	AL452882 T. brucei
C 525	6.4	37.6	20	17	AZ799305	AZ799305	2M0056N05	C 598	6.4	37.6	23	13	AL584237	AL584237
C 526	6.4	37.6	20	17	AZ823352	AZ823352	2M0097A22	C 599	6.4	37.6	23	13	BG926069	BG926069 HNC23-1-E
C 527	6.4	37.6	20	17	AZ853126	AZ853126	2M0156G10	C 600	6.4	37.6	23	17	AZ387861	AZ387861
C 528	6.4	37.6	20	17	AZ860554	AZ860554	2M0166C07	C 601	6.4	37.6	23	17	AZ390689	AZ390689
C 529	6.4	37.6	20	17	AZ895954	AZ895954	2M0227N12	C 602	6.4	37.6	23	17	AZ439149	AZ439149
C 530	6.4	37.6	20	17	AZ972315	AZ972315	2M0246E09	C 603	6.4	37.6	23	17	AZ451117	AZ451117
C 531	6.4	37.6	21	9	AL585450	AL585450	AL585450	C 604	6.4	37.6	23	17	AZ470337	AZ470337
C 532	6.4	37.6	21	10	AL585450	AL585450	2821108.3	C 605	6.4	37.6	23	17	AZ481838	AZ481838
C 533	6.4	37.6	21	13	BM398406	BM398406	5009-0-45	C 606	6.4	37.6	23	17	AZ514463	AZ514463
C 534	6.4	37.6	21	14	BM138406	BM138406	EST606692	C 607	6.4	37.6	23	17	AZ514463	AZ514463
C 535	6.4	37.6	21	14	BM138406	BM138406	EST606692	C 608	6.4	37.6	23	17	AZ514463	AZ514463
C 536	6.4	37.6	21	14	D20000	D20000	HUMG00970	C 609	6.4	37.6	23	17	AZ753387	AZ753387
C 537	6.4	37.6	21	17	AZ307929	AZ307929	1M0010F24	C 610	6.4	37.6	23	17	AZ780690	AZ780690
C 538	6.4	37.6	21	17	AZ309732	AZ309732	1M0016K01	C 611	6.4	37.6	23	17	AZ785466	AZ785466
C 539	6.4	37.6	21	17	AZ320773	AZ320773	1M0041C24	C 612	6.4	37.6	23	17	AZ818239	AZ818239
C 540	6.4	37.6	21	17	AZ345955	AZ345955	1M0080P19	C 613	6.4	37.6	23	17	AZ823567	AZ823567
C 541	6.4	37.6	21	17	AZ467734	AZ467734	1M0279N18	C 614	6.4	37.6	23	17	AZ833567	AZ833567
C 542	6.4	37.6	21	17	AZ479997	AZ479997	1M0301G11	C 615	6.4	37.6	23	17	AZ949056	AZ949056
C 543	6.4	37.6	21	17	AZ482019	AZ482019	1M0306117	C 616	6.4	37.6	23	17	BH790005	BH790005
C 544	6.4	37.6	21	17	AZ492310	AZ492310	1M0336D21	C 617	6.4	37.6	23	17	TA123G12Q	TA123G12Q
C 545	6.4	37.6	21	17	AZ503574	AZ503574	1M0343H19	C 618	6.4	37.6	23	17	TA158A06Q	TA158A06Q
C 546	6.4	37.6	21	17	AZ584607	AZ584607	1M0389E15	C 619	6.4	37.6	23	17	TA15C04Q	TA15C04Q
C 547	6.4	37.6	21	17	AZ598137	AZ598137	1M0412P16	C 620	6.4	37.6	23	17	TA162A12P	TA162A12P
C 548	6.4	37.6	21	17	AZ625565	AZ625565	1M0456H10	C 621	6.4	37.6	23	17	TA242D06P	TA242D06P
C 549	6.4	37.6	21	17	AZ651999	AZ651999	1M0545E01	C 622	6.4	37.6	23	17	TA296F01P	TA296F01P
C 550	6.4	37.6	21	17	AZ665199	AZ665199	1M0545E01	C 623	6.4	37.6	23	17	TA327G08Q	TA327G08Q
C 551	6.4	37.6	21	17	AZ676536	AZ676536	1M0562114	C 624	6.4	37.6	23	17	TA363D03Q	TA363D03Q
C 552	6.4	37.6	21	17	AZ745424	AZ745424	2M004M011	C 625	6.4	37.6	24	9	AL588263	AL588263
C 553	6.4	37.6	21	17	AZ785791	AZ785791	1M0030019	C 626	6.4	37.6	24	13	BM397860	BM397860
C 554	6.4	37.6	21	17	AZ796205	AZ796205	2M0051013	C 627	6.4	37.6	24	13	BM401141	BM401141
C 555	6.4	37.6	21	17	AZ819369	AZ819369	2M0089021	C 628	6.4	37.6	24	13	BM401311	BM401311
C 556	6.4	37.6	21	17	AZ819992	AZ819992	2M0091M21	C 629	6.4	37.6	24	17	AZ307229	AZ307229
C 557	6.4	37.6	21	17	AZ834089	AZ834089	2M0116C12	C 630	6.4	37.6	24	17	AZ307620	AZ307620
C 558	6.4	37.6	21	17	AZ862607	AZ862607	2M0170C23	C 631	6.4	37.6	24	17	AZ310221	AZ310221
C 559	6.4	37.6	21	17	AZ890424	AZ890424	2M0274F09	C 632	6.4	37.6	24	17	AZ339707	AZ339707
C 560	6.4	37.6	21	17	TA62F01P	TA62F01P	AL452946 T. brucei	C 633	6.4	37.6	24	17	AZ3411704	AZ3411704
C 561	6.4	37.6	22	9	AL465062 T. brucei	AL465062 T. brucei	AL465062 T. brucei	C 634	6.4	37.6	24	17	AZ409513	AZ409513
C 562	6.4	37.6	22	9	AL465062 T. brucei	AL465062 T. brucei	AL465062 T. brucei	C 635	6.4	37.6	24	17	AZ409513	AZ409513
C 563	6.4	37.6	22	9	AL465062 T. brucei	AL465062 T. brucei	AL465062 T. brucei	C 636	6.4	37.6	24	17	AZ409513	AZ409513
C 564	6.4	37.6	22	9	AL465062 T. brucei	AL465062 T. brucei	AL465062 T. brucei	C 637	6.4	37.6	24	17	AZ409513	AZ409513
C 565	6.4	37.6	22	9	AL465062 T. brucei	AL465062 T. brucei	AL465062 T. brucei	C 638	6.4	37.6	24	17	AZ409513	AZ409513
C 566	6.4	37.6	22	9	AL465062 T. brucei	AL465062 T. brucei	AL465062 T. brucei	C 639	6.4	37.6	24	17	AZ409513	AZ409513
C 567	6.4	37.6	22	9	AL465062 T. brucei	AL465062 T. brucei	AL465062 T. brucei	C 640	6.4	37.6	24	17	AZ409513	AZ409513
C 568	6.4	37.6	22	9	AL465062 T. brucei	AL465062 T. brucei	AL465062 T. brucei	C 641	6.4	37.6	24	17	AZ409513	AZ409513
C 569	6.4	37.6	22	9	AL465062 T. brucei	AL465062 T. brucei	AL465062 T. brucei	C 642	6.4	37.6	24	17	AZ409513	AZ409513
C 570	6.4	37.6	22	9	AL465062 T. brucei	AL465062 T. brucei	AL465062 T. brucei	C 643	6.4	37.6	24	17	AZ409513	AZ409513
C 571	6.4	37.6	22	9	AL465062 T. brucei	AL465062 T. brucei	AL465062 T. brucei	C 644	6.4	37.6	24	17	AZ409513	AZ409513
C 572	6.4	37.6	22	9	AL465062 T. brucei	AL465062 T. brucei	AL465062 T. brucei	C 645	6.4	37.6	24	17	AZ409513	AZ409513
C 573	6.4	37.6	22	13	BG926061	BG926061	HNC23-1-E	C 646	6.4	37.6	24	17	AZ409513	AZ409513
C 574	6.4	37.6	22	13	BM395019	BM395019	50072-2-7	C 647	6.4	37.6	24	17	AZ409513	AZ409513
C 575	6.4	37.6	22	13	BM395019	BM395019	50072-2-7	C 648	6.4	37.6	24	17	AZ409513	AZ409513
C 576	6.4	37.6	22	17	BM400797	BM400797	5009-0-79	C 649	6.4	37.6	24	17	AZ409513	AZ409513
C 577	6.4	37.6	22	17	AZ309879	AZ309879	1M0017D13	C 650	6.4	37.6	24	17	AZ409513	AZ409513
C 578	6.4	37.6	22	17	AZ311479	AZ311479	1M0026M24	C 651	6.4	37.6	24	17	AZ409513	AZ409513
C 579	6.4	37.6	22	17	AZ326642	AZ326642	1M0049D09	C 652	6.4	37.6	24	17	AZ409513	AZ409513
C 580	6.4	37.6	22	17	AZ341858	AZ341858	1M0074D03	C 653	6.4	37.6	24	17	AZ409513	AZ409513
C 581	6.4	37.6	22	17	AZ380277	AZ380277	1M0316D07	C 654	6.4	37.6	24	17	AZ409513	AZ409513
C 582	6.4	37.6	22	17	AZ480841	AZ480841	1M0302A19	C 655	6.4	37.6	24	17	AZ409513	AZ409513
C 583	6.4	37.6	22	17	AZ486653	AZ486653	1M0314A14	C 656	6.4	37.6	24	17	AZ409513	AZ409513
C 584	6.4	37.6	22	17	AZ493044	AZ493044	1M0432H09	C 657	6.4	37.6	24	17	AZ409513	AZ409513
C 585	6.4	37.6	22	17	AZ623308	AZ623308	1M0461F07	C 658	6.4	37.6	24	17	AZ409513	AZ409513
C 586	6.4	37.6	22	17	AZ633422	AZ633422	1M0461F07	C 659	6.4	37.6	24	17	AZ409513	AZ409513
C 587	6.4	37.6	22	17	AZ806109	AZ806109	2M0067O20	C 660	6.4	37.6	24	17	AZ409513	AZ409513
C 588	6.4	37.6	22	17	AZ829430	AZ829430	2M0107A09	C 661	6.4	37.6	24	17	AZ409513	AZ409513
C 589	6.4	37.6	22	17	AZ836104	AZ836104	2M0130C17	C 662	6.4	37.6	24	17	AZ409513	AZ409513
C 590	6.4	37.6	22	17	AZ958287	AZ958287	2M0255G02	C 663	6.4	37.6	24	17	AZ409513	AZ409513
					AL464946 T. brucei	AL464946 T. brucei	AL464946 T. brucei							

C 667	9.8	49.0	20	24	ABR95191	C. glutamicum air	C 740	9.8	49.0	24	21	AAA99024	H. influenzae adhe
C 668	9.8	49.0	20	24	ABR41160	Human obesity-asso	C 741	9.8	49.0	24	21	ABD01305	Primer EC280W-R to
C 669	9.8	49.0	20	24	ABR92994	Capture oligonucle	C 742	9.8	49.0	24	21	AAZ29056	PCR primer 3 for R
C 670	9.8	49.0	20	24	ABR93983	Capture oligonucle	C 743	9.8	49.0	24	21	AAH22236	Anti-A33 antigen a
C 671	9.8	49.0	20	24	ABR94202	Capture oligonucle	C 744	9.8	49.0	24	22	AAH20101	Chimeric antibody
C 672	9.8	49.0	20	24	ABR94281	Capture oligonucle	C 745	9.8	49.0	24	22	AAH39806	SNP specific lower
C 673	9.8	49.0	20	24	ABR94393	Capture oligonucle	C 746	9.8	49.0	24	22	AAH76329	Human C2-4-4 micro
C 674	9.8	49.0	20	24	ABR94404	Capture oligonucle	C 747	9.8	49.0	24	22	AAH44578	Mouse DSS-induced
C 675	9.8	49.0	20	24	ABR94627	Capture oligonucle	C 748	9.8	49.0	24	22	ABT03725	Human Olf-1-homol g
C 676	9.8	49.0	21	13	AAQ95063	3' - 5' DNA sequen	C 749	9.8	49.0	24	24	ABL54194	Streptococcus pneu
C 677	9.8	49.0	21	13	AAQ28665	ORL ANTISENSE I p	C 750	9.8	49.0	24	24	ABK68864	Escherichia canis p2
C 678	9.8	49.0	21	14	AAQ38853	Sequence of primer	C 751	9.8	49.0	24	24	ABQ00059	Oligonucleotide ad
C 679	9.8	49.0	21	14	AAQ50104	PCR primer used in	C 752	9.8	49.0	24	24	ABQ000310	Oligonucleotide ad
C 680	9.8	49.0	21	16	AAQ11981	CMV antisense olig	C 753	9.8	49.0	24	24	ABQ000324	Oligonucleotide ad
C 681	9.8	49.0	21	16	AAQ09021	Simple tandem repe	C 754	9.8	49.0	24	24	ABQ01080	Oligonucleotide ad
C 682	9.8	49.0	21	16	AAQ09024	PCR primer SK 69 d	C 755	9.8	49.0	24	24	ABQ004094	Oligonucleotide ad
C 683	9.8	49.0	21	16	AAQ09024	Antisense oligo RA	C 756	9.8	49.0	24	24	ABQ004135	Oligonucleotide ad
C 684	9.8	49.0	21	16	AAQ19822	Primer SK69 for HI	C 757	9.8	49.0	24	24	ABQ004587	Oligonucleotide ad
C 685	9.8	49.0	21	19	AAZ26484	Human polymorphic	C 758	9.8	49.0	24	24	ABQ004600	Oligonucleotide ad
C 686	9.8	49.0	21	19	AAZ26484	Human polymorphic	C 759	9.8	49.0	24	24	ABQ004628	Oligonucleotide ad
C 687	9.8	49.0	21	19	AAZ26484	Anti-CMV oligonucle	C 760	9.8	49.0	24	24	ABQ004641	Oligonucleotide ad
C 688	9.8	49.0	21	19	AAZ26484	Human biallelic po	C 761	9.8	49.0	24	24	ABQ006122	Oligonucleotide ad
C 689	9.8	49.0	21	19	AAZ26484	PCR primer 11LF-1	C 762	9.8	49.0	24	24	ABQ006163	Oligonucleotide ad
C 690	9.8	49.0	21	19	AAZ26484	Human BRCA1 exon 1	C 763	9.8	49.0	24	24	ABQ10422	Oligonucleotide ad
C 691	9.8	49.0	21	19	AAZ26484	Human BRCA1 PCR pr	C 764	9.8	49.0	24	24	ABQ10422	Oligonucleotide ad
C 692	9.8	49.0	21	19	AAZ26484	SK69 primer for am	C 765	9.8	49.0	24	24	ABQ10915	Oligonucleotide ad
C 693	9.8	49.0	21	20	AAZ23105	HIV-1 gp41 env gen	C 766	9.8	49.0	24	24	ABQ10928	Oligonucleotide ad
C 694	9.8	49.0	21	20	AAZ23105	Human cancer antiq	C 767	9.8	49.0	24	24	ABQ10956	Oligonucleotide ad
C 695	9.8	49.0	21	20	AAZ23105	BRCA1 gene specif	C 768	9.8	49.0	24	24	ABQ10969	Oligonucleotide ad
C 696	9.8	49.0	21	20	AAZ23105	Fehos exon 2 ampl	C 769	9.8	49.0	24	24	ABL55137	Oligonucleotide ad
C 697	9.8	49.0	21	21	AAZ22451	Human biallelic ma	C 770	9.8	49.0	24	24	ABL55137	Human ubiqutin C-
C 698	9.8	49.0	21	21	AAZ22451	Human biallelic ma	C 771	9.8	49.0	24	24	ABL82559	Random DNA arrange
C 699	9.8	49.0	21	21	AAZ22451	Human BRCA1 PCR pr	C 772	9.8	49.0	24	24	ABL82559	Capture oligonucle
C 700	9.8	49.0	21	21	AAZ22451	Sequence surroundi	C 773	9.8	49.0	24	24	ABL83920	Capture oligonucle
C 701	9.8	49.0	21	21	AAZ22451	Primer Ub3-3 used	C 774	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 702	9.8	49.0	21	21	AAZ22451	A. gossypii ribofl	C 775	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 703	9.8	49.0	21	21	AAZ22451	SSP1 cDNA amplifc	C 776	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 704	9.8	49.0	21	22	AAH48927	Human ERD gene ass	C 777	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 705	9.8	49.0	21	22	AAH48927	Human ERD gene ass	C 778	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 706	9.8	49.0	21	22	AAH23164	Nitric oxide synth	C 779	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 707	9.8	49.0	21	22	AAH23164	Nitric oxide synth	C 780	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 708	9.8	49.0	21	22	AAH23164	Arginine kinase an	C 781	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 709	9.8	49.0	21	22	AAH23164	Maize mRNAs DNA amp	C 782	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 710	9.8	49.0	21	22	AAH23164	Primer derived fro	C 783	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 711	9.8	49.0	21	22	AAH23164	Human ecNOS gene p	C 784	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 712	9.8	49.0	21	24	ABL49921	Methylation/activat	C 785	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 713	9.8	49.0	21	24	ABL49921	Human chromosome 2	C 786	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 714	9.8	49.0	21	24	ABL49921	Human PGE-2/NF-3 p	C 787	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 715	9.8	49.0	21	24	ABL49921	Human short inters	C 788	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 716	9.8	49.0	21	24	ABL49921	Helicobacter 16S r	C 789	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 717	9.8	49.0	21	24	ABL49921	Reverse PCR primer	C 790	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 718	9.8	49.0	21	24	ABL49921	PCR primer for pro	C 791	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 719	9.8	49.0	21	24	ABL49921	Probe for human po	C 792	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 720	9.8	49.0	21	24	ABL49921	Tail primer #247 f	C 793	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 721	9.8	49.0	21	24	ABL49921	Human ABCD1 gene r	C 794	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 722	9.8	49.0	21	24	ABL49921	Human androgen rec	C 795	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 723	9.8	49.0	21	24	ABL49921	Ras gene PCR prime	C 796	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 724	9.8	49.0	21	24	ABL49921	Human ATP-binding	C 797	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 725	9.8	49.0	21	24	ABL49921	Lactococcus lactis	C 798	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 726	9.8	49.0	21	24	ABL49921	Degenerate probe f	C 799	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 727	9.8	49.0	21	24	ABL49921	Mimip18 reverse pr	C 800	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 728	9.8	49.0	21	24	ABL49921	Elongation factor	C 801	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 729	9.8	49.0	21	24	ABL49921	Sequence of primer	C 802	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 730	9.8	49.0	21	24	ABL49921	PTEN/MMAC1 exon 6	C 803	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 731	9.8	49.0	21	24	ABL49921	PTEN/MMAC1 exon 6	C 804	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 732	9.8	49.0	21	24	ABL49921	Primer #16 used in	C 805	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 733	9.8	49.0	21	24	ABL49921	Lactococcus lactis	C 806	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 734	9.8	49.0	21	24	ABL49921	Non-coding strand	C 807	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 735	9.8	49.0	21	24	ABL49921	SK69 primer. Synt	C 808	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 736	9.8	49.0	21	24	ABL49921	Alkyl-galactoside	C 809	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 737	9.8	49.0	21	24	ABL49921	Oligonucleotide ch	C 810	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 738	9.8	49.0	21	24	ABL49921	HIV-1 PCR primer b	C 811	9.8	49.0	24	24	ABL84536	Capture oligonucle
C 739	9.8	49.0	21	24	ABL49921	Oligonucleotide pr	C 812	9.8	49.0	24	24	ABL84536	Capture oligonucle

810	6.2	36.5	23	9	AU014520	AU014520	883	6.2	36.5	25	17	AZ37071	AZ37071	IM031A16
C 811	6.2	36.5	23	9	AU256868	AU256868	C 884	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 812	6.2	36.5	23	9	AU258717	AU258717	C 885	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 813	6.2	36.5	23	10	AM063953	AM063953	C 886	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 814	6.2	36.5	23	13	BM395635	BM395635	C 887	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 815	6.2	36.5	23	13	BM396297	BM396297	C 888	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 816	6.2	36.5	23	13	BM397693	BM397693	C 889	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 817	6.2	36.5	23	13	BM398156	BM398156	C 890	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 818	6.2	36.5	23	13	BM398329	BM398329	C 891	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 819	6.2	36.5	23	13	BM399677	BM399677	C 892	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 820	6.2	36.5	23	13	BM400878	BM400878	C 893	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 821	6.2	36.5	23	14	L32041	L32041	C 894	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 822	6.2	36.5	23	17	AZ309461	AZ309461	C 895	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 823	6.2	36.5	23	17	AZ351113	AZ351113	C 896	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 824	6.2	36.5	23	17	AZ345108	AZ345108	C 897	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 825	6.2	36.5	23	17	AZ595375	AZ595375	C 898	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 826	6.2	36.5	23	17	AZ763749	AZ763749	C 899	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 827	6.2	36.5	23	17	AZ769365	AZ769365	C 900	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 828	6.2	36.5	23	17	AZ819914	AZ819914	C 901	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 829	6.2	36.5	23	17	AZ833228	AZ833228	C 902	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 830	6.2	36.5	23	17	AZ833407	AZ833407	C 903	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 831	6.2	36.5	23	17	AZ957043	AZ957043	C 904	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 832	6.2	36.5	23	17	TA251D05Q	TA251D05Q	C 905	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 833	6.2	36.5	24	9	AU256326	AU256326	C 906	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 834	6.2	36.5	24	13	BM397750	BM397750	C 907	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 835	6.2	36.5	24	13	BM399223	BM399223	C 908	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 836	6.2	36.5	24	17	AZ309298	AZ309298	C 909	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 837	6.2	36.5	24	17	AZ314246	AZ314246	C 910	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 838	6.2	36.5	24	17	AZ314670	AZ314670	C 911	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 839	6.2	36.5	24	17	AZ346816	AZ346816	C 912	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 840	6.2	36.5	24	17	AZ358150	AZ358150	C 913	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 841	6.2	36.5	24	17	AZ402579	AZ402579	C 914	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 842	6.2	36.5	24	17	AZ428700	AZ428700	C 915	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 843	6.2	36.5	24	17	AZ617422	AZ617422	C 916	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 844	6.2	36.5	24	17	AZ617463	AZ617463	C 917	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 845	6.2	36.5	24	17	AZ624698	AZ624698	C 918	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 846	6.2	36.5	24	17	AZ785162	AZ785162	C 919	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 847	6.2	36.5	24	17	AZ805942	AZ805942	C 920	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 848	6.2	36.5	24	17	AZ807126	AZ807126	C 921	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 849	6.2	36.5	24	17	AZ815479	AZ815479	C 922	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 850	6.2	36.5	24	17	TA313F10P	TA313F10P	C 923	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 851	6.2	36.5	24	17	TA313F10P	TA313F10P	C 924	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 852	6.2	36.5	24	17	TA313F10P	TA313F10P	C 925	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 853	6.2	36.5	24	17	TA313F10P	TA313F10P	C 926	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 854	6.2	36.5	24	17	TA313F10P	TA313F10P	C 927	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 855	6.2	36.5	24	17	TA313F10P	TA313F10P	C 928	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 856	6.2	36.5	24	17	TA313F10P	TA313F10P	C 929	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 857	6.2	36.5	24	17	TA313F10P	TA313F10P	C 930	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 858	6.2	36.5	24	17	TA313F10P	TA313F10P	C 931	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 859	6.2	36.5	24	17	TA313F10P	TA313F10P	C 932	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 860	6.2	36.5	24	17	TA313F10P	TA313F10P	C 933	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 861	6.2	36.5	24	17	TA313F10P	TA313F10P	C 934	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 862	6.2	36.5	24	17	TA313F10P	TA313F10P	C 935	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 863	6.2	36.5	24	17	TA313F10P	TA313F10P	C 936	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 864	6.2	36.5	24	17	TA313F10P	TA313F10P	C 937	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 865	6.2	36.5	24	17	TA313F10P	TA313F10P	C 938	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 866	6.2	36.5	24	17	TA313F10P	TA313F10P	C 939	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 867	6.2	36.5	24	17	TA313F10P	TA313F10P	C 940	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 868	6.2	36.5	24	17	TA313F10P	TA313F10P	C 941	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 869	6.2	36.5	24	17	TA313F10P	TA313F10P	C 942	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 870	6.2	36.5	24	17	TA313F10P	TA313F10P	C 943	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 871	6.2	36.5	24	17	TA313F10P	TA313F10P	C 944	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 872	6.2	36.5	24	17	TA313F10P	TA313F10P	C 945	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 873	6.2	36.5	24	17	TA313F10P	TA313F10P	C 946	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 874	6.2	36.5	24	17	TA313F10P	TA313F10P	C 947	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 875	6.2	36.5	24	17	TA313F10P	TA313F10P	C 948	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 876	6.2	36.5	24	17	TA313F10P	TA313F10P	C 949	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 877	6.2	36.5	24	17	TA313F10P	TA313F10P	C 950	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 878	6.2	36.5	24	17	TA313F10P	TA313F10P	C 951	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 879	6.2	36.5	24	17	TA313F10P	TA313F10P	C 952	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 880	6.2	36.5	24	17	TA313F10P	TA313F10P	C 953	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 881	6.2	36.5	24	17	TA313F10P	TA313F10P	C 954	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09
C 882	6.2	36.5	24	17	TA313F10P	TA313F10P	C 955	6.2	36.5	25	17	AZ62642	AZ62642	IM0269M09

C	959	9.6	48.0	24	22	AA169563	Bromo-structure do
C	960	9.6	48.0	24	22	AA164554	Human pterin methyl
C	961	9.6	48.0	24	24	ABK97947	Botulin toxin gene
C	962	9.6	48.0	24	24	ABK52391	Embryo implantatio
C	963	9.6	48.0	24	24	ABK49350	RNA polymerase II
C	964	9.6	48.0	24	24	ABA97311	Human alphasdelctaz
C	965	9.6	48.0	24	24	ABA97315	Human alphasdelctaz
C	966	9.6	48.0	24	24	ABO02407	Oligonucleotide ad
C	967	9.6	48.0	24	24	ABO08742	Oligonucleotide ad
C	968	9.6	48.0	24	24	ABO08783	Oligonucleotide ad
C	969	9.6	48.0	24	24	AB183094	Capture oligonucle
C	970	9.6	48.0	24	24	AB183095	Capture oligonucle
C	971	9.6	48.0	24	24	AB184126	Capture oligonucle
C	972	9.6	48.0	24	24	AB184127	Capture oligonucle
C	973	9.6	48.0	24	24	AB185376	Capture oligonucle
C	974	9.6	48.0	24	24	AB185377	Capture oligonucle
C	975	9.6	48.0	24	24	AB186382	Capture oligonucle
C	976	9.6	48.0	24	24	AB186383	Capture oligonucle
C	977	9.6	48.0	24	24	AB186236	Capture oligonucle
C	978	9.6	48.0	24	24	AB188237	Capture oligonucle
C	979	9.6	48.0	24	24	AB188306	Capture oligonucle
C	980	9.6	48.0	24	24	AB188307	Capture oligonucle
C	981	9.6	48.0	24	24	AB191642	Capture oligonucle
C	982	9.6	48.0	24	24	AB191643	Capture oligonucle
C	983	9.6	48.0	24	24	AB192360	Capture oligonucle
C	984	9.6	48.0	24	24	AB192361	Capture oligonucle
C	985	9.6	48.0	24	24	AA172285	CK-19 marker prime
C	986	9.6	48.0	25	19	AAV54130	Primer for human m
C	987	9.6	48.0	25	19	AAV16206	Oligonucleotide fo
C	988	9.6	48.0	25	19	AAV16202	Oligonucleotide fo
C	989	9.6	48.0	25	20	AAV52484	Reverse PCR primer
C	990	9.6	48.0	25	21	AAV52487	HLA HLA-A gene PCR
C	991	9.6	48.0	25	21	AAV52487	HLA HLA-A gene PCR
C	992	9.6	48.0	25	22	AAV52487	Novel signal trans
C	993	9.6	48.0	25	22	AAV52487	Novel signal trans
C	994	9.6	48.0	25	22	AAV52487	Human G-protein co
C	995	9.6	48.0	25	22	AAV52487	Human G-protein co
C	996	9.6	48.0	25	22	AAV52487	Human Rad51 mutat
C	997	9.6	48.0	25	22	AAV52487	Human Rad51 mutat
C	998	9.6	48.0	25	22	AAV52487	Human PRO polypept
C	999	9.6	48.0	25	22	AAV52487	Gastric acid produ
C	1000	9.6	48.0	25	22	AAV52487	Brome mosaic virus
C	1000	9.6	48.0	25	24	ABA85573	Human SP24 protein

ALIGNMENTS

RESULT 1
ID ABR99615 standard; DNA; 25 BP.

AC ABR99615;
DT 05-AUG-2002 (first entry)

DE Fungi PCR primer SEQ ID NO 187.

KW Fungus; bacteri; quantification; detection; infection; gastroenteritis;
KM ulcer; asthma; allergy; sinusitis; PCR; primer; ss.

OS Stachybotrys chartarum.

XX US6387652-B1.

XX 14-MAY-2002.

XX 13-JUN-2000; 2000US-0593012.

XX 15-APR-1998; 98US-081773P.

XX 14-APR-1999; 99US-0250990.

XX (USST) US ENVIRONMENTAL PROTECTION AGENCY.

PF Haugland R, Vesper S;
XX WPI; 2002-462353/49.
DR
XX
PT Detection and quantification of specific fungi or bacteria useful e.g.
PT in medical diagnosis and treatment of fungal and bacterial conditions;
PT by hybridizing and amplifying DNA using sequences unique to the species
PT or group of species -
XX
XX Claim 62; Column 97; 55pp; English.
XX
XX The invention relates to specific fungi or bacteria detected and
XX quantified in a sample by extracting and recovering DNA from the organism
XX in the sample and hybridizing and amplifying the DNA sequence using
XX sequences unique to the species/group of species but common to all
XX isolates of the species/group of species. The method especially employs
XX sequences selected from 225 fungal and bacterial primer and probe
XX sequences (ABN99429-ABN99653) for detection of specified fungi/fungal
XX groups or specified bacteria. The method enables detection and
XX quantification of specific fungi or bacteria, or groups of
XX fungal/bacterial species, useful medically for diagnosis and treatment of
XX fungi or bacteria associated with health problems such as infections,
XX gastroenteritis, ulcers, asthma, allergies and sinusitis. It is also
XX useful to detect and/or quantify microorganisms in the environment e.g.
XX to establish the risk of adverse health effects (e.g. pulmonary
XX haemorrhage from levels of Stachybotrys chartarum in air samples in
XX houses).
XX
XX Sequence 25 BP; 9 A; 5 C; 5 G; 6 T; 0 other;
XX
XX

Query Match 75.0%; Score 15; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GTTGGCAGTCAGAG 20
DB 1 GTTGGCAGTCAGAG 15

RESULT 2
ID ABR29212 standard; DNA; 25 BP.

AC ABR29212;

DT 23-APR-2002 (first entry)

DE Stachybotrys chartarum reverse PCR primer.

KW Fungal detection; bacterial detection; probe; primer; ss.

OS Stachybotrys chartarum.

XX WO200196612-A2.

XX 20-DEC-2001.

XX 13-JUN-2001; 2001WO-US18892.

XX 13-JUN-2000; 2000US-0593012.

XX (USST) US ENVIRONMENTAL PROTECTION AGENCY.

XX Haugland R, Vesper SJ;

XX WPI; 2002-098078/13.

XX Detecting and quantifying fungi and bacteria, involves obtaining a
XX sequence of the fungus, extracting the DNA from the sample, and
XX subjecting the DNA to polymerase chain reaction and fluorescent probe
XX analysis -
XX

PS Claim 62; Page 20; 110pp; English.

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 GCTTCGGCGGGA 15
 12 GCTTCGGCGGGA 23
 Db

RESULT 3
 AZ307451/c 21 bp DNA linear GSS 29-SEP-2000

LOCUS 1M0009509F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION

ACCESION AZ307451

VERSION 1

KEYWORDS GSS

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

REFERENCE 1 (bases 1 to 21)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Iselm,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
 and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00

Plate: 0009 row: E column: 09

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. 21

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0009509"

/clone_1ib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/note="Vector: PMD42ny; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (gi|4732114|gb|AF1207.1), a copy-number
 inducible derivative of plasmid RI. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 5 a 8 c 6 g 2 t

ORIGIN

Query Match 58.8%; Score 10; DB 17; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.8e+05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 GCTTCGGCGG 13
 12 GCTTCGGCGG 3
 Db

RESULT 4
 A1421881/c 25 bp mRNA linear EST 30-MAR-1999

LOCUS U15H03.X1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:2103221 3'
 DEFINITION similar to TF:P93237 P93237 PROLINE-RICH PROTEIN PRP2 PRECURSOR. 1,
 mRNA sequence.

ACCESION A1421881

VERSION 1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 25)

AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute / National Institute of Neurological
 Disorders and Stroke, Brain Tumor Genome Anatomy Project
 (CGAP/BRGAP), Tumor Gene Index
 Unpublished (1998)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgapbs-remail.nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
 Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILMW at:
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 764 Std Error: 0.00

Seq primer: -40UP from Gldco

High quality sequence stop: 1.

Location/Qualifiers

1. 25

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2103221"

/clone_1ib="NCI CGAP Brn23"

/tissue_type="Glioblastoma (pooled)"

/lab_host="DH10B"

/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer (5'
 TGTTACCAATCTGAAGTGGAGCGCGCCATATCTTTTCTTTTCTTTTCTTTT
 T 3'); double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified pT73 vector.
 Library is normalized, and was constructed by Bento
 Soares and M. Fatima Bonaldo."

BASE COUNT 8 a 13 c 3 g 1 t

ORIGIN

Query Match 57.6%; Score 9.8; DB 9; Length 25;

Best Local Similarity 84.6%; Pred. No. 4.9e+05;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGCTTCGGCGG 14

16 TTGCTTCGGCGG 4

Db

RESULT 5

Best Local Similarity 100.0%; Pred. No. 3.8e+05;

TM116120

CC diagnosis, prevention and treatment of conditions associated with Nck-2
CC expression, such as leukaemia and breast cancer.
XX
SQ Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 other;
Query Match 69.0%; Score 13.8; DB 22; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 TTGGGTTGGCCTCA 17
Db 19 TCTGGTTGCCACATCA 3
RESULT 5
AAZ59948
ID AAZ59948 standard; DNA; 21 BP.
XX
AC AAZ59948;
XX
XX 08-MAY-2000 (first entry)
XX
DE Human delta-like protein (DLK) PCR primer, SEQ ID NO:6.
XX
KM Drug exposure; drug abuse; gene expression; EST;
KM expressed sequence tag; identification; colerance; addiction; therapy;
KM screening; cellular response; ethanol; expression analysis;
KM Northern blot; delta-like protein; DLK; reverse transcriptase-PCR;
KM RT-PCR primer; ss.
XX
OS Homo sapiens.
XX
PM WO9967267-A1.
XX
PD 29-DEC-1999.
XX
PE 22-JUN-1999; 99WO-US1839.
XX
PR 22-JUN-1998; 98US-0090268.
PR 21-JUN-1999; 99US-0337022.
XX
PA (REGC) UNIV CALIFORNIA.
PI Miles MF, Lai C, Lockhart DJ;
DR WPI; 2000-147195/13.
XX
PT Novel methods for evaluating an organisms response to alcohol used to
PR evaluate drug treatment and identifying susceptibility to alcohol -
XX
XX Example 3; Page 69; 98pp; English.
XX
CC The invention relates the identification of genes whose expression
CC levels are altered by chronic exposure to one or more drugs of abuse
CC (e.g., ethanol, stimulants, opiates). The methods of the invention
CC monitor the response of a cell to a drug of abuse, and comprise
CC contacting the cell with the drug of abuse, and detecting the expression
CC of one or more of 218 expressed sequence tags (ESTs) via the use of
CC probes that specifically hybridise to the ESTs. The methods are used to
CC identify genes whose expression levels are altered by chronic or acute
CC exposure to one or more drugs of abuse. The identification of genes
CC whose regulation is altered in alcohol tolerance and/or addiction
CC provides a valuable tool to evaluate the response to one or more drugs of
CC abuse. Evaluation of the nature of this response provides information
CC useful in designing therapeutic and recovery regimens, and in evaluating
CC the susceptibility of an organism or patient to drugs in a medical
CC context. Monitoring the expression of identified genes and/or ESTs
CC provides a mechanism by which test agents can be screened for the ability
CC to alter or modulate the response of the organism to drugs of abuse.
CC Sequences AAZ59944-259951 represent reverse transcriptase-PCR (RT-PCR)
CC primers used to amplify 4 cDNA hybridisation probes from SH-SY5Y-AH1861
CC human neuroblastoma cell total RNA. The probes were used in Northern
CC blot analysis of gene expression in control and ethanol-treated

CC SH-SY5Y-AH1861 cells in an exemplification of the present invention. The
CC genes whose expression was analysed were dopamine beta-hydroxylase (DBH)
CC and sodium-dependent norepinephrine transporter (NET), both of which are
CC involved in norepinephrine metabolism; delta-like protein (DLK), and
CC monocyte chemoattractant peptide 1 (MCP-1). These genes are thought to
CC be important targets of ethanol. Primers AAZ59948-259949 were used to
CC generate the delta-like protein (DLK) probe.
XX
SQ Sequence 21 BP; 4 A; 6 C; 5 G; 6 T; 0 other;
Query Match 69.0%; Score 13.8; DB 21; Length 21;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 TTGGGTTGGCCTCAG 18
Db 4 TTGGGTTGCACACAG 20
RESULT 6
AAQ50799/C
ID AAQ50799 standard; RNA; 17 BP.
XX
AC AAQ50799;
XX
XX 26-MAY-1994 (first entry)
XX
DE HBV target sequence 25.
XX
KM RNA; enzyme; enzymatic RNA molecule; ERN; cleave; RNA; mRNA; HbRNA;
KM picornavirus; HIV; immunodeficiency virus; hepatitis B virus; HBV;
KM papilloma virus; HPV; Epstein-Barr virus; EBV; TGLV;
KM T-cell leukaemia virus; hepatitis C virus; HCV; cytomegalovirus;
KM influenza virus; HSV; herpes simplex virus; vector; immune response;
KM antibody; ribozyme; viral RNA; treatment; ss.
XX
OS Synthetic.
XX
PM WO9323569-A.
XX
PD 25-NOV-1993.
XX
PE 29-APR-1993; 93WO-US04020.
XX
XX 11-MAY-1992; 92US-0882689.
XX 14-MAY-1992; 92US-0882712.
XX 14-MAY-1992; 92US-0882713.
XX 14-MAY-1992; 92US-0882714.
XX 14-MAY-1992; 92US-0882823.
XX 14-MAY-1992; 92US-0882824.
XX 14-MAY-1992; 92US-0882886.
XX 14-MAY-1992; 92US-0882888.
XX 14-MAY-1992; 92US-0882889.
XX 14-MAY-1992; 92US-0882921.
XX 14-MAY-1992; 92US-0883823.
XX 14-MAY-1992; 92US-0883849.
XX 14-MAY-1992; 92US-0884073.
XX 14-MAY-1992; 92US-0884074.
XX 14-MAY-1992; 92US-0884333.
XX 14-MAY-1992; 92US-0884422.
XX 14-MAY-1992; 92US-0884431.
XX 14-MAY-1992; 92US-0884436.
XX 14-MAY-1992; 92US-0884521.
XX 31-JUL-1992; 92US-0923738.
XX 26-AUG-1992; 92US-0936086.
XX 18-SEP-1992; 92US-0948359.
XX 15-OCT-1992; 92US-0963322.
XX 07-DEC-1992; 92US-0967129.
XX 07-DEC-1992; 92US-0967130.
XX 07-DEC-1992; 92US-0967133.
XX
PA (RIBO-) RIBOZYME PHARM INC.

FEATURES
Source

Seq primer: T3.
Location/Qualifiers

1. 18
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_1lb="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+, Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT 1 a 7 c 6 g 4 t
ORIGIN

Query Match 54.1%; Score 9.2; DB 13; Length 18;
Best Local Similarity 78.6%; Pred. No. 9.6e+05;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCTTCGGCGGAGC 17
DB 17 GCCACGGCGGAGC 4

RESULT 8
AZ781461 19 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0019E20R Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCG2M0019E20 R, DNA sequence.
ACCESSION AZ781461
VERSION AZ781461.1 GI:12914177
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0019 row: E column: 20
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES
Source

1. 19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0019E20"
/clone_1lb="Mouse 10kb plasmid UGCGM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (914732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 0 a 1 c 11 g 7 t
ORIGIN

Query Match 54.1%; Score 9.2; DB 17; Length 19;
Best Local Similarity 78.6%; Pred. No. 9.7e+05;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGG 14
DB 3 GTTGCTTCGGCGG 16

RESULT 9
AZ432681 20 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0218N1F Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCG1M0218N1 F, DNA sequence.
ACCESSION AZ432681
VERSION AZ432681.1 GI:10556694
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0218 row: N column: 11
Seq primer: GGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
Source

1. 20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0218N1"
/clone_1lb="Mouse 10kb plasmid UGCGM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

PT therapy methods -
XX
PS Disclosure; Page 14; 44pp; English.
XX

CC The present invention relates to a member of the family of proteins known
CC as ADAMTS (A Disintegrin And Metalloprotease Thrombospondin domain)
CC protein, the new member being designated ADAMTS-S1. The invention also
CC relates to polynucleotides encoding ADAMTS-S1, antibodies to ADAMTS-S1,
CC assays for studying the function of ADAMTS-S1, assays for determining
CC agonists or antagonists of ADAMTS-S1, and to the use of ADAMTS-S1
CC polypeptides or polynucleotides in diagnostic, biotherapeutic, or gene
CC therapy methods. ADAMTS proteins and ADAMTS protein agonists and
CC antagonists are useful in the manufacture of a medicament for treating
CC arthritis (osteoarthritis and rheumatoid arthritis), inflammatory bowel
CC disease, Crohn's disease, emphysema, acute respiratory distress syndrome,
CC asthma, chronic obstructive pulmonary disease, Alzheimer's disease, organ
CC transplant toxicity and rejection, cachexia, allergy, cancer (such as
CC solid tumour cancer including colon, breast, lung, prostate, brain, and
CC haematopoietic malignancies including leukaemia and lymphoma), tissue
CC ulcerations, restenosis, periodical disease, epidermolysis bullosa,
CC osteoporosis, loosening of artificial joint implants, atherosclerosis
CC (including atherosclerotic plaque rupture), aortic aneurysm (including
CC abdominal aortic and aneurysm), congestive heart failure, myocardial
CC infarction, stroke, cerebral ischemia, head trauma, spinal cord injury,
CC neurodegenerative diseases (acute and chronic), autoimmune disorders,
CC Huntington's disease, Parkinson's disease, migraine, depression,
CC peripheral neuropathy, pain, cerebral amyloid angiopathy, noctropic or
CC cognitive enhancement, amyotrophic lateral sclerosis, multiple sclerosis,
CC ocular angiogenesis, corneal injury, macular degeneration, abnormal wound
CC healing, burns, infertility or diabetic shock. This polynucleotide
CC sequence represents the antisense primer used for amplification of the
CC ADAMTS-S1 DNA of the invention. This amplification was involved in the
CC expression of ADAMTS-S1 in chondrocytes derived from osteoarthritis (OA)
CC cartilage and induction by proinflammatory cytokines.

SO Sequence 23 BP; 7 A; 7 C; 5 G; 4 T; 0 other;

Query Match 66.0%; Score 13.2; DB 24; Length 23;
Best Local Similarity 83.3%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGGGTTGGCAGCTCAGG 20
DB 19 TGGGTTTCCAGCTCAGTG 2

RESULT 9

AB183724/C
ID AB183724 standard; DNA; 24 BP.

AC AB183724;
XX

DT 15-FEB-2002 (first entry)

DE Capture oligonucleotide zip ID#664 oligo #1.

XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
XX ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
XX infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
XX cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
XX environmental monitoring; food industry; feed industry; ss.

OS Synthetic.
XX

PN W0200179548-A2.
XX

PD 25-OCT-2001.
XX

PF 04-APR-2001; 2001WO-US10958.
XX

PR 14-APR-2000; 2000US-197271P.
XX

PA (CORR) CORNELL RES FOUND INC.

XX Barany F, Zivri M, Gerry NP, Favis R, Klaman R;
XX WPI; 2002-034366/04.
XX

PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch -
XX
PS Example 5; Fig 25; 300pp; English.
XX

CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where:
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting composite scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.

SO Sequence 24 BP; 3 A; 9 C; 6 G; 6 T; 0 other;

Query Match 64.0%; Score 12.8; DB 24; Length 24;
Best Local Similarity 87.5%; Pred. No. 3.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCGTTGGCAGCTCAGA 19
DB 16 GCGATTGCCAGCTCAGA 1

RESULT 10

AB183725
ID AB183725 standard; DNA; 24 BP.

AC AB183725;
XX

DT 15-FEB-2002 (first entry)

DE Capture oligonucleotide zip ID#664 oligo #2.

XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
XX ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
XX infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
XX cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
XX environmental monitoring; food industry; feed industry; ss.

OS Synthetic.
XX

PN W0200179548-A2.
XX

PD 25-OCT-2001.
XX

PF 04-APR-2001; 2001WO-US10958.
XX

PR 14-APR-2000; 2000US-197271P.
XX

PA (CORR) CORNELL RES FOUND INC.

sequence.
ACCESSION BH854200 GI:21425071
VERSION BH854200.1
KEYWORDS GSS.
SOURCE chalcid cress.
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 25)
AUTHORS Alonso,J.M., Leises,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrihab
C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (Signal)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of Atg49990 and
300 bases of the 3' end of Atg50000.
Class: TDNA tagged.
Location/Qualifiers
1. 25
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_078881.34.80.x"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT 5 a 5 c 5 g 10 t
ORIGIN
Query Match 54.1%; Score 9.2; DB 17; Length 25;
Best Local Similarity 78.6%; Pred. No. 1e+06; 3; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 TGCTTCGCGGAA 16
Db 9 TCCTTCGCGGAA 22
RESULT 13
AZ659612 20 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0537A07F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0537A07 F, DNA sequence.
ACCESSION AZ659612
VERSION AZ659612.1 GI:11796758
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,B., Pedersen,T., Rellily
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weis

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0537 Row: A Column: 07
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. 20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0537A07"
/note="UGCGIM0537A07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab_vector="PMD29uv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1473214[gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT 2 a 8 c 8 g 2 t
ORIGIN
Query Match 52.9%; Score 9; DB 17; Length 20;
Best Local Similarity 70.6%; Pred. No. 1.2e+06; 5; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 GTTGCTTCGCGGAA 17
Db 4 GGTGCTTCGCGGAA 20
RESULT 14
AZ663981 21 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0543J22R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0543J22 R, DNA sequence.
ACCESSION AZ663981
VERSION AZ663981.1 GI:11801127
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,B., Pedersen,T., Rellily
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weis

PT Novel protein LppQ of Mycoplasma mycoides subsp. mycoides SC, or its
PT parts useful for detection of Mycoplasma and for preparation of vaccine
PT for treating infection caused by Mycoplasma -
XX
PS Example 3; Page 26; 56pp; English.
XX
CC The present sequence is a PCR primer used for site directed mutagenesis
CC (to exchange Mycoplasma specific UGATP codons to universal UGATP
CC codons) of lipoprotein LppQ gene from Mycoplasma mycoides subsp.
CC mycoides SC (small colony type). LppQ is useful in a diagnostic method
CC for the direct or indirect detection of M. mycoides subsp. mycoides SC,
CC where the diagnostic method is an immunological method such as
CC immunoblotting, serological tests or ELISA (enzyme linked immunosorbent
CC assay). LppQ DNA and protein are useful for the preparation of a vaccine
CC against infection by M. mycoides subsp. mycoides SC. LppQ DNA is useful
CC for the preparation of live, attenuated or inactivated cells of
CC M. mycoides subsp. mycoides SC to be used as marker vaccine, where the
CC cells lack the ability to synthesize the LppQ lipoprotein. LppQ DNA is
CC also useful for expressing LppQ protein in a detection method for
CC M. mycoides subsp. mycoides SC, where the detection method is selected
CC from PCR and hybridisation. LppQ protein is useful for detecting
CC antibodies directed to it in a body fluid such as serum or bronchial
CC fluid from an animal. LppQ protein are also useful as a specific antigen
CC for sero-detection of contagious bovine pleuropneumonia (CBPP).
XX
SQ Sequence 25 BP; 15 A; 3 C; 5 G; 2 T; 0 other;
XX
Query Match 64.0%; Score 12.8; DB 22; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 2 TTGCGTTGGCACTCA 17
23 TTGTTTGGCACTCA 8
XX
RESULT 13
ABK41539 standard; DNA; 20 BP.
XX
AC ABK41539;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human CTNNA3 exon-specific lower PCR primer #15.
XX
KM Human; mouse; alpha-catenin; primer; ss; cytostatic; anti-infectivity;
KM cadherin-catenin related pathway; heart; testis; cancer; gene therapy;
KM cadherin-catenin related disease; specifically dilated cardiomyopathy;
KM cardiomyopathy; male infertility; CTNNA3; PCR; alpha T-catenin.
XX
OS Homo sapiens.
XX
PN WO200204636-A1.
XX
PD 17-JAN-2002.
XX
PF 28-JUN-2001; 2001WO-EP07392.
XX
PR 12-JUL-2000; 2000EP-0202472.
XX
PR 14-JUL-2000; 2000US-218309P.
XX
PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI Van Roy F, Goossens S, Janssens B, Vanpoucke G;
XX
XX WPI; 2002-171717/22.
XX
PT New alpha catenin polypeptides and polynucleotides encoding them,
PT useful for predicting, diagnosing or treating cadherin-catenin related
PT diseases, particularly cardiomyopathies, cancer and male infertility -
XX
PS Examples; Page 36; 132pp; English.

XX
CC The invention relates to human and mouse alpha-catenin polypeptides and
CC their associated polynucleotides. The polypeptides and related antibodies
CC are useful for modulating the cadherin-catenin related pathway in
CC selected organs, such as the heart and testis. The nucleic acids and the
CC antibodies are useful in the diagnosis and/or prediction of the
CC likelihood of developing cadherin-catenin related diseases. The nucleic
CC acids may also be used to predict the likelihood of developing cancer or
CC in diagnosing cancer, and in gene therapy. The polypeptide, the nucleic
CC acid or the antibody is useful in manufacturing a medicament for treating
CC cadherin-catenin related diseases, such as cancer, cardiomyopathy,
CC specifically dilated cardiomyopathy, and male infertility. Sequences
CC ABK41510-ABK41599 represent PCR primers used to amplify DNA encoding
CC human and mouse alpha-catenin polypeptides, including the CTNNA3 gene
CC which encodes human alpha T-catenin.
XX
SQ Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 other;
XX
Query Match 63.0%; Score 12.6; DB 24; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 2 TTGCGTTGGCACTCAGAG 20
1 TGGCACTTGACACTCAGAG 19
XX
DB 1 TGGCACTTGACACTCAGAG 19
XX
RESULT 14
AAC67562 standard; DNA; 21 BP.
XX
AC AAC67562;
XX
DT 14-FEB-2001 (first entry)
XX
DE Alzheimer's disease-linked mitochondrial SNP PCR primer #262.
XX
KM Human; mitochondrial genome; single nucleotide polymorphism; SNP;
KM Alzheimer's disease; mtDNA; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200063441-A2.
XX
PD 26-OCT-2000.
XX
PF 19-APR-2000; 2000WO-US10906.
XX
PR 20-APR-1999; 99US-0130447.
XX
PR 22-OCT-1999; 99US-0160901.
XX
PA (MITO-) MITOKOR.
XX
PI Hermsstadt C, Davis RE;
XX
XX WPI; 2000-672748/65.
XX
PT Diagnosing a subject at the risk for or having Alzheimer's disease
PT comprises determining at least one single nucleotide polymorphism in
PT mitochondrial DNA associated with the disease in the sample from the
PT subject -
XX
XX Example 9; Page 55; 89pp; English.
XX
CC The present invention describes a novel method for determining the risk
CC of or diagnosing Alzheimer's disease using single nucleotide
CC polymorphisms (SNPs) present in an individual's mitochondrial DNA
CC (mtDNA). In addition, the SNPs identified can be used to identify agents
CC suitable for use in treating Alzheimer's disease. Sequences
CC AAC67301-C67610 are PCR primers used to demonstrate the method of the
CC invention.
XX
SQ Sequence 21 BP; 5 A; 2 C; 6 G; 8 T; 0 other;

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

2 a 4 c 11 g 8 t

ORIGIN

Query Match 52.9%; Score 9; DB 17; Length 25;
Best Local Similarity 70.6%; Pred. No. 1.3e+06;
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCGGAC 17

Db 4 GTTGCTTCGGCGGAC 20

RESULT 17
AZ339811/c 23 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0071M19P Mouse 10kb plasmid UNGCM library Mus musculus genomic
DEFINITION clone UNGCM0071M19 F. DNA sequence.

ACCESSION AZ339811 GI:10414445

VERSION AZ339811.1

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 23)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 2C S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0071 row: M column: 19
Seq primer: CGTTGTAACAGCGCCACGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES

source

1. 23
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UNGCM0071M19"
/clone_lib="Mouse 10kb plasmid UNGCM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

11 a 7 c 3 g 2 t

ORIGIN

Query Match 51.8%; Score 8.8; DB 17; Length 23;
Best Local Similarity 83.3%; Pred. No. 1.6e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGCTTCGGCGG 13

Db 17 TTGCTTCGTCAG 6

RESULT 18
TA106C010/c 23 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 106c01, reverse sequence,
DEFINITION genomic survey sequence.

ACCESSION AL461896 GI:11831493

VERSION AL461896

KEYWORDS GSS.

SOURCE Trypanosoma brucei.

ORGANISM Trypanosoma brucei

REFERENCE 1 (bases 1 to 23)

AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajadream,M.A. and Barrell,B.G.

TITLE Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk

JOURNAL Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 CUTac 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

COMMENT Email: nelsaye@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1. 23
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="106c01"

BASE COUNT 8 a 6 c 8 g 1 t

ORIGIN

Query Match 51.8%; Score 8.8; DB 17; Length 23;
Best Local Similarity 83.3%; Pred. No. 1.6e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTGCTTCGGCG 12

|||||

CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NCO expression. The
CC present sequence is an amberzyme molecule of the invention.

Sequence 17 BP; 2 A; 6 C; 3 G; 6 U; 0 other;

Query Match	61.0%	Score 12.2;	DB 23;	Length 17;
Best Local Similarity	53.9%	Pred. No. 7.6e+03;		
Matches 9;	Conservative	5;	Mismatches 3;	Indels 0;
				Gaps 0

```

ay      1 TTGCGTTGCCACTCA 17
        : :| :| :| :| :| :|
Db      1 UCUGCUTUUGGCCACUCA 17

```

RESULT 17
ABK17746/c
ID ABK17746 standard; RNA; 17 BP

AC ABK17746;

DT. 09-APR-2002 (first entry)

DB	Human ERG hammerhead ribozyme target sequence, Seq ID No 393.
xx	

KM Human hammerhead ribozyme; cytosolic; antitumour; antidiabetic;
KM opththalmology; antirheumatic; antipsoriatic; virucide; osteoprotic;
KM vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KM tumour angiogenesis; diabetic retinopathy; macular degeneration;
KM neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris
KM angiolipoma of tubercous scleriosis; port-wine stain; wound healing;
KM Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KM Ostler-Weber-rendu syndrome; leukaemia; osteoporosis; DNasezyme; inozyme;
KM amberyzyme.

Homo sapiens.

PN WO200188124-A2.

PD 22-NOV-2001

PF 16-MAY-2001; 2001WO-US15866

PR 16-MAY-2000; 2000US-0572021

PA (RIBO-) RIBOZYME PHARM INC.

100

100

DR WPI; 2002-082995/11.

PT Novel polymulectide which down regulates expression of Ets-related
PT gene, useful for treating cancer, diabetic retinopathy, macular
PT degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber
PT syndrome -

PS Claim 4; Page 65; 149pp; English.

CC The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an ERS-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, vertica
CC vulgaris, angiolipoma of tuberosus sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunder-Weber syndrome, Osier-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or

chemotherapy treatment. (I) is useful for reducing ERG activity in a cell, by contacting the cell with (I). (I) is useful for cleaving RNA of ERG gene, by contacting (I) with RNA, in the presence of a divalent cation such as Mg²⁺. (I) is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically targeting genes that share homology with ERG gene or ERG fusion genes. ABK17554-ABK22719 represent nucleic acids, including antisense and enzymatic nucleic acid molecules which regulate expression of ERG, and related PCR primers of the invention.

Sequence 17 BP; 3 A; 5 C; 5 G; 4 U; 0 other,

Query Match	61.0%	Score 12.2;	DB 24	Length 17;
Best Local Similarity	82.4%	Pred. No. 7.6e+03;		
Matches 14;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps .0

```

QY      4 GCGTTGCCACTCAGAG 20
          ||||| ||||| ||
Db      17 GCGTTCGCGACTCAAG 1

```

RESULT 18	
AAQ90138/c	
ID	AAQ90138 standard; DNA; 22 BP.
XY	

AAQ90138;
AC
VV

DT 05-JAN-1996 (first entry)
YY

DE Transthyretin (TTR) gene exon 2 PCR primer 1791-1769.

KM Transchryletin; TTR; PCR primer 1791-1769; mutation Gly6-Ser6;
KM exon 2; familial Alzheimer's disease; amyloidosis; ss.

OS Synthetic

PN W09512815-A1.

PD 11-MAY-1995

PF 03-NOV-1994; 94WO-US12584

PR 04-NOV-1993; 93US-0148117

PA (UYNV) UNIV NEW YORK STATE RES FOUND

PI Eisenberg-grunberg M, Goldgaber DY, Schwartzman AL,

DR WPI; 1995-185876/24

PT Methods of preventing aggregation of free beta-amyloid protein
PT useful for diagnosis, prevention and treatment of amyloidosis
XX
PS Example 5; Page 32; 54pp; English.

CC AAQ90137 and AAQ90138 are a pair of

CC AAO90137 and AAO90138 are a pair of primers for the PCR amplification
CC of the transthyretin (TTR) gene exon 2. They were used in a
CC PCR-SSCP analysis for the identification of the TTR mutation Gly6
CC to Ser1. This mutation, as a genetic marker for familial Alzheimer's
CC disease, is useful for identifying people at risk of developing
CC amyloidosis.

Sequence 22 BP; 8 A; 2 C; 10 G; 2 T; 0 other;

Query Match	61.0%	Score 12.2	DB 16	Length 22
Best Local Similarity	82.4%	Pred. No. 7.9e+03		
Matches 14, Conservative	0	Mismatches 3	Indels 0	Gaps 0

QY 1 TTTCGCTTGCCACTCA 17
|||
Db 19 TTCCCGTTGCCCTCA 3

XX 13-JUN-2000; 2000US-0593012.
PR (USST) US ENVIRONMENTAL PROTECTION AGENCY.
XX
XX Haugland R, Vesper SJ;
PI MPI; 2002-098078/13.
XX
XX Detecting and quantifying fungi and bacteria, involves obtaining a
PT sequence of the fungus, extracting the DNA from the sample, and
PT subjecting the DNA to polymerase chain reaction and fluorescent probe
PT analysis.
XX
XX Claim 37; Page 14; 110pp; English.
XX
XX The invention relates to a method of detecting and quantifying fungi and
CC bacteria, involving obtaining a sequence of the microorganism to be
CC detected and quantified, extracting the DNA from the sample, and
CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
CC probe analysis. The method is useful for identifying and quantifying
CC specific fungi and bacteria using specific DNA sequences. The specific
CC DNA sequences are useful for the real time detection of PCR products with
CC a fluorescent probe system or other molecular probes like hybridisation.
CC ABK29026-ABK29474 represent fungal and bacterial PCR primers and probes
CC used in the method of the invention.
XX
XX Sequence 24 BP; 9 A; 4 C; 6 G; 5 T; 0 other;
SQ
XX
XX Query Match 61.0%; Score 12.2; DB 18; Length 25;
XX Best Local Similarity 82.4%; Pred. No. 8e+03; 3; Indels 0; Gaps 0;
XX Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 4 GCCTTGGCCACTCAGAG 20
Db 1 GCCTTGGCCACTCAGAG 17
XX
XX RESULT 22
XX AAT92300/c
XX ID AAT92300 standard; DNA; 25 BP.
XX
XX AAT92300;
XX
XX 20-JAN-1998 (first entry)
XX
XX Breast cancer tissue cDNA PCR primer from the IL-3R alpha gene.
XX
XX Breast cancer; PCR primer; cytokine; oncostatin M; prophylaxis;
XX leukaemia inhibitory factor; agonist; cell morphology; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX WO9716202-A1.
XX
XX 09-MAY-1997.
XX
XX 25-OCT-1996; 96WO-AU00676.
XX
XX 07-JUN-1996; 96AU-0000364.
XX 27-OCT-1995; 95AU-0006242.
XX 27-OCT-1995; 95AU-0006243.
XX 27-MAR-1996; 96AU-0008966.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Begley CG, Douglas AM;
XX MPI; 1997-271880/24.
XX
XX Use of cytokine(s), especially oncostatin M and leukaemia inhibitory
PT factor or functional derivatives or agonists - for the treatment or

PT prophylaxis of breast cancer by ameliorating the effects of or
XX delaying the onset of cancer.
XX
XX Example 3; Page 57; 83pp; English.
XX
XX A novel method has been developed for the treatment or prophylaxis of
CC breast cancer in a mammal. The method involves administering one or
CC more cytokines or functional derivatives or agonists of one or more
CC cytokines for a time and under conditions to ameliorate the effects
CC of or to delay onset of cancer. The present sequence represents a
CC PCR primer which amplifies the cDNA from breast cancer tissue. The
CC cytokines can inhibit the growth of breast cancer cells and also
CC detrimentally affect cell morphology.
XX
XX Sequence 25 BP; 5 A; 11 C; 5 G; 4 T; 0 other;
SQ
XX
XX Query Match 61.0%; Score 12.2; DB 18; Length 25;
XX Best Local Similarity 82.4%; Pred. No. 8e+03; 3; Indels 0; Gaps 0;
XX Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 3 TCGCTTGGCCACTCAGA 19
Db 20 TCGCTTGGCCACTCAGA 4
XX
XX RESULT 23
XX AAV95070
XX ID AAV95070 standard; RNA; 17 BP.
XX
XX AAV95070;
XX
XX 24-FEB-1999 (first entry)
XX
XX Canine IL-2 receptor g-chain substrate position 24.
XX
XX Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain;
XX hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;
XX autoimmune disease; psoriasis; allergy; inflammatory disease;
XX graft rejection; ss.
XX
XX Synthetic.
XX OS Canis sp.
XX
XX WO9824913-A2.
XX
XX 11-JUN-1998.
XX
XX 02-DEC-1997; 97WO-US21748.
XX
XX 03-DEC-1996; 96US-0758306.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX McSwigen JA, Stinchcomb DT;
XX MPI; 1998-33332/29.
XX
XX Ribozymes targeted to interleukin 2 - useful for treating e.g.
PT cancer, autoimmune disease and allergies
XX
XX Claim 4; Page 45; 61pp; English.
XX
XX The present sequence invention describes ribozymes targeted to modulate
CC the synthesis and/or expression of interleukin (IL)-2R gamma encoded
CC RNA. AAV93889 to AAV94574 represent specifically claimed substrate sequences
CC from the present invention. The ribozymes can be used for the treatment
CC of, e.g. graft rejection, autoimmune disease, cancer, psoriasis,
CC allergy and other inflammatory conditions. The ribozymes are also used
CC to induce tolerance in a recipient to alloantigen from a donor.
XX
XX Sequence 17 BP; 3 A; 7 C; 2 G; 5 U; 0 other;
SQ

```

Db          22 TSCCACC GCGGAGC 8

RESULT 26
LOCUS      TA307A070/c          25 bp    DNA       linear    GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 307A07, reverse sequence,
ACCESSION  AL488826
VERSION     AL488826.1  GI:11864396
SOURCE      Trypanosoma brucei.
ORGANISM    Trypanosoma brucei.
            Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrett,B.G.
TITLE       Direct Submission
JOURNAL     Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrett@sanger.ac.uk and
            nh@sanger.ac.uk
COMMENT     Constructed at the institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb) . The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaidin and B.
            Barrett, Oxford University Press, 1999) .
            Email: nelsayed@cligr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
            Location/Qualifiers
FEATURES             source
                     1..25
                        /organism="Trypanosoma brucei"
                        /strain="TREU927"
                        /db_xref="taxon:5691"
                        /clone="307A07"
BASE COUNT          7 a      11 c      4 g      3 t
ORIGIN
1
Query Match          50.6%; Score 8.6; DB 17; Length 25;
Best Local Similarity 73.3%; Pred. No. 2.1e+06;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy      3 TGCCTCGGCGGGAGC 17
          ||| ||| |||
          ||| ||| |||
Db      23 TGTTTGGGCGGAGC 9
RESULT 27
LOCUS      AA931484/c          22 bp    mRNA       linear    EST 03-JUN-1998
DEFINITION os91h03.s1 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1612757 3',
            similar to SM-BRM_HUMAN P10161 SALIVARY PROLINE-RICH PROTEIN PO
            1; contains MER22.c1 MSRI repetitive element ;, mRNA sequence.
ACCESSION  AA931484
VERSION     AA931484.1  GI:317973
SOURCE      EST.
            human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Cniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 22)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.

```

Email: ccgaps-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrrp/image/image.html

Trace considered overall poor quality
Seq primer: -40ml3 fwd. Et from Amer sham
High quality sequence stop: 1.

Location/Qualifiers

1. 22

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1612757"
/clone_11b="NCI CGAP GC3"
/tissue_type="pooled_germ cell tumors"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is not normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT

5 a 9 c 8 g 0 t

ORIGIN

Query Match 49.4%; Score 8.4; DB 9; Length 22;
Best Local Similarity 50.0%; Pred. No. 2.6e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

cy 5 CTTGGCGGG 14
|||||
|||||

Db 17 CTTGGCGGG 8

RESULT 28

A1352536/c

LOCUS

DEFINITION

22 bp mRNA linear EST 30-DEC-1998

A1352536

gt08f05.x1 NCI CGAP GC4 Homo sapiens CDNA clone IMAGE:1947009 3'

similar to SW:MG_N_DROME P49028 MAGO NASHI PROTEIN., mRNA

sequence.

A1352536

A1352536.1 GI:4089742

EST.

human.

ORGANISM

Homo sapiens

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 22)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Unpublished (1997)

Contact: Robert Straubeberg, Ph.D.
Email: ccgaps-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrrp/image/image.html

JOURNAL

COMMENT

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

XX ABK02000;
AC
XX 12-MAR-2002 (first entry)
XX
DE Human NOGO Zinzyne #322.
XX
KM Human, 86; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KM cerebroprotective; neuroprotective; antiparkinsonian;
KM muscular; CD20; neurite growth inhibitor gene; NOGO; haemorrhagic ribozyme;
KM DNAzyme; inozyme; G-cleaver; amberzyme; zinzyne; lymphoma; leukaemia;
KM B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KM human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KM MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
KM inflammatory arthropathy; central nervous system injury;
KM cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KM chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KM Parkinson's disease; ataxia; Huntington's disease;
KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200159103-A2.
XX
BD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04273.
XX
XX 11-FEB-2000; 2000US-181797P.
PR 28-FEB-2000; 2000US-185516P.
PR 06-MAR-2000; 2000US-187128P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
PI Blact L, McSwiggen J, Chowrira BM;
XX
DR WPI; 2001-607195/69.
XX
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
PT and central nervous system injury
XX
PS Claim 88; Page 101; 200pp; English.
XX
XX The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOCO).
CC The nucleic acid may be enzymatic nucleic acids (e.g., a ribozyme or a
CC DNAzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
CC possessing an NCR motif), a G-cleaver (cleaving RNA with a NYN
CC motif), or an amberyzyme (cleaving RNA with an NCR triplet), a zinzyne
CC (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used
CC to cleave RNA of CD20 in the presence of a divalent cation that is
CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce
CC CD20 activity of the cell and treat a patient having a condition
CC associated with the level of CD20. The treatment may further comprise the
CC use of one or more therapies. In particular, the CD20 targeting
CC nucleic acid may be used to treat lymphoma, the CD20 targeting
CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
CC low-grade or follicular NHL, lymphocytic leukaemia, HIV (human
CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
CC thrombocytopenia, and inflammatory arthropathy. The NOGO-targeting
CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a
CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
CC may be contacted with a cell to reduce NOGO activity of the cell and
CC treat a patient having a condition associated with the level of NOGO. The
CC treatment may further comprise the use of one or more therapies.

CC In particular, the NOGO-targeting nucleic acid may be used to treat
CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The
CC present sequence is a zinzyne molecule of the invention.
XX
SQ Sequence 17 BP; 3 A; 6 C; 3 G; 5 U; 0 other;
XX
Query Match 59.0%; Score 11.8; DB 23; Length 17;
Best Local Similarity 60.0%; Pred. No. 1.2e+04;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
XX
Dy 3 TGCCTTGGCAGCTCA 17
|||:|||||:
Db 2 UGCUUUGCCACUCA 16
XX
RESULT 27
AAV23720/C
ID AAV23720 standard; DNA; 20 BP.
XX
AC AAV23720;
XX
DT 20-AUG-1998 (first entry)
XX
DE PCR primer used in the course of the invention.
XX
KM Lipase; variant; improved wash performance; removal; lipid stain;
KM reduced calcium dependence; one-cycle wash efficiency; detergent;
KM cleaning composition; PCR primer; 86.
XX
OS Synthetic.
OS Pseudomonas pseudocaligenes.
XX
PN M09808939-A1.
XX
PD 05-MAR-1998.
XX
PF 26-AUG-1997; 97WO-DK0345.
XX
PR 29-AUG-1996; 96US-0029190.
PR 27-AUG-1996; 96DK-0000902.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Okkels JS, Svendsen A;
XX
DR WPI; 1998-230259/20.
XX
XX Variants of lipase from Pseudomonas containing specific amino acid
PT substitutions - deletions or additions, having improved wash
PT performance in detergent formulations
XX
PS Disclosure; Page 74; 104pp; English.
XX
CC PCR primers AAV23717-23 were used during the course of the invention.
CC The specification describes Pseudomonas pseudocaligenes lipase
CC variants. The variant lipases described in the specification has have
CC better wash performance than the original lipase. It has improved
CC removal of lipid stains, reduced calcium dependence, better compatibility
CC with detergents or their components, increased hydrophobicity, altered
CC substrate specificity and better one-cycle wash efficiency. The variant
CC lipase is used in detergent and cleaning compositions.
XX
SQ Sequence 20 BP; 8 A; 4 C; 7 G; 1 T; 0 other;
XX
Query Match 59.0%; Score 11.8; DB 19; Length 20;
Best Local Similarity 86.7%; Pred. No. 1.2e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0294 row: P column: 19
Seq primer: CACACAGGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source
1..22
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0294P19"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/note="Vector: PMD42uv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|473214|gb|AF1297.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
7 a 8 c 3 g 4 t

Query Match 49.4%; Score 8.4; DB 17; Length 22;
Best Local Similarity 90.0%; Pred. No. 2.6e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGCGCGGAAC 17
|||
Db 22 CGGTGGGAAC 13

RESULT 32
TA219C09P 22 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 219C09, forward sequence,
DEFINITION genomic survey sequence.
ACCESSION AL479371.1 GI:11845122
VERSION AL479371.1
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 22)
Hall, N., Bowman, S., Lennard, N. J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S. E., Rajandream, M. A. and Barrell, B. G.
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

COMMENT nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J. C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..22
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="219C09"

BASE COUNT
ORIGIN
3 a 8 c 4 g 7 t

Query Match 49.4%; Score 8.4; DB 17; Length 22;
Best Local Similarity 90.0%; Pred. No. 2.6e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTGCTTCGCG 11
|||
Db 10 TTGCTTCGCC 19

RESULT 33
A2475852 20 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0294A18f Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0294A18 F, DNA sequence.
ACCESSION A2475852
VERSION A2475852.1 GI:10633977
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenan, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0294 row: A column: 18
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source
1..20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0294A18"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

```

PN      WO200055325-A2.
XX
XX      21-SEP-2000.
XX
XX      17-MAR-2000; 2000WO-US07392.
XX
XX      18-MAR-1999; 99US-0125219.
XX      01-APR-1999; 99US-0127409.
XX      18-MAY-1999; 99US-0134770.
XX      13-SEP-1999; 99US-0153584.
XX      17-SEP-1999; 99US-0154603.
XX
XX      (UYCH-) UNIV CHICAGO.
XX
XX      Preuss D, Copenhaver G, Keith K;
XX      WPI; 2000-587529/55.
XX
XX      Recombinant DNA construct comprising a plant centromere, useful for
XX      producing stably inherited microchromosomes which can serve as vectors for
XX      the construction of transgenic plant and animal cells -
XX
XX      Disclosure; Page 279; 1449pp; English.
XX
XX      The present invention relates to a recombinant DNA construct of a plant
XX      (Arabidopsis thaliana) centromere. The constructs are useful for
XX      producing stably inherited microchromosomes which can serve as vectors for
XX      the construction of transgenic plant and animal cells expressing
XX      selected proteins such as hormones, enzymes, interleukins, clotting
XX      factors, cytokines, antibodies, and growth factors.
XX
XX      Sequence 20 BP; 9 A; 4 C; 5 G; 2 T; 0 other;
XX
XX      Query Match      59.0%; Score 11.8; DB 21; Length 20;
XX      Best Local Similarity 86.7%; Pred. No. 1.2e+04;
XX      Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX      1 TTTGCGTTGCGACT 15
XX      17 TTTCCGTTTGGCACT 3
XX
XX      Db
XX
XX      RESULT 31
XX      ABL44914
XX      ID ABL44914 standard; DNA; 20 BP.
XX      AC ABL44914;
XX      DT 11-APR-2002 (first entry)
XX      DE Human chromosome 1p36-35 PCR primer SEQ ID NO:1958.
XX      KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis;
XX      genome; PCR primer; ss.
XX      OS Homo sapiens.
XX      PN JP2001321190-A.
XX      PD 20-NOV-2001.
XX      PF 12-MAR-2001; 2001JP-0068285.
XX      PR 10-MAR-2000; 2000JP-0066716.
XX      PA (RIKA) RIKAGAKU KENKYUSHO.
XX      PA (GENO-) GENOTEX YG.
XX      DR WPI; 2002-144136/19.
XX      PT Arraying genome clones -
XX      PS Claim 4; Page 43; 528pp; Japanese.

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XX
XX      The present invention describes a method of arraying genome clones. The
XX      method comprises: (a) clones of the genomic libraries contained in
XX      multiwell plates numbered for discrimination are mixed in each of the
XX      multiwell plates; (b) a primer designed based on the chromosome marker
XX      sequence is added to the mixture to carry out an amplification reaction;
XX      (c) a signal corresponding to the marker is detected from the resultant
XX      amplified product to specify the discrimination Nos. of the multiwell
XX      plates containing the clones having said marker sequence; (d) the order
XX      of the markers is changed so that the same discrimination Nos. succeed to
XX      the maximum in the specified discrimination Nos. to array the multiwell
XX      plates; (e) the clones in the multiwell plates of the specified
XX      discrimination Nos. are mixed respectively in each well of longitudinal
XX      and lateral directions; (f) the mixed clones are cultured and the
XX      resultant cultures are amplified by using the above primer; (g) signals
XX      are detected from the amplified products; (h) the clones in the multiwell
XX      plates are specified from the detected result; and (i) the clones are
XX      microarrayed as the positions on the chromosome and arrayed. The
XX      microarray is useful for gene analysis. ABL42957 to ABL45322 represent
XX      PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
XX      represent PCR primers for human chromosome 21q22.1, which are
XX      specifically claimed for use in the present invention.
XX
XX      Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 other;
XX
XX      Query Match      59.0%; Score 11.8; DB 24; Length 20;
XX      Best Local Similarity 86.7%; Pred. No. 1.2e+04;
XX      Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX      6 GTTGGCACTCAGAG 20
XX      1 GTTAGCCACTCCGAG 15
XX
XX      Db
XX
XX      RESULT 32
XX      AAH24199/c
XX      ID AAH24199 standard; DNA; 23 BP.
XX      AC AAH24199;
XX      DT 11-SEP-2001 (first entry)
XX      DE PCR primer, SEQ ID NO:10, used to isolate ageing inhibition-related DNA.
XX      KW Mouse; ageing inhibition-related DNA; ageing inhibitory protein;
XX      recombinant production; transgenic animal; detection; drug screening;
XX      ligand identification; ageing-related disorder; premature ageing;
XX      PCR primer; ss.
XX      OS Synthetic.
XX      PN WO200138529-A1.
XX      PD 31-MAY-2001.
XX      PF 17-NOV-2000; 2000WO-JP08121.
XX      PR 19-NOV-1999; 99JP-0329649.
XX      PA (KYOW) KYOWA HAKKO KOGYO KK.
XX      PI Shirishi N, Sekine S, Nabeshima Y, Fujimori T, Ito S;
XX      DR WPI; 2001-367689/38.
XX      PT Polypeptide for treatment of premature aging -
XX      PS Example 1; Page 89; 94pp; Japanese.
XX
XX      The invention relates to 3 novel mouse proteins which inhibit ageing
XX      (AAH23664-AAH23666) and to the nucleic acids encoding them (AAH24193-
XX      AAH24195). The invention also relates to recombinant vectors, host
XX      cells and transgenic non-human animals comprising DNA encoding a

```

/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
Query Match
Best Local Similarity 48.2%; Score 8.2; DB 17; Length 20;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TTGCTTCGCGCG 14
Db 5 TTGCTTCGCGTG 17

RESULT 36
LOCUS AZ355490 21 bp DNA GSS 02-OCT-2000
DEFINITION clone UUGC1M0095N14 F, DNA sequence.
ACCESSION AZ355490
VERSION AZ355490.1 GI:10468057
KEYWORDS GSS.
SOURCE Mus musculus.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0095 row: N column: 14
Seq primer: CTTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1..21
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0095N14"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"

/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
Query Match
Best Local Similarity 48.2%; Score 8.2; DB 17; Length 21;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTTCTTCGCGCG 13
Db 4 GTTCTTCATGG 16

RESULT 37
LOCUS AA908627 22 bp mRNA EST 13-APR-1998
DEFINITION cg86e01.s1 NCI CGAP Ov8 Homo sapiens CDNA clone IMAGE:145192 3' similar to SW:U1A6_HUMAN P30041 24 KD PROTEIN ;, mRNA sequence.
ACCESSION AA908627
VERSION AA908627.1 GI:3048032
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 22)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbe-remail.nih.gov
unknown library type
Trace considered overall poor quality
Seq primer: -40m13 fwd. Et from Amerham
High quality sequence stop: 1.
Location/Qualifiers
1..22
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:145192"
/clone_lib="NCI CGAP_Ov8"
/issue_type="serous adenocarcinoma"
/lab_host="DH10B"
/note="Organ: ovary; Vector: pCMV-SPORT4; Site: 1; SalI, Site: 2; NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.1 kb. Life Technologies catalog #: 10982-015"

BASE COUNT
ORIGIN
Query Match
Best Local Similarity 48.2%; Score 8.2; DB 9; Length 22;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

SOURCE
house mouse.

ORGANISM
Mus musculus

REFERENCE
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)

AUTHORS
Dunn,D., Royagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A.
and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 1000 Std Error: 0.00
Plate: 0028 row: H column: 03
Seq primer: CACACAGGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.

FEATURES
source
1..23
location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0028H03"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN
4 a 3 c 12 g 4 t

Query Match
Best Local Similarity 48.2%; Score 8.2; DB 17; Length 23;
Best Local Similarity 76.9%; Pred. No. 3.3e+06;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY
4 GCTTGGCGGGA 16
||| ||| ||| |||
DB 10 GCTGAGGGGGA 22

Search completed: June 7, 2003, 09:43:43
Job time : 1020.33 secs

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XX OS Naja naja siamensis.
XX PN WO200170173-A2.
XX PD 27-SEP-2001.
XX PF 14-MAR-2001; 2001WO-US08150.
XX PR 23-MAR-2000; 2000US-0533454.
XX PA (PHYL-) PHYLAMED CORP.
XX PI Mundschchenk DD, Reid PF;
XX DR WPI; 2001-616350/71.
XX PT Composition for preventing HIV infection of mammalian cells comprises
XX PT an anti-immunodeficiency virus immunokine capable of binding to a
XX PT cellular protein by which HIV infection of the cell is prevented.
XX PS Example 1; Page 30; 54pp; English.
XX CC The present invention relates to a composition for preventing HIV
XX CC infection of mammalian cells. The composition comprises an
XX CC anti-immunodeficiency virus immunokine (a neurotoxin) capable of binding
XX CC to a cellular protein in a manner that prevents HIV infection of the
XX CC cell. One such neurotoxin is alpha-cobratoxin from Naja naja siamensis
XX CC (Thailand cobra). The present sequence is a PCR primer which was used to
XX CC amplify alpha-cobratoxin cDNA for use in the present invention.
XX SQ Sequence 21 BP; 4 A; 6 C; 3 G; 8 T; 0 other;
XX
XX Query Match 58.0%; Score 11.6; DB 22; Length 21;
XX Best Local Similarity 77.8%; Pred. No. 1.6e+04;
XX Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TTTGGCTTGGCAGTCAG 18
Db 2 TTTTCATTGCGCATTGAG 19
XX
RESULT 40
XX ABL43246
XX ID ABL43246 standard; DNA; 21 BP.
XX AC ABL43246;
XX DT 11-APR-2002 (first entry)
XX DE Human chromosome 1p36-35 PCR primer SEQ ID NO:290.
XX KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis;
XX KW genome; PCR primer; se.
XX OS Homo sapiens.
XX PN JP2001321190-A.
XX PD 20-NOV-2001.
XX PF 12-MAR-2001; 2001JP-0068285.
XX PR 10-MAR-2000; 2000JP-0066716.
XX PA (RIKA) RIKAGAKU KENKUSHO.
XX PA (GENO-) GENOTEX YG.
XX DR WPI; 2002-144136/19.
XX PT Arraying genome clones -
XX PS Claim 4; Page 10; 528pp; Japanese.

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XX CC The present invention describes a method of arraying genome clones. The
XX CC method comprises: (a) clones of the genomic libraries contained in
XX CC multiwell plates numbered for discrimination are mixed in each of the
XX CC multiwell plates; (b) a primer designed based on the chromosome marker
XX CC sequence is added to the mixture to carry out an amplification reaction;
XX CC (c) a signal corresponding to the marker is detected from the resultant
XX CC amplified product to specify the discrimination Nos. of the multiwell
XX CC plates containing the clones having said marker sequence; (d) the order
XX CC of the markers is changed so that the same discrimination Nos. succeed to
XX CC the maximum in the specified discrimination Nos. to array the multiwell
XX CC plates; (e) the clones in the multiwell plates of the specified
XX CC discrimination Nos. are mixed respectively in each well of longitudinal
XX CC and lateral directions; (f) the mixed clones are cultured and the
XX CC resultant cultures are amplified by using the above primer; (g) signals
XX CC are detected from the amplified products; (h) the clones in the multiwell
XX CC plates are specified from the detected result; and (i) the clones are
XX CC reconstituted as the positions on the chromosome and arrayed. The
XX CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
XX CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
XX CC represent PCR primers for human chromosome 21q22.1, which are
XX CC specifically claimed for use in the present invention.
XX SQ Sequence 21 BP; 3 A; 9 C; 1 G; 8 T; 0 other;
XX
XX Query Match 58.0%; Score 11.6; DB 24; Length 21;
XX Best Local Similarity 77.8%; Pred. No. 1.6e+04;
XX Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TTTGGCTTGGCAGTCAG 18
Db 1 TTTACATTTCCTCTCAG 18

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Search completed: June 7, 2003, 08:30:37
Job time : 180.727 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 07:18:59 ; Search time 164.727 Seconds
(without alignments)
273.421 Million cell updates/sec

Title: US-10-080-959a-2

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Sequence: 1 ttgcgttcgcaccacagag 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 1698378

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.0	25	24	ABN99615	Fungi PCR primer S
2	15.0	25	24	ABK29212	Stachybotrys chart
3	14.4	24	22	AAH56097	Human SCNA3 PCR-SS
4	13.8	20	22	AAK2656	Human NCK-2 phosph
5	13.8	21	21	AAQ59948	Human delta-like p
6	13.4	17	14	AAQ50799	HBV taget sequenc
7	13.4	24	19	AAV5581	STS probe GV10 gen
8	13.2	23	24	AAK98779	Antisense primer f
9	12.8	24	24	AB183724	Capture oligonucle

10	12.8	64.0	24	AB183725	Capture oligonucle
11	12.8	64.0	25	AAD07981	M. mycoides LppQ 5
12	12.8	64.0	25	AAD07982	M. mycoides LppQ 5
13	12.6	63.0	20	ABK41539	Human CTNNA3 exon-
14	12.6	63.0	21	AAK67562	Alzheimer's disease
15	12.6	63.0	21	AAQ58843	Human NABH virus primer
16	12.2	61.0	17	ABK02611	Human NOGO Ambertz
17	12.2	61.0	17	ABK17746	Human ERG hamerthe
18	12.2	61.0	22	AAQ90138	Transhyretin (TTR
19	12.2	61.0	24	AAZ30442	Degenerate primer
20	12.2	61.0	24	ABN99536	Fungi PCR primer S
21	12.2	61.0	24	ABK29133	Paecilomyces lilac
22	12.2	61.0	25	AAK92300	Breast cancer tlas
23	12.2	61.0	17	AAV95070	Canine IL-2 recept
24	12.2	61.0	21	AAK64985	Rat OB receptor PC
25	12.2	61.0	23	AAK21460	RT-PCR primer, 232
26	11.8	59.0	17	ABK02000	Human NOGO Zinzyme
27	11.8	59.0	20	AAV23720	PCR primer used in
28	11.8	59.0	20	AAK95488	PCR primer used to
29	11.8	59.0	20	AAK02576	PCR primer #7. Sy
30	11.8	59.0	20	AAK23122	Arabidopsis thalia
31	11.8	59.0	20	ABL44914	Human chromosome 1
32	11.8	59.0	23	AAH24199	PCR primer, SEQ ID
33	11.8	59.0	24	ABK49704	Human kinase uridy
34	11.8	59.0	24	AB188868	Capture oligonucle
35	11.8	59.0	24	AB188869	Capture oligonucle
36	11.6	58.0	19	AAQ34205	Upstream PCR prime
37	11.6	58.0	20	AAI66253	s-cervistoxin potas
38	11.6	58.0	21	AAI69969	alpha-cobratoxin p
39	11.6	58.0	21	AAI69969	Human chromosome 1
40	11.6	58.0	21	ABL43246	Sequence upstream
41	11.6	58.0	22	AAQ33559	Oligonucleotide ch
42	11.6	58.0	24	AAV05057	Oligonucleotide ad
43	11.6	58.0	24	ABQ08241	Oligonucleotide ad
44	11.6	58.0	24	ABQ08372	Oligonucleotide ad
45	11.6	58.0	24	ABQ08413	Oligonucleotide ad
46	11.6	58.0	25	AAH59820	Primer for JNK2 nu
47	11.6	58.0	25	AAH41882	JNK2 gene PCR prim
48	11.6	58.0	25	AAH39055	SNP specific SNR
49	11.4	57.0	15	ABK63990	Human Bf gene alle
50	11.4	57.0	17	AAK07448	Hammerhead ribozym
51	11.4	57.0	20	AAK08249	p212, PCR primer f
52	11.4	57.0	21	AAK05684	Binary vector back
53	11.4	57.0	24	AAQ21129	Primer FPCRPROR fo
54	11.4	57.0	24	AAK8841	PCR primer 2 used
55	11.4	57.0	24	AAH25008	Nucleotide sequenc
56	11.4	57.0	25	AAK71006	Single nucleotide
57	11.4	57.0	25	AAK82988	HIV6 detecting pro
58	11.4	57.0	25	AAK90744	Human secretory pr
59	11.4	57.0	25	ABK66421	Human gene specif
60	11.2	56.0	17	ABK00505	Human NOGO Hamerh
61	11.2	56.0	17	ABK18676	Human ERG G-cleave
62	11.2	56.0	19	AAQ13541	Probe JFL329 to co
63	11.2	56.0	19	AAK44568	Antisense oligo HU
64	11.2	56.0	19	AAK80607	Oligonucleotide IS
65	11.2	56.0	19	AAZ59338	Human STR2 inton
66	11.2	56.0	19	AAK00702	Sequencing primer
67	11.2	56.0	19	AAK38170	NOV2 gene specific
68	11.2	56.0	20	AAQ13447	Probe to mutant co
69	11.2	56.0	20	AAV06902	Modified oligonuc
70	11.2	56.0	20	AAZ00682	Human GPC exon 9
71	11.2	56.0	20	AAZ00604	Human GPC4 exon 7B
72	11.2	56.0	20	AAK06128	Human Sema7A codin
73	11.2	56.0	20	AB196581	Capture oligonucle
74	11.2	56.0	21	AAK58076	ICAM-1 antisense o
75	11.2	56.0	21	AAV38612	Human ICAM-1, E-se
76	11.2	56.0	21	AAV17884	Human albumin forw
77	11.2	56.0	22	AAV57864	Human chromosome 1
78	11.2	56.0	24	AB189732	Capture oligonucle
79	11.2	56.0	24	AB189733	Capture oligonucle
80	11.2	55.0	19	AAK60163	Human ATM gene exo
81	11.2	55.0	20	AAK97421	Interferon regulat
82	11.2	55.0	20	AAK95546	PCR primer used to

Capture oligonucle
M. mycoides LppQ 5
M. mycoides LppQ 5
Human CTNNA3 exon-
Alzheimer's disease
Human NABH virus primer
Human NOGO Ambertz
Human ERG hamerthe
Transhyretin (TTR
Degenerate primer
Fungi PCR primer S
Paecilomyces lilac
Breast cancer tlas
Canine IL-2 recept
Rat OB receptor PC
RT-PCR primer, 232
Human NOGO Zinzyme
PCR primer used in
PCR primer used to
PCR primer #7. Sy
Arabidopsis thalia
Human chromosome 1
PCR primer, SEQ ID
Human kinase uridy
Capture oligonucle
Upstream PCR prime
s-cervistoxin potas
alpha-cobratoxin p
Human chromosome 1
Sequence upstream
Oligonucleotide ch
Oligonucleotide ad
Oligonucleotide ad
Oligonucleotide ad
Primer for JNK2 nu
JNK2 gene PCR prim
SNP specific SNR
Human Bf gene alle
Hammerhead ribozym
p212, PCR primer f
Binary vector back
Primer FPCRPROR fo
PCR primer 2 used
Nucleotide sequenc
Single nucleotide
HIV6 detecting pro
Human secretory pr
Human gene specif
Human NOGO Hamerh
Human ERG G-cleave
Probe JFL329 to co
Antisense oligo HU
Oligonucleotide IS
Human STR2 inton
Sequencing primer
NOV2 gene specific
Probe to mutant co
Modified oligonuc
Human GPC exon 9
Human GPC4 exon 7B
Human Sema7A codin
Capture oligonucle
ICAM-1 antisense o
Human ICAM-1, E-se
Human albumin forw
Human chromosome 1
Capture oligonucle
Capture oligonucle
Human ATM gene exo
Interferon regulat
PCR primer used to

80	7.6	44.7	19	17	A2345359	A2345359	1M0079D23	C	153	7.4	43.5	25	9	AU257776	AU257776	1M0079D23	
C	81	7.6	44.7	19	17	A2361152	A2361152	1M0104A16	C	154	7.4	43.5	25	13	BM400880	A2345359	1M0079D23
C	82	7.6	44.7	19	17	A2480905	A2480905	1M0302N22	C	155	7.4	43.5	25	13	A2372385	A2345359	1M0124A16
C	83	7.6	44.7	19	17	A2586436	A2586436	1M0392016	C	156	7.4	43.5	25	17	A2768960	A2768960	1M0559G07
C	84	7.6	44.7	20	13	BM397553	BM397553	5009-0-34	C	157	7.4	43.5	25	17	A27979075	A27979075	2M0255G08
C	85	7.6	44.7	20	13	BM398892	BM398892	5009-0-50	C	158	7.2	42.4	15	13	BM398834	BM398834	5009-0-5-
C	86	7.6	44.7	20	13	BM399755	BM399755	5009-0-60	C	159	7.2	42.4	16	9	AA936037	AA936037	n253F05.8
C	87	7.6	44.7	20	17	A2595239	A2595239	1M0407B18	C	160	7.2	42.4	19	9	A1625518	A1625518	1M0407B18
C	88	7.6	44.7	20	17	A2662848	A2662848	1M0524K07	C	161	7.2	42.4	19	17	A2453412	A2453412	1M0524K07
C	89	7.6	44.7	20	17	A2964089	A2964089	2M0207A13	C	162	7.2	42.4	19	17	A2805995	A2805995	2M0207A13
C	90	7.6	44.7	21	17	A2309054	A2309054	1M0012A18	C	163	7.2	42.4	19	17	A2805995	A2805995	2M0207A13
C	91	7.6	44.7	21	17	A2645640	A2645640	1M0511N07	C	164	7.2	42.4	19	17	A2805995	A2805995	2M0207A13
C	92	7.6	44.7	21	17	A2780653	A2780653	2M0018E17	C	165	7.2	42.4	19	17	A2805995	A2805995	2M0207A13
C	93	7.6	44.7	22	17	A2583690	A2583690	1M0378E16	C	166	7.2	42.4	20	17	A2309963	A2309963	1M0378E16
C	94	7.6	44.7	22	17	A2589849	A2589849	1M0399A09	C	167	7.2	42.4	20	17	A2512414	A2512414	1M0399A09
C	95	7.6	44.7	23	13	BM398474	BM398474	5009-0-45	C	168	7.2	42.4	20	17	A2810573	A2810573	2M0076K11
C	96	7.6	44.7	23	13	BM398474	BM398474	5009-0-45	C	169	7.2	42.4	21	17	A2359244	A2359244	1M0102D03
C	97	7.6	44.7	23	17	A2737746	A2737746	1M0137D15	C	170	7.2	42.4	21	17	A2792515	A2792515	1M0137D15
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C	99	7.6	44.7	23	17	A2779607	A2779607	2M0016E18	C	172	7.2	42.4	21	17	BH758186	BH758186	2M0016E18
C	100	7.6	44.7	23	17	A2784648	A2784648	2M0027P11	C	173	7.2	42.4	22	9	AA931331	AA931331	2M0027P11
C	101	7.6	44.7	23	17	A2823400	A2823400	2M0097K24	C	174	7.2	42.4	22	13	BM398732	BM398732	5009-0-49
C	102	7.6	44.7	23	17	A2831999	A2831999	2M0116N24	C	175	7.2	42.4	22	17	A2592243	A2592243	1M0403F05
C	103	7.6	44.7	24	17	A2650143	A2650143	1M0520I11	C	176	7.2	42.4	22	17	TA47B10P	TA47B10P	1M0520I11
C	104	7.6	44.7	24	17	TR238D04Q	TR238D04Q	1M0520I11	C	177	7.2	42.4	23	17	A2328328	A2328328	1M046B16
C	105	7.6	44.7	25	9	A1000280	A1000280	ov10e04.s	C	178	7.2	42.4	23	17	A2350054	A2350054	1M0087L18
C	106	7.6	44.7	25	9	A1049424	A1049424	ubj3f08.r	C	179	7.2	42.4	23	17	A2430197	A2430197	1M024M02
C	107	7.6	44.7	25	9	A1471696	A1471696	cl199F05.x	C	180	7.2	42.4	23	17	A2456925	A2456925	1M0260J06
C	108	7.6	44.7	25	12	BF732128	BF732128	EST-NGR-1	C	181	7.2	42.4	23	17	A2475927	A2475927	1M0294B21
C	109	7.6	44.7	25	17	A2645830	A2645830	1M0513I04	C	182	7.2	42.4	23	17	A2511153	A2511153	1M0356M01
C	110	7.6	44.7	25	17	A2779686	A2779686	2M0016J20	C	183	7.2	42.4	23	17	A2824724	A2824724	2M0095D06
C	111	7.6	44.7	25	17	A2788397	A2788397	2M0035N19	C	184	7.2	42.4	23	17	TA101C01Q	TA101C01Q	1M0356M01
C	112	7.6	44.7	25	17	A2802728	A2802728	2M0061B18	C	185	7.2	42.4	23	17	TA178H03P	TA178H03P	1M0356M01
C	113	7.6	44.7	25	17	BH847831	BH847831	SALX.0595	C	186	7.2	42.4	24	17	A2341147	A2341147	1M0073F24
C	114	7.4	43.5	17	2	HSM007757	HSM007757	1M042907 Homo sapi	C	187	7.2	42.4	24	17	A2415688	A2415688	1M0190C03
C	115	7.4	43.5	19	13	BM397268	BM397268	5009-0-30	C	188	7.2	42.4	24	17	A2443113	A2443113	1M0237G08
C	116	7.4	43.5	19	13	CO1584	CO1584	HUMS000858	C	189	7.2	42.4	24	17	A2451051	A2451051	1M0230D12
C	117	7.4	43.5	19	17	A2475079	A2475079	1M0293B17	C	190	7.2	42.4	24	17	A2465432	A2465432	1M0257B19
C	118	7.4	43.5	20	13	BM4001334	BM4001334	5009-0-9-	C	191	7.2	42.4	24	17	A2762096	A2762096	1M0575B19
C	119	7.4	43.5	20	17	A2308179	A2308179	1M0100K19	C	192	7.2	42.4	24	17	A2781101	A2781101	1M0193J01
C	120	7.4	43.5	20	17	A2377739	A2377739	1M0132A14	C	193	7.2	42.4	24	17	BH814314	BH814314	1M0193J01
C	121	7.4	43.5	20	17	A2478502	A2478502	1M0298B09	C	194	7.2	42.4	24	17	TR115E01P	TR115E01P	1M0298B09
C	122	7.4	43.5	20	17	A2497572	A2497572	1M0334B14	C	195	7.2	42.4	25	9	AA953687	AA953687	1M0334B14
C	123	7.4	43.5	20	17	A2655977	A2655977	1M0531E13	C	196	7.2	42.4	25	9	AA9594917	AA9594917	1M0531E13
C	124	7.4	43.5	21	17	A2659612	A2659612	1M0537A07	C	197	7.2	42.4	25	17	A2472671	A2472671	1M0537A07
C	125	7.4	43.5	21	17	A2794301	A2794301	2M0048G05	C	198	7.2	42.4	25	17	A2643950	A2643950	1M0507L11
C	126	7.4	43.5	21	17	A2803575	A2803575	2M0064K04	C	199	7.2	42.4	25	17	A2760227	A2760227	1M0553L18
C	127	7.4	43.5	21	17	A2955804	A2955804	2M0222L03	C	200	7.2	42.4	25	17	A2799596	A2799596	2M0048M20
C	128	7.4	43.5	21	17	TA232G12Q	TA232G12Q	1M0480787 T. brucei	C	201	7.2	42.4	25	17	BH813291	BH813291	1M0480787
C	129	7.4	43.5	21	17	TA629F01P	TA629F01P	1M0465062 T. brucei	C	202	7.2	42.4	25	17	CSN06D19	CSN06D19	1M0465062
C	130	7.4	43.5	22	13	BM395774	BM395774	5009-0-11	C	203	7.2	42.4	15	13	BM396119	BM396119	5009-0-18
C	131	7.4	43.5	22	17	A2474957	A2474957	1M0245C24	C	204	7.2	42.4	19	17	A2768918	A2768918	1M0569F08
C	132	7.4	43.5	22	17	A2651001	A2651001	1M0521O23	C	205	7.2	42.4	19	17	A2812572	A2812572	2M0079O15
C	133	7.4	43.5	22	17	TR328D01P	TR328D01P	1M0531I07	C	206	7.2	42.4	19	17	A2858978	A2858978	2M0164F24
C	134	7.4	43.5	23	17	A2481657	A2481657	1M0306K01	C	207	7.2	42.4	20	14	BO901238	BO901238	1M0306K01
C	135	7.4	43.5	23	17	A2621487	A2621487	1M0454A17	C	208	7.2	42.4	20	14	BO901239	BO901239	1M0454A17
C	136	7.4	43.5	23	17	A2653869	A2653869	1M0527D14	C	209	7.2	42.4	20	17	A2434383	A2434383	1M0220C17
C	137	7.4	43.5	23	17	A2784963	A2784963	2M0028F20	C	210	7.2	42.4	20	17	A2455752	A2455752	1M0258F17
C	138	7.4	43.5	23	17	TR266D01P	TR266D01P	1M0488313 T. brucei	C	211	7.2	42.4	20	17	A2489864	A2489864	1M0323I01
C	139	7.4	43.5	24	13	BM396107	BM396107	5009-0-17	C	212	7.2	42.4	20	17	A2622553	A2622553	1M0455O24
C	140	7.4	43.5	24	17	AQ050534	AQ050534	dbxb00004b	C	213	7.2	42.4	20	17	A2779169	A2779169	2M0015N08
C	141	7.4	43.5	24	17	A2592133	A2592133	1M0402K15	C	214	7.2	42.4	21	9	AU264725	AU264725	1M0402K15
C	142	7.4	43.5	24	17	A2812679	A2812679	2M0079H03	C	215	7.2	42.4	21	17	A2323997	A2323997	1M0045B18
C	143	7.4	43.5	24	17	A2946136	A2946136	2M0207K14	C	216	7.2	42.4	21	17	A2420773	A2420773	1M0198E18
C	144	7.4	43.5	24	17	TR11D1D1P	TR11D1D1P	1M0466360 T. brucei	C	217	7.2	42.4	21	17	A2458050	A2458050	1M0261C14
C	145	7.4	43.5	24	17	TA190D03Q	TA190D03Q	1M0477644 T. brucei	C	218	7.2	42.4	21	17	A2487925	A2487925	1M0317G22
C	146	7.4	43.5	25	9	AA9378803	AA9378803	of86e04.s	C	219	7.2	42.4	21	17	A2651849	A2651849	1M0522I13
C	147	7.4	43.5	25	9	AA9382866	AA9382866	oo97e01.s	C	220	7.2	42.4	21	17	A2775804	A2775804	2M0009D01
C	148	7.4	43.5	25	9	A1261405	A1261405	qfK08C04.x	C	221	7.2	42.4	21	17	TA45E03Q	TA45E03Q	2M0072A04
C	149	7.4	43.5	25	9	A1471576	A1471576	cl199D02.x	C	222	7.2	42.4	21	17	TA45E03Q	TA45E03Q	2M0072A04
C	150	7.4	43.5	25	9	A1474586	A1474586	cm12b02.x	C	223	7.2	42.4	22	9	A1128721	A1128721	qae2h06.8
C	151	7.4	43.5	25	9	A1624446	A1624446	ts48C07.x	C	224	7.2	42.4	22	9	A1682443	A1682443	wc53D06.x
C	152	7.4	43.5	25	9	A1638719	A1638719	clt24e01.x	C	225	7.2	42.4	22	9	AU008996	AU008996	1M0508996

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C 230	10.4	52.0	21	22	AAF97523	Human gene single
C 231	10.4	52.0	21	24	ABL51363	Rat phospholipase
C 232	10.4	52.0	22	16	AAT02312	P. cepacia 16S rRNA
C 233	10.4	52.0	22	16	AAT02314	P. cepacia 16S rRNA
C 234	10.4	52.0	22	16	AAT02316	P. cepacia 16S rRNA
C 235	10.4	52.0	22	20	AAZ31624	PCR primer for hum
C 236	10.4	52.0	22	20	AAI18130	GI tract binding p
C 237	10.4	52.0	22	21	AAZ95089	Human UGT2B7 exon
C 238	10.4	52.0	22	24	ABL45189	Human chromosome 1
C 239	10.4	52.0	23	16	AAQ90329	Human interleukin-
C 240	10.4	52.0	23	17	AAI34035	Nycobacteria 16S-2
C 241	10.4	52.0	23	18	AAT50760	Cytine IL-5 gene fo
C 242	10.4	52.0	23	24	ABN99533	Fungi PCR primer S
C 243	10.4	52.0	23	24	ABX29130	Human angiotensin
C 244	10.4	52.0	23	24	ABX29130	Myrothecium vertiru
C 245	10.4	52.0	24	12	AAQ11104	Probe/primer E to
C 246	10.4	52.0	24	16	AAT02310	P. cepacia 16S rRNA
C 247	10.4	52.0	24	16	AAT02311	P. cepacia 16S rRNA
C 248	10.4	52.0	24	16	AAT02313	P. cepacia 16S rRNA
C 249	10.4	52.0	24	16	AAT02315	P. cepacia 16S rRNA
C 250	10.4	52.0	24	18	AAT60453	MCSF PCR primer P2
C 251	10.4	52.0	24	19	AAV22022	PCR primer for fun
C 252	10.4	52.0	24	20	AAZ24967	Primer A for yeast
C 253	10.4	52.0	24	21	AAH45873	E. coli CCT PCR pr
C 254	10.4	52.0	24	22	ABO00906	Oligonucleotide ad
C 255	10.4	52.0	24	24	ABO01478	Oligonucleotide ad
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C 258	10.4	52.0	24	24	ABO04281	Oligonucleotide ad
C 259	10.4	52.0	24	24	ABO06922	Oligonucleotide ad
C 260	10.4	52.0	24	24	ABO10500	Oligonucleotide ad
C 261	10.4	52.0	24	24	ABO10541	Oligonucleotide ad
C 262	10.4	52.0	24	24	ABA05300	Detection PCR prim
C 263	10.4	52.0	24	24	AB191574	Capture oligonucle
C 264	10.4	52.0	24	24	AB191575	Capture oligonucle
C 265	10.4	52.0	25	16	AAO99098	Extension/ligation
C 266	10.4	52.0	25	16	AAO99101	Ligation primer us
C 267	10.4	52.0	25	19	AAV07443	Synthetic peptide-
C 268	10.4	52.0	25	19	AAV07443	Recombinant heat-x
C 269	10.4	52.0	25	21	AAV82471	HLA HLA-C gene PCR
C 270	10.4	52.0	25	21	AAV82471	HLA HLA-C gene PCR
C 271	10.4	52.0	25	21	AAV82471	HLA HLA-C gene PCR
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C 293	10.4	52.0	25	21	AAV82471	HLA HLA-C gene PCR
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C 301	10.4	52.0	25	21	AAV82471	HLA HLA-C gene PCR

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ALIGNMENTS

RESULT 1
 LOCUS B1094828
 DEFINITION EST-CD34N-028 cDNA library of human CD 34+ stem/progenitor cells
 EST-CD34N-028 cDNA library of human CD 34+ stem/progenitor cells
 Homo sapiens cDNA 3', mRNA sequence.

ACCESSION B1094828
 VERSION B1094828.1
 KEYWORDS GI:117373705
 SOURCE
 ORGANISM

Homo sapiens
 human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 25)
 Zhou, G., Chen, J., Lee, S., Terry, C., Rowley, J. D. and Wang, S. M.
 The pattern of gene expression in human hematopoietic CD34+
 stem/progenitor cells
 Unpublished (2001)
 Contact: Wang SM
 Hem/Onc
 University of Chicago Medical Center
 5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA
 Tel: 773-702-6788
 Fax: 773-702-3002

Email: swanglemidway.uchicago.edu
 This EST fragment was amplified from cDNA library of human CD 34+
 stem/progenitor cells with G1G1 technique (Generation of Longer
 cDNA fragments from SAGE tags for Gene Identification, Proc. Natl.
 Acad. Sci. USA 97, 349, 2000), which starts from the 3' end till
 the first CATG site of the target cDNA sequence.
 Seq primer: M13 Forward.
 Location/Qualifiers

FEATURES

source
 1..25
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="cDNA library of human CD 34+ stem/progenitor
 cells"
 /cissue_type="Bone marrow"
 /cell_type="CD34+ stem/progenitor cells"
 /note="3 ESTs converted from the SAGE tag sequences using
 G1G1 method"

BASE COUNT

Query Match 65.9%; Score 11.2; DB 13; Length 25;
 Best Local Similarity 81.2%; Pred. No. 9.1e+04;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 TTGCTTCGGCGGAC 17
 6 TTTTTCGGCTGGAC 21

RESULT 2

LOCUS TA352B06Q
 DEFINITION T. brucei sheared genomic DNA clone 352b06, reverse sequence.
 T. brucei sheared genomic DNA clone 352b06, reverse sequence.
 genomic survey sequence.
 AL496495
 AL496495.1 GI:11870199
 GSS.
 Trypanosoma brucei.
 Trypanosoma brucei.
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE

1 (bases 1 to 25)
 Hall, N., Bowman, S., Lennard, N. J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S. E., Rajandream, M. A. and Barrell, B. G.
 Direct Submission

TITLE

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TRU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (~
 4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J. C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaundin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers

FEATURES

source
 1..25
 /organism="Trypanosoma brucei"
 /strain="TRU927"
 /db_xref="taxon:5691"
 /clone="352b06"

BASE COUNT

Query Match 61.2%; Score 10.4; DB 17; Length 25;
 Best Local Similarity 91.7%; Pred. No. 2.4e+05;

XX The invention relates to a method of detecting and quantifying fungi and
CC bacteria, involving obtaining a sequence of the microorganism to be
CC detected and quantified, extracting the DNA from the sample, and
CC subjecting the DNA to polymerase chain reaction (PCR) and fluorescent
CC probe analysis. The method is useful for identifying and quantifying
CC specific fungi and bacteria using specific DNA sequences. The specific
CC DNA sequences are useful for the real time detection of PCR products with
CC a fluorescent probe system or other molecular probes like hybridisation.
CC AAK29026-ABK29474 represent fungal and bacterial PCR primers and probes
CC used in the method of the invention.

XX Sequence 25 BP; 9 A; 5 C; 5 G; 6 T; 0 other;

Query Match 75.0%; Score 15; DB 24; Length 25;

Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GTTTGCCACTCAG 20

1 GTTTGCCACTCAG 15

RESULT 3

AAH56097 standard; DNA; 24 BP.

AAH56097;

04-SBP-2001 (first entry)

Human SCN3A PCR-SSCP PCR primer SEQ ID NO:341.

Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
anticonvulsant; neuroprotective; PCR primer; ss.

Homo sapiens.
Synthetic.

WO200138564-A2.

31-MAY-2001.

24-NOV-2000; 2000MO-CA01404.

26-NOV-1999; 99US-0167623.

(UWMC-) UNIV MCGILL.

Rouleau GA, LaFreniere RG, Rochefort D, Cossette P, Ragsdale D;

WPI; 2001-355945/37.

Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a
PT DNA variant, equivalent, or mutation which shows a linkage
PT disequilibrium -

Example 5; Fig 6; 268pp; English.

XX The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The
CC method comprises determining the genotype of at least one gene selected
CC from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation
CC which shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all
CC sodium channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome
CC 2q33-q31. Compounds identified as modulators of the biological activity
CC of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating
CC epilepsy or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH5763 to AAH56164 and AAB99674 to

CC AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR
CC primers, oligonucleotides and proteins given in the exemplification of
CC the present invention.

XX Sequence 24 BP; 6 A; 5 C; 2 G; 10 T; 1 other;

Query Match 72.0%; Score 14.4; DB 22; Length 24;

Best Local Similarity 83.3%; Pred. No. 5.9e+02;

Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTGCGTTTGCCTCAG 18

6 TTTGCGTTTGCCTCAG 23

RESULT 4

AAC92656/c standard; DNA; 20 BP.

AAC92656;

27-MAR-2001 (first entry)

Human Nck-2 phosphothioate antisense oligonucleotide, SEQ ID NO:17.

Human Nck-2; adapter protein; Nck adapter protein; hNck-beta; Grb4;
signal transduction; SH2 domain; SH3 domain; src homology domain;
integrin signalling; receptor tyrosine kinase signalling;
growth factor receptor signalling; PINCH; v-Abl; Ras; Sos;
transcriptional activation; cancer; tumour; leukaemia; breast cancer;
expression inhibition; phosphothioate; antisense oligonucleotide; ss.

Homo sapiens.

US6165728-A.

26-DEC-2000.

19-NOV-1999; 99US-0444053.

19-NOV-1999; 99US-0444053.

(ISIS-) ISIS PHARM INC.

Ward DT, Cowseert LM;

WPI; 2001-090480/10.

Novel antisense compound which inhibits expression of human nck-2
PT useful for treating disease or condition associated with expression of
PT nck-2, and as research reagents, kits and diagnostics -

Claim 1; Column 41-42; 38pp; English.

XX Sequences AAC92649-C92728 represent antisense oligonucleotides
CC targeted to the human Nck-2 gene, which inhibit its expression.
CC The antisense oligonucleotides were designed to target different
CC regions of the human Nck-2 mRNA, and were analysed for their effect on
CC Nck-2 mRNA levels by quantitative real-time PCR. Nck-2 (also known
CC as Nck adapter protein, hNck-beta and Grb4), contains both SH2 and SH3
CC src homology domains and functions as an adapter protein in
CC integrin-mediated and receptor tyrosine kinase-mediated signal
CC transduction, particularly in growth factor receptor signalling.
CC Moreover, Nck-2 participates in pathways that connect growth factor
CC receptor signalling and integrin signalling via its interaction with
CC PINCH, a LIM domain-containing adapter protein which is involved in
CC integrin, growth factor and Wnt signalling pathways. Nck-2 also
CC interacts with Egr (epidermal growth factor) and PDGF (platelet-derived
CC growth factor) receptors, inhibiting EGF- and PDGF-stimulated DNA
CC synthesis in an SH2-dependent manner. Nck-2 is also able to interact with
CC v-Abl, Ras and Sos proteins to induce transcriptional activation, and is
CC therefore implicated in the development of cancer, particularly leukaemia
CC and breast cancer. The oligonucleotides of the invention are useful for

LOCUS	TA1146120	22 bp	DNA	linear	GSS 13-DEC-2000
DEFINITION	T. brucei sheared genomic DNA clone 114g12, reverse sequence,				
ACCESSION	AL462379				
VERSION	AL462379.1 GI:11832660				
KEYWORDS	GSS.				
SOURCE	Trypanosoma brucei.				
ORGANISM	Trypanosoma brucei Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;				
REFERENCE	Eukaryota.				
AUTHORS	1 (bases 1 to 22) Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajadream,M.A. and Barrell,B.G.				
TITLE	Direct Submission				
JOURNAL	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk				
COMMENT	Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrell, Oxford University Press, 1999). Email: nelsayed@tigr.org Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/ .				
FEATURES	location/Qualifiers				
source	1..22 /organism="Trypanosoma brucei" /strain="TREU927" /db_xref="taxon:5691" /clone="114g12"				
BASE COUNT	6 a 5 c 7 g 4 t				
ORIGIN					
Query Match	56.5%; Score 9.6; DB 17; Length 22;				
Best Local Similarity	75.0%; Pred. No.6.1e+05;				
Matches	12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;				
Qy	1 GTTGCTTCGGCGGAA 16 2 GTTGATCGGACAGAA 17				
Db					
RESULT 6					
A2786547	24 bp DNA linear GSS 16-FEB-2001				
LOCUS	2M0032B10F Mouse 10kb plasmid UGCM1 library Mus musculus genomic				
DEFINITION	clone UGCM0032B10 F, DNA sequence.				
ACCESSION	A2786547				
VERSION	A2786547.1 GI:13924417				
KEYWORDS	GSS.				
SOURCE	house mouse.				
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclirognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 24) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islem H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly, M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.				
AUTHORS	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT				
JOURNAL					
COMMENT					

B4112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0032 row: B column: 10
 Seq primer: CGTGTAAACGACGGCCACT
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1. 24
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U96C2M0032B10"
 /clone_lib="Mouse 10kb plasmid library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 3 c 5 g 13 t
 ORIGIN
 Query Match 55.3%; Score 9.4; DB 17; Length 24;
 Best Local Similarity 90.9%; Pred. No. 7.9e+05;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
 Oy 1 GTTGCTTGGC 11
 |||||
 |||||
 10 GTTGCTTGGC 20
 DB 10 GTTGCTTGGC 20
 RESULT 7
 BM398017/c 18 bp mRNA EST 17-JAN-2001
 LOCUS 5009-0-4-D05.c.1 Chllocat/Turkewitz cDNA (large fraction)
 DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM398017
 VERSION BM398017.1 GI:18198070
 KEYWORDS EST.
 SOURCE Tetrahymena thermophila.
 ORGANISM Tetrahymena thermophila.
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymena.
 Turkewitz, A.P., Karter, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J., and Klobucher, L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

PI Draper KG, Dudycz LW, Holeczek JJ, Macejak DG, Mamine JA;
 PI MeSwiggen JA;
 XX WPI, 1993-386599/48.
 XX
 XX Enzymatic RNA molecules - used to inhibit viral replication,
 PT infection and gene expression
 XX
 PS Claim 5, Fig 8, 287pp; English.
 XX
 CC The sequences (AA050775-99) and (AA052551-8) are pref. hepatitis B
 CC virus-target sequences for enzymatic RNA molecules. The RNA
 CC molecules are complementary to a substrate binding region in the
 CC specified gene target. They also have enzymatic activity, in that
 CC they specifically cleave RNA in the target. The RNAs interfere with
 CC viral replication and therefore have anti-viral properties. They can
 CC be used to attenuate viruses to be used in vaccines.
 XX
 SQ Sequence 17 BP; 4 A; 6 C; 4 G; 3 U; 0 other;
 XX
 QY Query Match 67.0%; Score 13.4; DB 14; Length 17;
 Best Local Similarity 93.3%; Pred. No. 1.8e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 4 GCCTTGCCACTCAG 18
 15 GAGTTGCCACTCAG 1
 XX
 RESULT 7
 ID AAV35581/c
 ID AAV35581 standard; DNA; 24 BP.
 AC AAV35581;
 DT 04-SEP-1998 (first entry)
 XX
 XX STS probe GVI0 generating lower primer.
 DE
 XX Hydronephrosis gene; HNG gene; USF2 gene; renal disease; renal aplasia;
 KW vesical-ureteral reflux; pelvi-ureteral junction obstruction;
 KW multicystic renal dysplasia; renal agenesis; hydronephrosis; MMD;
 KW von Mayer-Rokitansky-Kuester disorder; bifid ureter; STS probe;
 KW sequence tagged site; PCR primer; ss.
 XX
 OS Synthetic.
 XX Homo sapiens.
 PN NO9815650-A2.
 XX
 PD 16-APR-1998.
 XX
 PF 09-OCT-1997; 97MO-EP05583.
 XX
 PR 09-OCT-1996; 96EP-0202820.
 XX
 PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
 XX
 XX Frysne JFGJ, Groenen PMA, Van De Ven WJM;
 XX WPI, 1998-240833/21.
 DR
 XX Hydronephrosis gene - useful to treat or diagnose renal diseases and
 PT disorders, e.g. vesical-ureteral reflux, pelvi-ureteral junction
 PT obstruction, multicystic renal dysplasia or renal agenesis
 XX
 PS Example 3; Page 46, 73pp; English.
 XX
 CC This primer is used for the generation of sequence tagged sites (STS)
 CC probes used for pinpointing chromosome 6 breakpoint. This was used for
 CC isolating the human hydronephrosis (HNG) gene of the invention. A
 CC translocation partner to this HNG gene on chromosome 6 is the
 CC chromosome 19 USF2 gene. The HNG gene can be used as a starting point

CC to design suitable compounds or techniques for the treatment of renal
 CC diseases or disorders, or nucleotide probes for diagnosing cells
 CC involved in renal diseases or disorders. A protein or a fragment
 CC encoded by HNG gene can be used as a starting point for preparing
 CC suitable antibodies for diagnosing cells involved in renal diseases and
 CC disorders. The products and method can be used to treat or diagnose
 CC renal diseases and disorders selected from vesical-ureteral reflux,
 CC uni or bilateral pelvi-ureteral junction obstruction, multicystic renal
 CC dysplasia (MRD), renal agenesis, renal aplasia, hydronephrosis,
 CC von Mayer-Rokitansky-Kuester disorder and bifid ureter.
 CC
 SQ Sequence 24 BP; 3 A; 6 C; 8 G; 7 T; 0 other;
 XX
 QY Query Match 67.0%; Score 13.4; DB 19; Length 24;
 Best Local Similarity 93.3%; Pred. No. 1.9e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 6 GTTGGCCACTCAG 20
 23 GTTAGCCACTCAG 9
 XX
 RESULT 8
 ID AAK98779/c
 ID AAK98779 standard; DNA; 23 BP.
 AC AAK98779;
 DT 13-MAY-2002 (first entry)
 XX
 XX Antisense primer for amplification of ADAMTS-SI.
 DE
 XX Antiarthritic; osteopathic; antirheumatic; antiinflammatory; nocrotic;
 KW antiasthmatic; neuromodulator; cyostatic; vasotropic;
 KW antiallergic; dermatological; antiarteriosclerotic; cerebroprotective;
 KW cardiant; immunosuppressive; anticonvulsant; antiparkinsonian; analgesic;
 KW antimitigraine; antidepressant; ophthalmological; vulnery; antidiabetic;
 KW antifertility; a disintegrin and metalloprotease thrombospondin domain;
 KW ADAMTS; ADAMTS-SI; agonist; antagonist; bioterpentic; gene therapy;
 KW arthritis; inflammatory bowel disease; Crohn's disease; atherosclerosis;
 KW perididial disease; emphysema; acute respiratory distress syndrome;
 KW asthma; chronic obstructive pulmonary disease; Alzheimer's disease;
 KW organ transplant toxicity; rejection; cachexia; allergy; restenosis;
 KW cancer; tissue ulcerations; epidermolysis bullosa; aortic aneurysm;
 KW osteoporosis; artificial joint implant; congestive heart failure; stroke;
 KW myocardial infarction; cerebral ischemia; head trauma; corneal injury;
 KW spinal cord injury; neurodegenerative disease; autoimmune disorder;
 KW Huntington's disease; Parkinson's disease; migraine; multiple sclerosis;
 KW depression; peripheral neuropathy; pain; cerebral amyloid angiopathy;
 KW nocrotic; cognition enhancement; amyotrophic lateral sclerosis;
 KW ocular angiogenesis; macular degeneration; abnormal wound healing; burn;
 KW infertility; diabetic shock; chondrocyte; osteoarthritis; OA; cartilage;
 KW proinflammatory cytokine; human; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1136547-A2.
 XX
 PD 26-SEP-2001.
 XX
 PF 21-MAR-2001; 2001EP-0302634.
 XX
 PR 22-MAR-2000; 2000US-191382P.
 XX
 PA (PFIZ) PFIZER PROD INC.
 XX
 XX Buckbinder L, Mitchell PG, Schaefer JF, Walsh RT;
 PI WPI, 2002-229167/29.
 DR
 XX Novel isolated polynucleotide encoding A Disintegrin And
 PT Metalloprotease family of metalloproteases, containing Chromospondin
 PT domain, termed ADAMTS-SI, useful for diagnostic, bioterpentic or gene

XX Barany F, Zivvi M, Gerry NP, Favis R, Kilman R;
 XX WPI, 2002-034366/04.
 XX
 XX Designing capture oligonucleotide probes for use on a support to which
 XX complementary oligonucleotides hybridize with little mismatch -
 XX
 XX Example 5, Fig 25; 300pp; English.
 XX
 XX The present invention describes a method (M1) for designing capture
 XX oligonucleotide probes (I) for use on a support to which complementary
 XX oligonucleotide probes (II) will hybridize with little mismatch, where
 XX (i) have melting temperatures within a narrow range. The method is useful
 XX for detecting infectious diseases caused by bacterial infectious agents
 XX e.g. *Salmonella*, *Listeria monocytogenes* and *Haemophilus influenza*, fungal
 XX infectious agents e.g. *Cryptococcus neoformans*, *Candida albicans* and
 XX *Aspergillus fumigatus*, viruses e.g. T-cell lymphocytotropic virus,
 XX Epstein-Barr virus and polio virus, and parasitic infectious agents
 XX selected from *Onchocerca volvulus*, *Entamoeba histolytica* and *Dracontulus*
 XX medinensis. The method is also useful for detecting genetic diseases such
 XX as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 XX Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 XX involved in DNA amplification, replication, recombination or repair, the
 XX cancer is specifically associated with a gene selected from BRCA1 gene,
 XX p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 XX method is also used for environmental monitoring, forensics and the food
 XX and feed industry, detecting comprises scanning (using e.g. a scanning
 XX electron microscope and infrared microscope) the support at the
 XX particular sites and identifying if ligation of the oligonucleotide probe
 XX sets occurred and correlating (using a computer) identified ligation to a
 XX presence or absence of the target nucleotide sequences. AB182074 to
 XX AB19546 represent oligonucleotide sequences used in the exemplification
 XX of the present invention.
 XX
 XX Sequence 24 BP; 6 A; 6 C; 9 G; 3 T; 0 other;
 XX
 XX Query Match 64.0%; Score 12.8; DB 24; Length 24;
 XX Best Local Similarity 87.5%; Pred. No. 3.9e+03;
 XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX 4 GCGTTGCCACTCAGA 19
 XX | | | | | | | | | | | | | | | | | | | | | |
 XX Db 9 GCGATTGCCACTCAGA 24
 XX
 XX
 XX RESULT 11
 XX AAD07981
 XX ID AAD07981 standard; DNA; 25 BP.
 XX
 XX AAD07981;
 XX
 XX 06-AUG-2001 (first entry)
 XX
 XX M. mycoides LppQ gene site directed mutagenesis PCR primer MMMLP482.
 XX
 XX Lipoprotein; LppQ; antibacterial; vaccine; Mycoplasma infection;
 XX bovine pleuropneumonia; CBPP; site directed mutagenesis; PCR primer; ss.
 XX
 XX Mycoplasma mycoides subsp. mycoides SC.
 XX
 XX Key Location/Qualifiers
 XX mlec_feature 17
 XX /tag= a
 XX /note= "Nucleotide G is present at this location in the
 XX sequence shown in sequence listing of the specification"
 XX
 XX MO200140471-A1.
 XX
 XX 07-JUN-2001.
 XX
 XX 24-NOV-2000; 2000WO-EP11798.
 XX
 XX

PR 29-NOV-1999; 99EP-0123676.
 XX
 XX (ALKU) AKZO NOBEL NV.
 XX
 XX Frey JU, Nicolet JU, Abdo EB;
 XX
 XX WPI; 2001-381385/40.
 XX
 XX Novel protein LppQ of Mycoplasma mycoides subsp. mycoides SC, or its
 XX parts useful for detection of Mycoplasma and for preparation of vaccine
 XX for treating infection caused by Mycoplasma -
 XX
 XX Example 3; Page 26; 56pp; English.
 XX
 XX The present sequence is a PCR primer used for site directed mutagenesis
 XX (to exchange Mycoplasma specific UGACtrp codons to universal UGCtrp
 XX codons) of lipoprotein LppQ gene from Mycoplasma mycoides subsp.
 XX mycoides SC (small colony type). LppQ is useful in a diagnostic method
 XX for the direct or indirect detection of M. mycoides subsp. mycoides SC,
 XX where the diagnostic method is an immunological method such as
 XX immunoblotting, serological tests or ELISA (enzyme linked immunosorbent
 XX assay). LppQ DNA and protein are useful for the preparation of a vaccine
 XX against infection by M. mycoides subsp. mycoides SC. LppQ DNA is useful
 XX for the preparation of live, attenuated or inactivated cells of
 XX M. mycoides subsp. mycoides SC to be used as marker vaccine, where the
 XX cells lack the ability to synthesise the LppQ lipoprotein. LppQ DNA is
 XX also useful for expressing LppQ protein in a detection method for
 XX M. mycoides subsp. mycoides SC, where the detection method is selected
 XX from PCR and hybridisation. LppQ protein is useful for detecting
 XX antibodies directed to it in a body fluid such as serum or bronchial
 XX fluid from an animal. LppQ protein are also useful as a specific antigen
 XX for sero-detection of contagious bovine pleuropneumonia (CBPP).
 XX
 XX Sequence 25 BP; 2 A; 5 C; 3 G; 15 T; 0 other;
 XX
 XX Query Match 64.0%; Score 12.8; DB 22; Length 25;
 XX Best Local Similarity 87.5%; Pred. No. 3.9e+03;
 XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX 2 TTGCGTTTGCCACTCA 17
 XX | | | | | | | | | | | | | | | | | | | | | |
 XX Db 3 TTGTTTGGCCACTCA 18
 XX
 XX
 XX RESULT 12
 XX AAD07982/c
 XX ID AAD07982 standard; DNA; 25 BP.
 XX
 XX AAD07982;
 XX
 XX 06-AUG-2001 (first entry)
 XX
 XX M. mycoides LppQ gene site directed mutagenesis PCR primer MMMLP483.
 XX
 XX Lipoprotein; LppQ; antibacterial; vaccine; Mycoplasma infection;
 XX bovine pleuropneumonia; CBPP; site directed mutagenesis; PCR primer; ss.
 XX
 XX Mycoplasma mycoides subsp. mycoides SC.
 XX
 XX MO200140471-A1.
 XX
 XX 07-JUN-2001.
 XX
 XX 24-NOV-2000; 2000WO-EP11798.
 XX
 XX 29-NOV-1999; 99EP-0123676.
 XX
 XX (ALKU) AKZO NOBEL NV.
 XX
 XX Frey JU, Nicolet JU, Abdo EB;
 XX
 XX WPI; 2001-381385/40.
 XX

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0543 row: 3 column: 22
 Seq primer: CACACGAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.

FEATURES

source

1..21
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0543422"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

6 a 3 c 6 g 6 t

Query Match 52.9%; Score 9; DB 17; Length 21;

Best Local Similarity 70.6%; Pred. No. 1.3e+06;

Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 GTTGCTGGCGGGAAC 17
 2 GGTCCTCATGCGTAC 18

RESULT 15

BM399936

LOCUS 5009-0-63-D08.t.1 Chilcoat/Turkewitz CDNA (large fraction)
 DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM399936

VERSION 1

KEYWORDS EST.

SOURCE Tetrahymena thermophila.

ORGANISM Tetrahymena thermophila

REFERENCE Turkewitz, A.P., Karver, K.M., John, C., Orlas, E., Kirk, K.E., Frankel, J., and Klobutcher, L.

AUTHORS EST from Tetrahymena thermophila, strain CUA23.1, growing cells

JOURNAL Unpublished (2002)

COMMENT Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apurkew@midway.uchicago.edu
 Seq primer: T3.

FEATURES

source

1..25
 Location/Qualifiers
 /organism="Tetrahymena thermophila"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_1lb="Chilcoat/Turkewitz CDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT

2 a 8 c 11 g 4 t

Query Match 52.9%; Score 9; DB 13; Length 25;

Best Local Similarity 70.6%; Pred. No. 1.3e+06;

Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 GTTGCTGGCGGGAAC 17
 8 GTGCGTGGCGCGTAC 24

RESULT 16

A2478429

LOCUS 25 bp DNA GSS 04-OCT-2000
 DEFINITION 1M029806R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M029806 R, DNA sequence.

ACCESSION A2478429

VERSION A2478429.1

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A., and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0298 row: C column: 06
 Seq primer: CACACGAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 25.

FEATURES

source

1..25
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M029806"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA

Query Match 63.0%; Score 12.6; DB 21; Length 21;
 Best Local Similarity 78.9%; Pred. No. 4.9e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TTGCGTTTGGCACTCAGA 19
 |||||
 1 TTGAGTTTCTAGGACAGA 19

RESULT 15
 AAQ58843 standard; cDNA; 25 BP.
 AC AAQ58843;
 XX 24-NOV-1994 (first entry)
 DT NANBH virus primer group C14-5, primer 14-17.
 XX
 XX Antigen; structural; non-structural; non A non B hepatitis virus;
 KM NANBHV, NANBH, patient; plasma; diagnosis; detection; carrier; PCR;
 KM polymerase chain reaction; amplify; primer; ss.
 XX
 OS Synthetic.
 XX JP6070778-A.
 XX 15-MAR-1994.
 PD 01-JUN-1993; 93JP-0156087.
 XX 10-JUL-1992; 92JP-0207391.
 XX
 XX (KOKU-) KOKUSAI SHIYAKU KK.
 PA (SANW) SANWA KAGAKU KENKYUSHO CO.
 PA (TOFU) TONEN CORP.
 PA (TKR-) ZH TOKYO RINGHO IGAKU SOGO KENKYUSHO.
 DR WPI; 1994-128677/16.

XX Nucleic acid fragment coding non-A non-B hepatitis virus antigen
 PT - useful in diagnosis of NANB patient and detection of virus
 PT carrier

XX Disclosure; Page 10; 37pp; Japanese.

XX The sequences given in AAQ58828-72 are primers which were used to
 CC amplify cDNA sequences encoding antigens of structural and non-
 CC structural regions of non A non B hepatitis virus (NANBHV). The
 CC amplified sequences were derived from the plasma of a NANBH patient by
 CC recombinant DNA techniques. The amplified fragments are useful for
 CC the diagnosis of NANBH patients and the detection of NANBH carriers.

XX Sequence 25 BP; 5 A; 7 C; 8 G; 5 T; 0 other:

OY 2 TTGCGTTTGGCACTCAGAG 20
 |||||
 1 TCGCGTATGCCGCTCAGGG 19

Query Match 63.0%; Score 12.6; DB 15; Length 25;
 Best Local Similarity 78.9%; Pred. No. 5e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

RESULT 16
 ABK02611 standard; RNA; 17 BP.
 AC ABK02611;
 XX 12-MAR-2002 (first entry)

DE Human NOGO Amberyne #283.
 XX
 XX Human; ss; antisense therapy; cytostratic; antiinflammatory; haemostatic;
 KM cerebroprotective; neurotrophic; neuroprotective; antiparkinsonian;
 KM muscular; CD20; neurite growth inhibitor gene; NOGO; hammethead ribozyme;
 KM DNazyme; Inozyme; G-cleaver; Amberyne; zinzyme; lymphoma; leukemia;
 KM B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukemia;
 KM human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KM MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
 KM inflammatory arthropathy; central nervous system injury;
 KM cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KM chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KM Parkinson's disease; ataxia; Huntington's disease;
 KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX W0200159103-A2.
 XX 16-AUG-2001.
 PD 09-FEB-2001; 2001WO-US04273.
 XX 11-FEB-2000; 2000US-181797P.
 PR 28-FEB-2000; 2000US-185516P.
 PR 06-MAR-2000; 2000US-187128P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, McSwiggen J, Chowrira BM;
 DR WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
 PT and central nervous system injury -

XX Claim 88; Page 137; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO).
 CC The nucleic acids may be enzymatic nucleic acids (e.g., a ribozyme or a
 CC DNazyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN
 CC motif) or an amberyne (cleaving RNA with an NGN triplet), a zinzyme
 CC (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used
 CC to cleave RNA of CD20 in the presence of a divalent cation that is
 CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce
 CC CD20 activity of the cell and treat a patient having a condition
 CC associated with the level of CD20. The treatment may further comprise the
 CC use of one or more therapies. In particular, the CD20 targeting
 CC nucleic acid may be used to treat lymphoma, leukemia, B-cell
 CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
 CC low-grade or follicular NHL, lymphocytic leukemia, HIV (human
 CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
 CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
 CC thrombocytopenia, and inflammatory arthropathy. The NOGO-targeting
 CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a
 CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
 CC may be contacted with a cell to reduce NOGO activity of the cell and
 CC treat a patient having a condition associated with the level of NOGO. The
 CC treatment may further comprise the use of one or more therapies.
 CC In particular, the NOGO-targeting nucleic acid may be used to treat
 CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
 CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob

Db 16 GTTGCTGGCGGCG 5

RESULT 19
TA266D03P/c

LOCUS
DEFINITION T. brucei sheared genomic DNA clone 266d03, forward sequence,
genomic survey sequence.

ACCESSION
VERSION AL488313
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrett, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrett@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..23
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="266d03"

BASE COUNT
2 a 9 c 5 g 7 t

ORIGIN

Query Match 51.8%; Score 8.8; DB 17; Length 23;
Best Local Similarity 83.3%; Pred. No. 1.6e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 TTGCGCGCGGAC 17
Db 17 TTCAGGCGGAC 6

RESULT 20
AZ345583/c

LOCUS
DEFINITION 20 bp DNA linear GSS 29-SEP-2000
clone UGCG1M080L18 F, DNA sequence.

ACCESSION
VERSION AZ345583
KEYWORDS
SOURCE
ORGANISM
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Bacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts

JOURNAL
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: 1 column: 18
Seq primer: CCTGTAAACGACGCGCAT
Clase: plasmid ends
High quality sequence stop: 20.

FEATURES
source
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M080L18"
/clone_1b="Mouse 10kb plasmid UGCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42ny. Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMW42 (g1473214|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptor complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
5 a 12 c 0 g 3 t

ORIGIN

Query Match 50.6%; Score 8.6; DB 17; Length 20;
Best Local Similarity 73.3%; Pred. No. 2e+06;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTTGCTGGCGGCGA 15
Db 16 GTTGCTGGCGGCGA 2

RESULT 21
AM247820

LOCUS
DEFINITION 22 bp mRNA linear EST 07-JAN-2000
2820485, Sprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820485 3',
mRNA sequence.

ACCESSION
VERSION AM247820
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_BESTs: 2820485.Sprime
Contact: Robert Strauberg, Ph.D.
Email: cgabs-r@mail.nih.gov


```

Query Match      60.0%; Score 12; DB 19; Length 17;
Best Local Similarity 75.0%; Pred. No. 9.6e+03;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      8 TTGGCACTCAGA 19
        ::|||:|||
Db      1 UUGCCACUCACAGA 12

RESULT 24
AAT64985
ID AAT64985 standard; DNA; 21 BP.
XX
XX AAT64985;
XX
XX 23-FEB-1998 (first entry)
XX
XX Rat OB receptor PCR primer ROBR 27.
XX
XX Ob receptor; obesity; leptin; rat; rodent; animal model; ligand;
XX fatty; fa mutation; therapy; PCR; primer; MspI; ss.
XX
XX Synthetic.
XX Rattus sp.
XX
XX M09731015-A1.
XX
XX 28-AUG-1997.
XX
XX 18-FEB-1997; 97MO-US02397.
XX
XX 25-APR-1996; 96GB-0008473.
XX 22-FEB-1996; 96US-0090405.
XX 22-MAR-1996; 96US-0013969.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Caskey CT, Hesse JW, Liu Q, Phillips MS;
XX
XX WPI; 1997-435085/40.
XX
XX Rat wild-type and mutant ob receptor protein - useful for
XX identification of new ligands for prevention and treatment of
XX obesity
XX
XX Example 8; Page 15; 35pp; English.
XX
XX This oligonucleotide comprises forward PCR primer ROBR 27. Its
XX sequence corresponds to bases 796-816 of a rat ob receptor (OB-R)
XX cDNA sequence (see AAT64961). It was used with rat OB-R reverse
XX primer ROBR 28 (see AAT64986) to amplify 1.8 kb fragments of rat
XX genomic DNA from lean and fa/fa (fatty) Zucker rats. Subsequent
XX digestion of the PCR product from a homozygous lean rat using
XX restriction endonuclease MspI yielded 2 fragments of 1100 bp and
XX 700 bp. MspI digestion of the PCR product from a fa/fa rat
XX fragments of 950, 130 bp and 700 bp. The fa mutant OB-R gene
XX (see AAT64962) contains an A to C transversion at bp 880 that creates
XX an extra MspI site. This allows genotype analysis of lean and
XX fa/fa rats.
XX
XX Sequence 21 BP; 5 A; 3 C; 7 G; 6 T; 0 other;

Query Match      60.0%; Score 12; DB 18; Length 21;
Best Local Similarity 75.0%; Pred. No. 9.9e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 TTTCGCTTGCCTCAGAG 20
        |||||
Db      2 TTTCGCTATGAAATCAGAG 21

```

```

ID AAD21460 standard; DNA; 23 BP.
XX
AC AAD21460;
XX
DT 28-JAN-2002 (first entry)
DE RT-PCR primer, 2323-70 to examine the expression of human agp-96614-al.
XX
KM Human; CD20/IgE-receptor like protein; immunoglobulin E; agp-96614-al;
KW agp-69406-al; cancer; abnormal cell proliferation; autoimmune disease;
KW ovarian cancer; brain cancer; arteriosclerosis; vascular stenosis;
KW rheumatoid arthritis; multiple sclerosis; allergy; dermatitis; asthma;
KM reproductive disease; diabetes; transplant rejection; endometriosis;
KM infertility; gene therapy; reverse transcription PCR; RT-PCR primer; ss.
XX
OS Homo sapiens.
XX
PN M0200174903-A2.
XX
FD 11-OCT-2001.
XX
PF 29-MAR-2001; 2001MO-USI0048.
PR 30-MAR-2000; 2000US-193728P.
PR 27-NOV-2000; 2000US-0723258.
PA (AMGE-) AMGEN INC.
XX
PI Welcher AA, Calzone FJ;
XX
DR WPI; 2001-662968/76.
PT Novel CD20/IgE-receptor like polypeptides and polymucleotides,
PT antagonists and antibodies of the polypeptide useful for treating
PT ameliorating or preventing diseases associated with the polypeptide
PT e.g. cancer, asthma
PS Example 3; Page 112; 145pp; English.
XX
CC The invention relates to human CD20/immunoglobulin E (IgE)-receptor
CC like polypeptides designated as agp-96614-al and agp-69406-al and
CC nucleic acid molecules encoding such polypeptides. Polypeptides of
CC the invention are useful for treating, preventing or ameliorating
CC a disease, condition, or disorder which includes cancer such as
CC brain cancer, ovarian cancer; abnormal cell proliferation such as
CC arteriosclerosis, vascular stenosis; pathology from allergens
CC such as allergies, asthma, dermatitis; dysfunction of immune system
CC as rheumatoid arthritis, autoimmune disease, multiple sclerosis,
CC diabetes, transplant rejection and reproductive diseases such as
CC infertility, preterm labour and delivery, endometriosis etc. They
CC are also useful for identifying antagonists and as immunogens, for
CC raising antibodies which may also be used to prevent, treat or
CC diagnose a number of diseases and disorders. Polymucleotides of the
CC invention are used to map the location of CD20/IgE-receptor like
CC gene and related genes on chromosomes and as hybridisation probes.
CC They are also useful in gene therapy. The present sequence is
CC reverse transcription PCR (RT-PCR) primer used to examine the
CC expression of human agp-96614-al sequence.
XX
SQ Sequence 23 BP; 7 A; 7 C; 4 G; 5 T; 0 other;
OY Query Match 60.0%; Score 12; DB 22; Length 23;
DB Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
          9 TGCCACTCAGAG 20
            |||||
            |||||
            |||||
DB      23 TGCCACTCAGAG 12
RESULT 26
ABK02000
ABK02000 standard; RNA; 17 BP.

```

FEATURES
source

Location/Qualifiers
1..22
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI CGAP_G4"
/ribose_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pTR73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTR73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT
5 a 7 c 5 g 5 t

Query Match 49.4%; Score 8.4; DB 9; Length 22;
Best Local Similarity 90.0%; Pred. No. 2.6e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TTGGGGCGGA 15
21 TTGGGGCGGA 12

Db

RESULT 29
LOCUS AU006620 22 bp mRNA linear EST 31-JUL-1998
DEFINITION Schizosaccharomyces pombe late log phase cDNA
ACCESSION AU006620
VERSION AU006620
KEYWORDS fission yeast.
SOURCE Schizosaccharomyces pombe
ORGANISM Schizosaccharomycetes; Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomycetes.
REFERENCE 1 (bases 1 to 22)
Moriyomo, M. and Mita, K.
AUTHORS Identification of expressed sequence tags of Schizosaccharomyces pombe
TITLE Unpublished (1998)
JOURNAL Contact: Mitsunori Moriyomo
COMMENT Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba 263-8555, Japan
Email: moriyomo@nirs.go.jp

FEATURES
source

Location/Qualifiers
1..22
/organism="Schizosaccharomyces pombe"
/strain="972"
/db_xref="taxon:4896"
/clone_lib="spc00195"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/sex="h minus"
/note="Vector: M13mp19. The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL: <http://www.nirs.go.jp>)"

BASE COUNT
3 a 2 c 6 g 11 t

Query Match 49.4%; Score 8.4; DB 9; Length 22;
Best Local Similarity 90.0%; Pred. No. 2.6e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCTTCGG 10

Db

Db 1 GTTCTTCGG 10

RESULT 30
LOCUS AU006633 22 bp mRNA linear EST 31-JUL-1998
DEFINITION Schizosaccharomyces pombe late log phase cDNA
ACCESSION AU006633
VERSION AU006633
KEYWORDS fission yeast.
SOURCE Schizosaccharomyces pombe
ORGANISM Schizosaccharomycetes; Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomycetes.
REFERENCE 1 (bases 1 to 22)
Moriyomo, M. and Mita, K.
AUTHORS Identification of expressed sequence tags of Schizosaccharomyces pombe
TITLE Unpublished (1998)
JOURNAL Contact: Mitsunori Moriyomo
COMMENT Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba 263-8555, Japan
Email: moriyomo@nirs.go.jp

FEATURES
source

Location/Qualifiers
1..22
/organism="Schizosaccharomyces pombe"
/strain="972"
/db_xref="taxon:4896"
/clone_lib="spc00210"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/sex="h minus"
/note="Vector: M13mp19. The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL: <http://www.nirs.go.jp>)"

BASE COUNT
3 a 2 c 6 g 11 t

Query Match 49.4%; Score 8.4; DB 9; Length 22;
Best Local Similarity 90.0%; Pred. No. 2.6e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCTTCGG 10

Db 1 GTTCTTCGG 10

RESULT 31
LOCUS AZ476310 22 bp DNA linear GSS 04-OCT-2000
DEFINITION IM029494P19R Mouse 10kb plasmid UGCGIM library Mus musculus genomic clone UGCGIM0294P19 R, DNA sequence.
ACCESSION AZ476310
VERSION AZ476310
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiser, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)

```

QY      1 TTGGCTTGGCACT 15
      |||||
      16 TTGGCTTGGCGCT 2

RESULT 28
AAK95488
ID      AAK95488 standard; DNA; 20 BP.
XX
AC      AAK95488;
XX
DT      13-SEP-1999 (first entry)
XX
DE      PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KM      Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KM      sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KM      vaccine; neutralising epitope; PCR primer; ss.
XX
OS      Synthetic.
XX
OS      Chlamydia pneumoniae.
XX
PN      WO927105-A2.
XX
PD      03-JUN-1999.
XX
PF      20-NOV-1998; 98WO-1B01890.
XX
PR      04-NOV-1998; 98US-0107078.
PR      21-NOV-1997; 97FR-0014673.
XX
PA      (GEST ) GENSET.
XX
PI      Griffiths R;
XX
DR      WPI; 1999-357842/30.
XX
PT      Genome sequence of Chlamydia pneumoniae
XX
PS      Page 1752; Disclosure; 191pp; English.
XX
CC      AAY91991-X97517 represent PCR primers used to amplify open reading
CC      frames and other nucleic acid sequences from the genome of
CC      Chlamydia pneumoniae (see AAY91990). C. pneumoniae causes respiratory
CC      disease such as pneumonia and bronchitis and is thought to be a
CC      contributing factor in heart disease, sarcoidosis, sinusitis, purulent
CC      otitis media, erythema nodosum or pharyngitis. The polypeptides encoded
CC      by the open reading frames of the C. pneumoniae genome (see AAY34584-
CC      AAY35879) can be used in immunogenic compositions as vaccines. Vectors
CC      containing C. pneumoniae nucleotide sequences can also be used as
CC      immunogenic compositions, especially where the vector directs the
CC      expression of a neutralising epitope of C. pneumoniae.
XX
SQ      Sequence 20 BP; 6 A; 3 C; 7 G; 4 T; 0 other;
XX

Query Match      59.0%; Score 11.8; DB 20; Length 20;
Best Local Similarity 86.7%; Pred. No. 1.2e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 GTTGGCACTCAGAG 20
      |||||
      2 GTTGGCACTCAGAG 16

RESULT 29
AAK02576/c
ID      AAK02576 standard; DNA; 20 BP.
XX
AC      AAK02576;
XX
DT      07-MAY-1999 (first entry)
XX
DB      PCR primer #7.
XX

```

```

XX      plant artificial chromosome; PLAC; foreign gene expression; trait; oil;
XX      herbicide; resistance; tolerance; insect; disease; stress; drought;
XX      heat; chilling; freezing; salt; moisture; oxidative; yield; food content;
XX      physical appearance; male sterility; drydown; standability; prolificacy;
XX      starch; detection; PCR primer; ss.
XX
OS      Synthetic.
XX
OS      Arabidopsis thaliana.
XX
PN      MO9855637-A1.
XX
PD      10-DEC-1998.
XX
PF      03-JUN-1998; 98WO-US11288.
XX
PR      05-FEB-1998; 98US-0073741.
PR      03-JUN-1997; 97US-0048451.
XX
PA      (ARCH-) ARCH DEV CORP.
XX
PI      Copenhagen G, Preuss D;
XX
DR      WPI; 1999-080832/07.
XX
PT      New isolated Arabidopsis thaliana centromeres - used for the
PT      production of plant artificial chromosomes for the production of
PT      transgenic plants having desirable agronomic traits
XX
PS      Disclosure; Page 77; 150pp; English.
XX
CC      This invention describes a recombinant DNA construct which comprises a
CC      functional Arabidopsis thaliana centromere. This centromeric region can
CC      be used for the production of plant artificial chromosomes (PLAC's)
CC      which can be used for the production of plants which can express
CC      foreign genes. PLACs can be used to provide desirable traits such as
CC      herbicide resistance or tolerance, insect resistance or tolerance,
CC      disease resistance or tolerance (viral, bacterial, fungal, nematode),
CC      stress tolerance and/or resistance, as exemplified by resistance or
CC      tolerance to drought, heat, chilling, freezing, excessive moisture, salt
CC      stress, oxidative stress, increased yields, food content and makeup,
CC      physical appearance, male sterility, drydown, standability, prolificacy,
CC      starch quantity and quality, oil quantity and quality, protein quality
CC      and quantity, or amino acid composition. The centromeric regions can
CC      also be used to detect the presence of similar centromeric regions in
CC      other plants or animals. This sequence is a PCR primer used in the
CC      method of the invention.
XX
SQ      Sequence 20 BP; 9 A; 4 C; 5 G; 2 T; 0 other;
XX

Query Match      59.0%; Score 11.8; DB 20; Length 20;
Best Local Similarity 86.7%; Pred. No. 1.2e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTGGCTTGGCACT 15
      |||||
      17 TTGGCTTGGCGACT 3

RESULT 30
AAF22122/c
ID      AAF22122 standard; DNA; 20 BP.
XX
AC      AAF22122;
XX
DT      20-MAR-2001 (first entry)
XX
DE      Arabidopsis thaliana chromosome centromere associated primer #6.
XX
KM      Centromere; mitochondrion; vector; ds.
XX
OS      Arabidopsis thaliana.
XX

```

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

1 a 3 c 12 g 4 t

Query Match 48.2%; Score 8.2; DB 17; Length 20;
Best Local Similarity 76.9%; Pred. No. 3.3e+06;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 TTGCTCGGCGGG 14
1 TTTCTGCGGCGGG 13

Db

RESULT 34
AZ511616 20 bp DNA linear GSS 05-OCT-2000
LOCUS 1M035B18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M035B18 F, DNA sequence.
ACCESSION AZ511616
VERSION
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A., and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0356 row: B column: 15
Seq primer: CACACGAAACAGCATATAC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. 20

FEATURES

source
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M035B18"
/clone_1ib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

1 a 1 c 9 g 9 t

Query Match 48.2%; Score 8.2; DB 17; Length 20;
Best Local Similarity 76.9%; Pred. No. 3.3e+06;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 TTGCTCGGCGGG 14
7 TTGTTTGGGCGGG 19

Db

RESULT 35
AZ789409 20 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0037H1F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0037H1 F, DNA sequence.
ACCESSION AZ789409
VERSION
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A., and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0037 row: H column: 11
Seq primer: CGTGTAAACAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. 20

FEATURES

source
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0037H1"
/clone_1ib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "phosphorothioate"
FEATURE:
NAME/KEY: -
LOCATION: 1..21
OTHER INFORMATION: /note = "885-905 primer"
US-08-974-549A-510

Query Match 63.5%; Score 10.8; DB 4; Length 21;
Best Local Similarity 85.7%; Pred. No. 3.1e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGCTTCGGCGG 14
Db 6 GCTTCTTCGGCGG 19

Search completed: June 7, 2003, 09:45:18
Job time : 48.8545 secs

CC mouse ageing inhibitory protein of the invention; the recombinant
 CC production of a mouse ageing inhibitory protein; antibodies against
 CC the ageing inhibitory proteins; methods for immunologically assaying
 CC the proteins; and methods for identifying ligands or other modulators
 CC of the ageing inhibitory proteins; and the ligands and modulators thus
 CC identified. The ageing inhibitory proteins, nucleic acids encoding
 CC them, and antibodies, ligands and modulators, may be used in the
 CC diagnosis and treatment of ageing (particularly premature ageing),
 CC and ageing-related disorders. Sequences AAH24198-AAH24199 represent
 CC PCR primers used in an exemplification of the invention to isolate a
 CC mouse ageing inhibition-related DNA sequence (AAH24197).

CC Sequence 23 BP; 8 A; 6 C; 5 G; 4 T; 0 other;

Query Match 59.0%; Score 11.8; DB 22; Length 23;

Best Local Similarity 86.7%; Pred. No. 1.3e+04; Mismatches 2; Indels 0; Gaps 0;

Matches 13; Conservative 0; Indels 0; Gaps 0;

1 TTTCGCTTGGCACT 15
 |||||
 16 TTTCGCTTGGCACT 4

RESULT 33
 ID ABK49704/C
 ABK49704 standard; DNA; 24 BP.

AC ABK49704;

DT 15-JUL-2002 (first entry)

DE Human kinase uridylylate 12 protein, RT-PCR primer 2.

KM Human, kinase uridylylate 12; malignant neoplasm; tumour; haemopathy; HIV;
 KM human immunodeficiency virus infection; immunological disease; RT-PCR;
 KM inflammation; sterility; pregnancy pathology; growth disorder; primer;
 KM embryonic development disorder; hereditary disease;
 KM reverse transcriptase PCR; ss.

OS Homo sapiens.

PN WO200183726-A1.

PD 08-NOV-2001.

PF 28-APR-2001; 2001WO-CN00649.

PR 29-APR-2000; 2000CN-0115551.

PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

PI Mao Y, Xie Y;

DR WPI; 2002-062122/08.

PT Human uridylylate kinase 12 and encoded polynucleotide, applicable in
 PT diagnosis and treatment of developmental disorders, malignant tumour,
 PT haemopathy, HIV infection, immunological diseases and various
 PT inflammations

PS Example 2; Page 17; 36pp; Chinese.

CC The present invention relates to a new polypeptide of human uridylylate
 CC kinase 12, its fragment, analogue or derivative. The polypeptide of the
 CC invention and its encoding polynucleotide are applicable in diagnosis
 CC and treatment of malignant neoplasm, haemopathy, human immunodeficiency
 CC virus (HIV) infection, immunological diseases, various inflammations,
 CC sterility, pregnancy pathology, embryonic development disorders, growth
 CC and development disorders and hereditary diseases. The present nucleic
 CC acid sequence represents reverse transcriptase (RT)-PCR primer 2 that
 CC was used in the methods of the invention to isolate the coding sequence
 CC of the human kinase uridylylate 12 protein.

SQ Sequence 24 BP; 10 A; 3 C; 3 G; 8 T; 0 other;

Query Match 59.0%; Score 11.8; DB 24; Length 24;

Best Local Similarity 86.7%; Pred. No. 1.3e+04; Mismatches 2; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 TTTCGCTTGGCACT 15
 |||||
 15 TTTCGCTTGGCACT 1

RESULT 34
 ID AB188868/C
 AB188868 standard; DNA; 24 BP.

AC AB188868;

DT 15-FEB-2002 (first entry)

DE Capture oligonucleotide zip ID#3236 oligo #1.

KM Human, K-ras; PCR primer; probe; capture probe; mutation detection;
 KM ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KM infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
 KM cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
 KM environmental monitoring; food industry; feed industry; ss.

OS Synthetic.

PN WO200179548-A2.

PD 25-OCT-2001.

PF 04-APR-2001; 2001WO-US10958.

PR 14-APR-2000; 2000US-197271P.

PA (CORR) CORNELL RES FOUND INC.

PI Barany F, Zilvi M, Gerry NP, Favis R, Klaman R;

DR WPI; 2002-034366/04.

PT Designing capture oligonucleotide probes for use on a support to which
 PT complementary oligonucleotides hybridize with little mismatch -

PS Example 5; Fig 25; 300pp; English.

CC The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridise with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medinensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting complex scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. AB182074 to
 CC AB17546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention.


```

RESULT 37
AAI66253/c
ID AAI66253 standard; DNA; 20 BP.
XX
XX AAI66253;
AC
XX
XX 22-JAN-2002 (first entry)
DT
XX
XX S cerevisiae potassium translocation gene mutagenic primer Kan-antisense.
DE
XX
XX S. cerevisiae; yeast; potassium translocation system; TRK1; TRK2;
KM TOKI; human erg potassium ion channel; HERG; antiarrhythmic;
KM antiinflammatory; antifibrillatory; HERG modulator; mutagenic primer; ss.
XX
XX Saccharomyces cerevisiae.
OS
XX Synthetic.
XX
XX DE19953478-A1.
XX
XX 11-OCT-2001.
PD
XX
XX 06-NOV-1999; 99DE-1053478.
PF
XX
XX 06-NOV-1999; 99DE-1053478.
PR
XX
XX (LICH/) LICHTENBERG-FRATE H.
PA (LUDW/) LUDWIG J.
XX
XX LICHTENBERG-FRATE H, Ludwig J;
PI WPI; 2001-603577/69.
XX
XX Genetically modified yeast lacking endogenous potassium transport
PT activity; useful for identifying e.g. antiarrhythmic agents; includes a
PR functional human potassium channel
XX
XX Example 1; Fig 2; 40pp; German.
XX
XX The present invention relates to a genetically modified Saccharomyces
CC cerevisiae in which the endogenous potassium-translocation systems (TRK1,
CC TRK2 and TOKI) are specifically deleted and the human erg potassium ion
CC channel (HERG) is stably integrated and expressed. This can be used to
CC identify specific modulators of HERG, which are potentially useful as
CC antiarrhythmic, antifibrillatory and antiinflammatory agents. The present
CC sequence is a mutagenic primer used to disrupt the yeast TRK1 gene.
XX
XX Sequence 20 BP; 6 A; 7 C; 3 G; 4 T; 0 other;
SQ
Query Match 58.0%; Score 11.6; DB 22; Length 20;
Best Local Similarity 77.8%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TTGGCGTTGGCCACTCAG 18
DB 19 TTAGGATTTCACACTGAG 2
RESULT 38
AAT89508
ID AAT89508 standard; DNA; 21 BP.
XX
XX AAT89508;
AC
XX
XX 15-MAY-1998 (first entry)
DT
XX
XX a-cobratoxin gene amplifying primer LAS 3.
DE
XX
XX a-cobratoxin; neurotoxin; inactivated bioactive polypeptide;
KM disulphide bridge; LAS 2; wound healing; toxin; PCR primer; ss.
XX
XX Synthetic.
OS
XX Naja naja siamensis.

```

```

XX
XX MO9743407-A1.
PN
XX
XX 20-NOV-1997.
PD
XX
XX 08-MAY-1997; 97WO-US08074.
PF
XX
XX 10-MAY-1996; 96US-0644399.
PR
XX
XX (PHYL-) PHYLONED CORP.
PA
XX
XX Mundschenk DD, Smith LA;
PI WPI; 1998-008876/01.
XX
XX Production of inactivated bioactive polypeptide(s), particularly
PT neurotoxin(s) - by expression of DNA encoding the polypeptide in
PR such a way that one or more disulphide bridges are not formed
XX
XX Example 1; Page 16; 32pp; English.
PS
XX
XX This primer is used for the asymmetric PCR amplification of the gene
CC a-cobratoxin. A Naja naja siamensis cDNA is used as a template. This was
CC used for the DNA sequencing of a-cobratoxin. This was used in a novel
CC method for producing an inactivated neurotoxin with post translational
CC modifications. A novel method for preparing a composition comprising
CC an inactivated bioactive polypeptide comprises identifying a polypeptide
CC having a biological activity dependent on the presence of one or more
CC disulphide bridges in its tertiary structure, preparing a cDNA strand
CC encoding the polypeptide, expressing the cDNA under conditions in which
CC the polypeptide is recovered in an inactive form due to the failure to
CC form one or more disulphide bridges and recovering the inactive
CC polypeptide and formulating it into an aqueous composition. The
CC polypeptide can be treated with onated water under conditions to
CC oxidise any disulphide bonds in order to form corresponding pairs of
CC cysteine residues, and to then stabilise the resultant cysteine residues
CC and prevent the reformation of disulphide bonds. The methods can be used
CC for producing bioactive polypeptides which are inactivated but still
CC retain other useful properties such as immunogenicity and antiviral,
CC anti-tumour or wound healing activity. They can be used with toxins
CC affecting the presynaptic neurojunction such as norexin, crotoxin,
CC beta-bungarotoxin, taipoxin, textilotoxin and a-latrotoxin, toxins
CC affecting the postsynaptic neurojunction such as a-conotoxins, ion
CC erabutoxin, a-cobratoxin and a-bungarotoxin, toxins affecting ion
CC channels such as dendrotoxins, scorpion toxins, m-conotoxins, and sea
CC anemone toxins, or cell membrane-damaging toxins such as mycotoxins,
CC cardiotoxins, melittin, and phospholipases. The inactivated neurotoxin
CC composition can be used for the study and treatment of viral and
CC neurological diseases.
XX
XX Sequence 21 BP; 4 A; 6 C; 3 G; 8 T; 0 other;
SQ
Query Match 58.0%; Score 11.6; DB 19; Length 21;
Best Local Similarity 77.8%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TTGGCGTTGGCCACTCAG 18
DB 2 TTTCATTGCCATTTCAG 19
RESULT 39
AAI69969
ID AAI69969 standard; DNA; 21 BP.
XX
XX AAI69969;
AC
XX
XX 18-DEC-2001 (first entry)
DT
XX
XX alpha-cobratoxin PCR primer, LAS 3.
DE
XX
XX alpha-cobratoxin; PCR primer; anti-HIV; HIV infection; immunokine;
KM neurotoxin; Thailand cobra; ss.

```


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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 08:19:34 ; Search time 42.1818 Seconds

(Without alignments)
145,407 Million cell updates/sec

Title: US-10-080-959A-2

Perfect score: 20
Sequence: 1 ttgtgctgcctcctcagag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 364038

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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4: /cgn2_6/prodata/2/ina/6B.COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCrUS.COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	75.0	25	4	US-09-593-012-187
2	13.8	69.0	20	4	US-09-444-053-17
3	13.4	67.0	17	3	US-08-193-627-25
4	12.2	61.0	22	1	US-08-148-117A-2
5	12.2	61.0	24	4	US-09-593-012-108
6	12	60.0	21	1	US-08-758-306-999
7	12	60.0	21	4	US-08-803-346-29
8	11.8	59.0	20	4	US-09-553-231-7
9	11.6	58.0	21	1	US-07-994-423-4
10	11.6	58.0	21	1	US-08-421-891-4
11	11.6	58.0	21	2	US-08-908-212A-3
12	11.4	57.0	25	2	US-08-859-998-509
13	11.4	57.0	25	4	US-09-225-928-509
14	11.2	56.0	19	1	US-08-164-200-9
15	11.2	56.0	19	1	US-08-327-363-7
16	11.2	56.0	19	4	US-09-328-174A-96
17	11.2	56.0	21	1	US-08-136-118-6
18	11.2	55.0	22	4	US-09-091-952A-83
19	11	55.0	19	4	US-09-360-416-65
20	11	55.0	20	1	US-08-393-997-1
21	11	55.0	21	4	US-08-977-219-12
22	11	55.0	22	3	US-09-064-964-17
23	11	55.0	23	1	US-08-821-119-21
24	11	55.0	23	2	US-08-821-118-4
25	11	55.0	23	3	US-08-481-335-18
26	11	55.0	24	1	US-08-574-763-6
27	10.8	54.0	15	2	US-08-292-620A-10

28	10.8	54.0	15	3	US-09-071-845-10	Sequence 10, Appl
29	10.8	54.0	20	2	US-08-484-956-68	Sequence 68, Appl
30	10.8	54.0	20	2	US-08-757-653-68	Sequence 68, Appl
31	10.8	54.0	20	2	US-08-117-952-652	Sequence 652, Appl
32	10.8	54.0	20	3	US-09-358-685-23	Sequence 23, Appl
33	10.8	54.0	20	4	US-09-428-696-29	Sequence 29, Appl
34	10.8	54.0	20	4	US-09-270-933-2	Sequence 2, Appl
35	10.8	54.0	20	4	US-08-520-946-68	Sequence 68, Appl
36	10.8	54.0	21	1	US-08-415-818-8	Sequence 8, Appl
37	10.8	54.0	21	1	US-08-894-236-8	Sequence 8, Appl
38	10.8	54.0	21	5	PCT-US96-0144A-8	Sequence 8, Appl
39	10.8	54.0	22	1	US-08-203-198-31	Sequence 31, Appl
40	10.8	54.0	22	3	US-09-358-685-2	Sequence 2, Appl
41	10.8	54.0	23	4	US-08-821-994-29	Sequence 29, Appl
42	10.6	53.0	25	2	US-08-466-103A-28	Sequence 28, Appl
43	10.6	53.0	18	1	US-08-371-942A-118	Sequence 118, Appl
44	10.6	53.0	18	1	US-08-639-363-11	Sequence 11, Appl
45	10.6	53.0	18	3	US-09-161-244-74	Sequence 74, Appl
46	10.6	53.0	18	3	US-08-779-916A-118	Sequence 118, Appl
47	10.6	53.0	18	5	PCT-US95-0860A-118	Sequence 118, Appl
48	10.6	53.0	20	2	US-08-117-952-366	Sequence 366, Appl
49	10.6	53.0	20	4	US-09-021-701-1041	Sequence 1041, Appl
50	10.6	53.0	20	4	US-09-021-701-1042	Sequence 1042, Appl
51	10.6	53.0	20	4	US-09-021-701-1043	Sequence 1043, Appl
52	10.6	53.0	20	4	US-09-021-701-1044	Sequence 1044, Appl
53	10.6	53.0	20	4	US-08-803-346-21	Sequence 21, Appl
54	10.6	53.0	21	2	US-08-117-952-405	Sequence 405, Appl
55	10.6	53.0	21	3	US-08-882-046-19	Sequence 19, Appl
56	10.6	53.0	21	4	US-09-470-443-91	Sequence 91, Appl
57	10.6	53.0	24	3	US-08-513-974B-218	Sequence 218, Appl
58	10.6	52.0	15	2	US-08-292-620A-11	Sequence 11, Appl
59	10.4	52.0	15	3	US-09-071-845-11	Sequence 11, Appl
60	10.4	52.0	18	1	US-08-363-585-39	Sequence 59, Appl
61	10.4	52.0	18	1	US-08-440-787A-112	Sequence 112, Appl
62	10.4	52.0	18	1	US-08-440-787A-114	Sequence 114, Appl
63	10.4	52.0	20	2	US-08-448-267A-10	Sequence 10, Appl
64	10.4	52.0	20	2	US-08-874-266-17	Sequence 17, Appl
65	10.4	52.0	20	2	US-08-442-809A-18	Sequence 18, Appl
66	10.4	52.0	20	2	US-08-480-655-32	Sequence 32, Appl
67	10.4	52.0	20	3	US-09-280-799-40	Sequence 40, Appl
68	10.4	52.0	20	3	US-09-280-799-65	Sequence 65, Appl
69	10.4	52.0	20	3	US-08-765-743-4	Sequence 4, Appl
70	10.4	52.0	20	4	US-09-487-445-76	Sequence 76, Appl
71	10.4	52.0	20	4	US-09-455-683-32	Sequence 32, Appl
72	10.4	52.0	21	3	US-08-840-316-45	Sequence 45, Appl
73	10.4	52.0	21	4	US-08-809-523-45	Sequence 45, Appl
74	10.4	52.0	21	4	US-08-471-971-45	Sequence 45, Appl
75	10.4	52.0	21	4	US-09-402-776-45	Sequence 45, Appl
76	10.4	52.0	21	5	PCT-US93-08849A-45	Sequence 45, Appl
77	10.4	52.0	22	2	US-09-197-008-2	Sequence 2, Appl
78	10.4	52.0	22	2	US-08-694-835-5	Sequence 5, Appl
79	10.4	52.0	23	3	US-08-765-332-25	Sequence 25, Appl
80	10.4	52.0	23	4	US-09-448-894-25	Sequence 25, Appl
81	10.4	52.0	23	4	US-09-593-012-105	Sequence 105, Appl
82	10.4	52.0	24	2	US-08-447-430A-9	Sequence 9, Appl
83	10.4	52.0	25	1	US-08-694-835-5	Sequence 5, Appl
84	10.4	52.0	25	1	US-08-694-835-8	Sequence 8, Appl
85	10.4	52.0	25	2	US-08-929-101-5	Sequence 5, Appl
86	10.4	52.0	25	2	US-08-929-101-8	Sequence 8, Appl
87	10.4	52.0	25	2	US-09-476-124-25	Sequence 25, Appl
88	10.4	52.0	25	5	PCT-US95-01639-5	Sequence 5, Appl
89	10.4	52.0	25	5	PCT-US95-01639-8	Sequence 8, Appl
90	10.2	51.0	15	1	US-08-136-118-12	Sequence 12, Appl
91	10.2	51.0	15	3	US-08-805-633A-69	Sequence 69, Appl
92	10.2	51.0	15	3	US-08-805-633A-69	Sequence 69, Appl
93	10.2	51.0	15	4	US-09-569-344-69	Sequence 69, Appl
94	10.2	51.0	17	2	US-08-292-620A-1866	Sequence 1866, Appl
95	10.2	51.0	17	2	US-08-292-620A-1996	Sequence 1996, Appl
96	10.2	51.0	17	2	US-08-292-620A-2004	Sequence 2004, Appl
97	10.2	51.0	17	3	US-09-071-845-1866	Sequence 1866, Appl
98	10.2	51.0	17	3	US-09-071-845-1996	Sequence 1996, Appl
99	10.2	51.0	17	3	US-09-071-845-2004	Sequence 2004, Appl
100	10.2	51.0	17	4	US-08-584-040-6023	Sequence 6023, Appl

US-09-593-012-187
Sequence 187, Application US/09593012
Patent No. 6387652
GENERAL INFORMATION:
APPLICANT: HAUGLAND, Richard
APPLICANT: VESPER, Stephen
TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
FILE REFERENCE: HAUGLAND-1A
CURRENT APPLICATION NUMBER: US/09/593,012
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 09/280,990
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 60/081,773
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 225
SOFTWARE: Patentin version 3.0
SEQ ID NO 187
LENGTH: 25
TYPE: DNA
ORGANISM: Stachybotrys chartarum.
US-09-593-012-187

ALIGNMENTS

Sequence 3, Appl1
Sequence 9, Appl1
Sequence 3, Appl1
Sequence 18, Appl1
Sequence 57, Appl1
Sequence 49, Appl1
Sequence 51, Appl1
Sequence 52, Appl1
Sequence 8, Appl1
Sequence 58, Appl1
Sequence 27, Appl1
Sequence 28, Appl1
Sequence 19, Appl1
Sequence 28, Appl1
Sequence 42, Appl1
Sequence 13, Appl1
Sequence 12, Appl1
Sequence 360, Appl1
Sequence 35, Appl1
Sequence 36, Appl1
Sequence 35, Appl1
Sequence 7, Appl1

RESULT 1
US-09-593-012-187
Sequence 187, Application US/09593012
Patent No. 6387652
GENERAL INFORMATION:
APPLICANT: HAUGLAND, Richard
APPLICANT: VESPER, Stephen
TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
FILE REFERENCE: HAUGLAND-1A
CURRENT APPLICATION NUMBER: US/09/593,012
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 09/280,990
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 60/081,773
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 225
SOFTWARE: Patentin version 3.0
SEQ ID NO 187
LENGTH: 25
TYPE: DNA
ORGANISM: Stachybotrys chartarum.
US-09-593-012-187

Query Match 75.0%; Score 15; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GTTGGCACTCAGAG 20
DB 1 GTTGGCACTCAGAG 15

RESULT 2
US-09-444-053-17/c
Sequence 17, Application US/09444053A
Patent No. 6165728
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Lex M. Cowart
TITLE OF INVENTION: ANTISENSE MODULATION OF NCK-2 EXPRESSION
FILE REFERENCE: RTS-0122
CURRENT APPLICATION NUMBER: US/09/444,053A
CURRENT FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 89

SEQ ID NO 17
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-444-053-17

Query Match 69.0%; Score 13.8; DB 4; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTGGTTGCACTCA 17
DB 19 TTTGGTTGCACTCA 3

RESULT 3
US-08-193-627-25/c
Sequence 25, Application US/08193627
Patent No. 6017756
GENERAL INFORMATION:
APPLICANT: KENNETH G. DRAPER
TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING HEPATITIS B VIRUS
TITLE OF INVENTION: INHIBITING HEPATITIS B VIRUS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,627
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/882,712
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Marbury, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 197/072

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 17
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-193-627-25

Query Match 67.0%; Score 13.4; DB 3; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCGTTGGCACTCAG 18
DB 15 GCGTTGGCACTCAG 1

RESULT 4
US-08-148-117A-2/c

Sequence 2, Application US/08148117A
Patent No. 5744368
GENERAL INFORMATION:
APPLICANT: GOLDBER, DMITRY, Y.;
APPLICANT: SCHMARZMAN, ALEXANDER, L.; EISENBERG-
APPLICANT: GRNEERG, MOISES.
TITLE OF INVENTION: METHOD OF PREVENTING
NUMBER OF INVENTIONS: AGGREGATION OF AMYLOID - PROTEIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148.117A
FILING DATE: 04-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KENNETH H. SONNENFELD
REGISTRATION NUMBER: 33,285
REFERENCE/DOCKET NUMBER: 0867-4113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 22
TYPE: NUCLEOTIDE
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
US-08-148-117A-2

Query Match 61.0%; Score 12.2; DB 1; Length 22;
Best Local Similarity 82.4%; Pred. No. 8.3e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTGGCTTGCCTCA 17
DB 19 TTCCGTTGCCCTCA 3

RESULT 5
US-09-593-012-108
Sequence 108, Application US/09593012
Patent No. 6387652
GENERAL INFORMATION:
APPLICANT: HAUGLAND, Richard
APPLICANT: VESPER, Stephen
TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
FILE REFERENCE: HAUGLAND-1A
CURRENT APPLICATION NUMBER: US/09/593.012
PRIOR FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 09/290.990
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 60/081.773
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 108
LENGTH: 24
TYPE: DNA
ORGANISM: Paecilomyces lilacinus
US-09-593-012-108

Query Match 61.0%; Score 12.2; DB 4; Length 24;
Best Local Similarity 82.4%; Pred. No. 8.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCGTTGGCACTCAG 20
DB 1 GCTTGCACTCAG 17

RESULT 6
US-08-758-306-999
Sequence 999, Application US/08758306
Patent No. 5807743
GENERAL INFORMATION:
APPLICANT: Scinccomb, Dan T.
APPLICANT: McSwigen, James A.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES
TITLE OF INVENTION: ASSOCIATED WITH
TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
NUMBER OF SEQUENCES: 1379
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: storage
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758.306
FILING DATE: December 3, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wardlaw, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/132
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 999:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-758-306-999

Query Match 60.0%; Score 12; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 1e+03;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTGGCACTCAGA 19
DB 1 TUGCCACTCAGA 12

RESULT 7
US-08-803-346-29
Sequence 29, Application US/08803346
Patent No. 6281346
GENERAL INFORMATION:

APPLICANT: HESS, JOHN W.
APPLICANT: CASKEY, C. THOMAS
APPLICANT: LIU, QINGYUN
APPLICANT: PHILLIPS, MICHAEL SEAN
TITLE OF INVENTION: RAT OB RECEPTORS AND NUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOANNE M. GIESSEY - MERCK & CO., INC.
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,346
FILING DATE: 20-FEB-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GIESSEY, JOANNE M
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 19642Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3046
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-803-346-29

Query Match 60.0%; Score 12; DB 4; Length 21;
Best Local Similarity 75.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TTGGGTTTGGCCACTCAGAG 20
DB 2 TTGGGTTTGGAGATCAG 21

RESULT 8
US-09-553-231-7/C
Sequence 7, Application US/09553231
Patent No. 6432647
GENERAL INFORMATION:
APPLICANT: PREUS, DAPHNE
APPLICANT: COENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:257--2
CURRENT APPLICATION NUMBER: US/09/553,231
CURRENT FILING DATE: 2000-04-19
PRIOR APPLICATION NUMBER: 60/073,741
PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: 60/048,451
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 7
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Primer
US-09-553-231-7

Query Match 59.0%; Score 11.8; DB 4; Length 20;
Best Local Similarity 86.7%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCGTTTGGCCACT 15
DB 17 TTTCGTTTGGCCACT 3

RESULT 9
US-07-994-423-4/C
Sequence 4, Application US/07994423
Patent No. 5432080
GENERAL INFORMATION:
APPLICANT: HAMMOND, Geoffrey L.
APPLICANT: AVAKUMOV, George V.
TITLE OF INVENTION: Variants of Corticosteroid Binding
TITLE OF INVENTION: Globulin
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/994,423
FILING DATE: 16-DEC-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16777/197/ALLE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-994-423-4

Query Match 58.0%; Score 11.6; DB 1; Length 21;
Best Local Similarity 77.8%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TCGGTTTGGCCACTCAGAG 20
DB 20 TCGGTTTGGCCACTCAGT 3

RESULT 10
US-08-421-891-4/C
Sequence 4, Application US/08421891
Patent No. 5395969
GENERAL INFORMATION:
APPLICANT: HAMMOND, Geoffrey L.
APPLICANT: AVAKUMOV, George V.
TITLE OF INVENTION: Variants of Corticosteroid Binding
TITLE OF INVENTION: Globulin

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/421,891
FILING DATE: 14-Apr-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/994,423
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16777/197/ALLE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-421-891-4

Query Match 58.0%; Score 11.6; DB 1; Length 21;
Best Local Similarity 77.8%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TGGCTTGGCACTCAG 20
DB 20 TGGCTTGGCACTCAG 3

RESULT 11
US-08-908-212A-3
Sequence 3, Application US/08908212A
Patent No. 5989857
GENERAL INFORMATION:
APPLICANT: Mundschien, David
APPLICANT: Smith, Leonard
TITLE OF INVENTION: Polypeptide Compositions and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fredrickson & Byron, P.A.
STREET: 900 Second Avenue South
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402-3397
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows-95
SOFTWARE: ASCII files
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,212A
FILING DATE: 07 August 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/644,399
FILING DATE: 10 May 1996
ATTORNEY/AGENT INFORMATION:

NAME: Goldman, Philip M.
REGISTRATION NUMBER: 31,162
REFERENCE/DOCKET NUMBER: 15050.1.2.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 347-7088
TELEFAX: (612) 347-7077
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-908-212A-3

Query Match 58.0%; Score 11.6; DB 2; Length 21;
Best Local Similarity 77.8%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTGGCTTGGCACTCAG 18
DB 2 TTTTCATTGGCACTCAG 19

RESULT 12
US-08-859-998-509/c
Sequence 509, Application US/08859998
Patent No. 5994076
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Jekhadze, George
APPLICANT: Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 509:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-08-859-998-509

Query Match 57.0%; Score 11.4; DB 2; Length 25;
Best Local Similarity 92.3%; Pred. No. 2.2e+03;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TTGCCACTCAGAG 20
Db 17 TTGCCACTCTGAG 5

RESULT 13

US-09-225-928-509/C

Sequence 509, Application US/09225928

Patent No. 6352829

GENERAL INFORMATION:

APPLICANT: Chenchik, Alex

Biblashvili, Robert

Jokhadze, George

TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL

NUMBER OF SEQUENCES: 1375

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 2200 Sand Hill Road, Suite 100

CITY: Menlo Park

STATE: CA

COUNTRY: US

ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/225,928

FILING DATE: 05-Jan-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/859,998

FILING DATE: 21-May-1997

ATTORNEY/AGENT INFORMATION:

NAME: Field, Bret E.

REGISTRATION NUMBER: 37,620

REFERENCE/DOCKET NUMBER: 09096/002001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-322-5070

TELEFAX: 415-854-0875

INFORMATION FOR SEQ ID NO: 509:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

OTHER INFORMATION: oligonucleotide primer

SEQUENCE DESCRIPTION: SEQ ID NO: 509:

US-09-225-928-509

Query Match 57.0%; Score 11.4; DB 4; Length 25;

Best Local Similarity 92.3%; Pred. No. 2.2e+03;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TTGCCACTCAGAG 20

Db 17 TTGCCACTCTGAG 5

RESULT 14

US-08-164-200-9/C

Sequence 9, Application US/08164200

Patent No. 5552390

GENERAL INFORMATION:

APPLICANT: Scholar, Eric M.

APPLICANT: Iversen, Patrick L.

TITLE OF INVENTION: Phosphorothioate Inhibitors of Metastatic

US-08-164-200-9/C

Sequence 9, Application US/08164200

Patent No. 5552390

GENERAL INFORMATION:

APPLICANT: Scholar, Eric M.

APPLICANT: Iversen, Patrick L.

TITLE OF INVENTION: Phosphorothioate Inhibitors of Metastatic

US-08-164-200-9/C

Sequence 9, Application US/08164200

Patent No. 5552390

GENERAL INFORMATION:

APPLICANT: Scholar, Eric M.

APPLICANT: Iversen, Patrick L.

TITLE OF INVENTION: Breast Cancer

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zarley, McKee, Thome, Voorhees, & Sease

STREET: 801 Grand Avenue Suite 3200

CITY: Des Moines

STATE: Iowa

COUNTRY: United States

ZIP: 50309

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/164,200

FILING DATE: December 9, 1993

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Nebel, Heidi Sease

REGISTRATION NUMBER: P-37,719

REFERENCE/DOCKET NUMBER: UMC #63054

TELECOMMUNICATION INFORMATION:

TELEPHONE: (515) 288-3667

TELEFAX: (515) 288-1338

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: mRNA

HYPOTHETICAL: NO

ANTI-SENSE: YES

US-08-164-200-9

Query Match 56.0%; Score 11.2; DB 1; Length 19;

Best Local Similarity 81.2%; Pred. No. 2.7e+03;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTGCGTTGCCACTCA 17

Db 19 TTGCCCTGCCACCCA 4

RESULT 15

US-08-327-363-7/C

Sequence 7, Application US/08327363

Patent No. 5643780

GENERAL INFORMATION:

APPLICANT: Isis Pharmaceuticals and

APPLICANT: Brenda Baker

TITLE OF INVENTION: Compositions and Methods for Modulating

TITLE OF INVENTION: RNA Activity Through Modification of the 5' Cap Structure of

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5643780

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/327,363

FILING DATE: herewith

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 847,054
FILING DATE: April 3, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Kathryn Leary, Ph.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: ISIS-1719
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 19
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-327-363-7

Query Match 56.0%; Score 11.2; DB 1; Length 19;
Best Local Similarity 81.2%; Pred. No. 2.7e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CGTTGCCACTCAGAG 20
DB 16 CCTCTGCTACTCAGAG 1

RESULT 16
US-09-328-174A-96
Sequence 96, Application US/09328174A
Patent No. 6448003
GENERAL INFORMATION:
APPLICANT: Guida, Marco
TITLE OF INVENTION: Genotyping Human Phenol Sulfotransferase
FILE REFERENCE: 4389-6 (formerly SEQ-16P)
CURRENT APPLICATION NUMBER: US/09/328,174A
PRIORITY FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: 09/328,174
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 96:
LENGTH: 19
TYPE: DNA
ORGANISM: H. sapiens
US-09-328-174A-96

Query Match 56.0%; Score 11.2; DB 4; Length 19;
Best Local Similarity 81.2%; Pred. No. 2.7e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CGTTGCCACTCAGAG 20
DB 1 CCTTGGCCACCAAGAG 16

RESULT 17
US-08-136-118-6/c
Sequence 6, Application US/08136118
Patent No. 5580969
GENERAL INFORMATION:
APPLICANT: HOKE, Glenn D
APPLICANT: BRADLEY, Matthews O
APPLICANT: WILLIAMS, Taffy J
APPLICANT: LEE, Che-Hung
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES DIRECTED
AGAINST HUMAN ICAM-1
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Naval Medical Res. & Dev. Cmd.
STREET: 8901 Wisconsin Ave.
CITY: Bethesda

STATE: Maryland
COUNTRY: USA
ZIP: 20889-5606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,118
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,259
FILING DATE: 24-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Spevack, A. David
REGISTRATION NUMBER: 24,743
REFERENCE/DOCKET NUMBER: N.C. 75,776
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 295-6759
TELEFAX: (202) 295-1022
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-136-118-6

Query Match 56.0%; Score 11.2; DB 1; Length 21;
Best Local Similarity 81.2%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CGTTGCCACTCAGAG 20
DB 16 CCTCTGCTACTCAGAG 1

RESULT 18
US-09-091-952A-83
Sequence 83, Application US/09091952A
Patent No. 6458532
GENERAL INFORMATION:
APPLICANT: Deterra-Wadleigh, Sevilla D.
Gershon, Elliot S.
Badner, Judith A.
Goldin, Lynn R.
Berrettini, Wade H.
Yoshikawa, Takeo
Sanders, Alan R.
Barelling, Lisa E.
TITLE OF INVENTION: Chromosomal Markers and Diagnostic
Tests for Manic-Depressive Illness
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1...22
OTHER INFORMATION: D18S1066 forward primer
SEQUENCE DESCRIPTION: SEQ ID NO: 83:
US-09-091-952A-83

Query Match 56.0%; Score 11.2; DB 4; Length 22;
Best Local Similarity 81.2%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TTGGTTGGCACTCAG 18
DB 1 TGCTGTGCTCTCAG 16

RESULT 19
US-09-360-416-65
Sequence 65, Application US/09360416
Patent No. 6458536
GENERAL INFORMATION:
APPLICANT: Richard A. Gatti
TITLE OF INVENTION: METHODS FOR DETECTION OF ATAXIA
FILE REFERENCE: 510015-222
CURRENT FILING DATE: 1999-07-23
CURRENT APPLICATION NUMBER: US/09/360,416
NUMBER OF SEQ ID NOS: 143
SOFTWARE: PasteSeq for Windows Version 3.0
SEQ ID NO 65
LENGTH: 19
TYPE: DNA
ORGANISM: Human
US-09-360-416-65

Query Match 55.0%; Score 11; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGCCACTCAGA 19
DB 2 TGCCACTCAGA 12

RESULT 20
US-08-393-997-1
Sequence 1, Application US/08393997
Patent No. 5633729
GENERAL INFORMATION:
APPLICANT: Taniguchi, Tadatsugu
APPLICANT: Harada, Hisaaki
TITLE OF INVENTION: Methods for Diagnosing Cancer, Precancerous
TITLE OF INVENTION: State, or Susceptibility to Other Forms of

TITLE OF INVENTION: Diseases by Detecting an Acceleration of Exon
TITLE OF INVENTION: Skipping in IRE-1 mRNA
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA: US/08/393,997
APPLICATION NUMBER: US/08/393,997
FILING DATE: herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 0652.1420000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-393-997-1

Query Match 55.0%; Score 11; DB 1; Length 20;
Best Local Similarity 73.7%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TTGGTTGGCACTCAG 20
DB 1 TTCCCTTCCTCCAG 19

RESULT 21
US-08-927-219-12/c
Sequence 12, Application US/08927219
Patent No. 6187533
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Yamagata, Kazuya
APPLICANT: Oda, Naohisa
APPLICANT: Katsuki, Pamela J.
APPLICANT: Furuta, Hiroko
APPLICANT: Horikawa, Yukio
APPLICANT: Menzel, Stephen
TITLE OF INVENTION: MUTATIONS IN THE DIABETES SUSCEPTIBILITY
TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA
TITLE OF INVENTION: AND HNF-4ALPHA
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/927,219
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,679
FILING DATE: 30-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,056
FILING DATE: 02-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/025,719
FILING DATE: 10-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:272
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/474-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-927-219-12

Query Match 55.0%; Score 11; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGCGTTGCC 12
DB 15 TTGCGTTGCC 5

RESULT 22
US-09-064-964-17
Sequence 17, Application US/09064964
Patent No. 6080399
GENERAL INFORMATION:
APPLICANT: Gajewski, Thomas F.
TITLE OF INVENTION: VACCINE ADJUVANTS FOR IMMUNOTHERAPY OF
TITLE OF INVENTION: MELANOMA
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,964
FILING DATE: Concurrently Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:280
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512)418-3000
TELEFAX: (512)474-7577
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
US-09-064-964-17

Query Match 55.0%; Score 11; DB 3; Length 22;
Best Local Similarity 73.7%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TTGCGTTGCCACTCAG 20
DB 4 TAGCGATGCTCTCAAG 22

RESULT 23
US-08-821-119-21
Sequence 21, Application US/08821119
Patent No. 5821104
GENERAL INFORMATION:
APPLICANT: Holm, Kaj Andre
APPLICANT: Rasmussen, Grethe
APPLICANT: Haikier, Torben
TITLE OF INVENTION: Tripeptidyl Aminopeptidase
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58211040 No. 5821104disk of No. 5821104th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,119
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4107,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-821-119-21

Query Match 55.0%; Score 11; DB 1; Length 23;
Best Local Similarity 64.7%; Pred. No. 3.6e+03;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTGCGTTGCCACTCAG 18
DB 7 YTGRTTYTGCAYTCG 23

RESULT 24
US-08-821-118-4
Sequence 4, Application US/08821118
Patent No. 5989889
GENERAL INFORMATION:
APPLICANT: Rey, Michael
APPLICANT: Golightly, Elizabeth

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES
TITLE OF INVENTION: HAVING TRIPEPTIDE AMINOPEPTIDASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSSEE: No. 59898890 No. 59898890 of No. 59898890th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,118
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambirth, Elia J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4107,400-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-821-118-4

Query Match 55.0%; Score 11; DB 2; Length 23;
Best Local Similarity 64.7%; Pred. No. 3.6e+03;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TTGGCTTGCCACTCAG 18
Db 7 YTGRTYTGCCAYTCGG 23

RESULT 25
US-08-481-435-18
Sequence 18, Application US/08481435
Patent No. 6027906
GENERAL INFORMATION:
APPLICANT: Balganes, Tanjore S
TITLE OF INVENTION: No. 6027906e1 Polypeptides
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,435
FILING DATE: 10-JUL-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IN 580/MAS/94

FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9404072-2
FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid (synthetic DNA primer)
US-08-481-435-18

Query Match 55.0%; Score 11; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCGTTGCCAC 14
Db 13 GCGTTGCCAC 23

RESULT 26
US-08-574-763-6/C
Sequence 6, Application US/08574763
Patent No. 5736376
GENERAL INFORMATION:
APPLICANT: Yanagisawa, Masashi
TITLE OF INVENTION: RECOMBINANT ENDOTHELIN CONVERTING
ENZYME-2 AND ITS USE IN ECG INHIBITOR SCREENING
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/574,763
FILING DATE: Concurrently herewith
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Corder, Timothy S.
REGISTRATION NUMBER: 38,414
REFERENCE/DOCKET NUMBER: UTXD:472
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-574-763-6

Query Match 55.0%; Score 11; DB 1; Length 24;
Best Local Similarity 73.7%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TTGGCTTGCCTCAGAG 20
| | | | | | | | | | | | | | | | | | | | | |
DB 22 TAGCACTTGCTCAGAG 4

RESULT 27

US-08-292-620A-10
Sequence 10, Application US/08292620A

PATENT No. 5837542
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ. ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

two

US-08-292-620A-10

Query Match 54.0%; Score 10.8; DB 2; Length 15;
Best Local Similarity 64.3%; Pred. No. 4.2e+03;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 TTGGCACTCAGAG 20
: | | | | | | | | | | | | | | | | | | | | | |
DB 2 UCUGCUACUCAGAG 15

RESULT 28
US-09-071-845-10

Sequence 10, Application US/09071845

PATENT No. 6132967
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ. ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-071-845-10

Query Match 54.0%; Score 10.8; DB 3; Length 15;
Best Local Similarity 64.3%; Pred. No. 4.2e+03;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 TTGGCACTCAGAG 20
: | | | | | | | | | | | | | | | | | | | | | |
DB 2 UCUGCUACUCAGAG 15

RESULT 29
US-08-484-956-68/C
Sequence 68, Application US/08484956
PATENT No. 5843654
GENERAL INFORMATION:
APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
APPLICANT: OLDENBURG, MARY C.

APPLICANT: HEISLER, LAURA
TITLE OF INVENTION: DETECTION OF p53 MUTATIONS
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,956
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/402,601
FILING DATE: 09-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,164
FILING DATE: 09-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/254,359
FILING DATE: 06-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 04-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL J., PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01801
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-484-956-68

Query Match 54.0%; Score 10.8; DB 2; Length 20;
Best Local Similarity 85.7%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 7 TTGGCCTGAG 20
Db 19 TTGGCCTGAG 6

RESULT 30
US-08-757-653-68/c
Sequence 68, Application US/08/757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichay, Victor I.
APPLICANT: Lyamichay, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
NUMBER OF SEQUENCES: 190
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,952
FILING DATE: 07-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,471
FILING DATE: 15-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9423
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-68

Query Match 54.0%; Score 10.8; DB 2; Length 20;
Best Local Similarity 85.7%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 7 TTGGCCTGAG 20
Db 19 TTGGCCTGAG 6

RESULT 31
US-08-117-952-652/c
Sequence 652, Application US/08/117952
Patent No. 5851760
GENERAL INFORMATION:
APPLICANT: Evans, Glen A.
APPLICANT: Smith, Michael W.
TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
NUMBER OF SEQUENCES: 797
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,952
FILING DATE: 07-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,471
FILING DATE: 15-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9423
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737

TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 652:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-08-117-952-652

Query Match 54.0%; Score 10.8; DB 2; Length 20;
Best Local Similarity 85.7%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TTGGCCACTCAG 20
Db 19 TTGGCCACTCAG 6

RESULT 32
US-09-358-685-23/c
; Sequence 23, Application US/09358685
; Patent No. 6121047
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowart
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHP-1 EXPRESSION
; FILE REFERENCE: RTS-0081
; CURRENT APPLICATION NUMBER: US/09/358,685
; CURRENT FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-358-685-23

Query Match 54.0%; Score 10.8; DB 3; Length 20;
Best Local Similarity 85.7%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GTTGGCACTCAGA 19
Db 14 GTTGGCACTCAGA 1

RESULT 33
US-09-428-696-29/c
; Sequence 29, Application US/09428696
; Patent No. 6165789
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowart
; TITLE OF INVENTION: ANTISENSE MODULATION OF HNRNP A1 EXPRESSION
; FILE REFERENCE: RTS-0111
; CURRENT APPLICATION NUMBER: US/09/428,696
; CURRENT FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-428-696-29

Query Match 54.0%; Score 10.8; DB 4; Length 20;
Best Local Similarity 85.7%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTTCGTTGGCAC 14
Db 18 TTTCGTTGGCAC 5

RESULT 34
US-09-270-933-2/c
; Sequence 2, Application US/09270933
; Patent No. 6365375
; GENERAL INFORMATION:
; APPLICANT: Dietmarer, Wolfgang
; APPLICANT: Ruschoff, Josef
; TITLE OF INVENTION: IMPROVED METHOD OF PRIMER-EXTENSION PREAMPLIFICATION
; TITLE OF INVENTION: PCR
; FILE REFERENCE: 4802
; CURRENT APPLICATION NUMBER: US/09/270,933
; CURRENT FILING DATE: 1999-03-16
; EARLIER APPLICATION NUMBER: DE 198 13 317.0
; EARLIER FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer for
US-09-270-933-2

Query Match 54.0%; Score 10.8; DB 4; Length 20;
Best Local Similarity 85.7%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TTTCGCACTCAG 20
Db 19 TTTCGCACTCAG 6

RESULT 35
US-08-520-946-68/c
; Sequence 68, Application US/08520946
; Patent No. 6372424
; GENERAL INFORMATION:
; APPLICANT: BROW, MARY ANN D.
; APPLICANT: LYAMICHEV, VICTOR I.
; APPLICANT: OLIVE, DAVID M.
; TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,946
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: FORS-01756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-520-946-68

Query Match 54.0%; Score 10.8; DB 4; Length 20;
Best Local Similarity 85.7%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 7 TTGCGCTTGCAGC 20
Db 19 TTGCGCAGCTGAG 6

RESULT 36
US-08-415-818-8/c
Sequence 8, Application US/08415818
Patent No. 5621079
GENERAL INFORMATION:
APPLICANT: Cascleri, Margaret A.
APPLICANT: Linemeyer, David L.
APPLICANT: Macneil, Douglas J.
APPLICANT: Shiao, Lin-Lin
APPLICANT: Strader, Catherine D.
APPLICANT: Tan, Carina P.
APPLICANT: Weinberg, David H.
TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mary A. Appollina
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,818
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/383,746
FILING DATE: 03-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Appollina, Mary A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19390
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-4720
TELEFAX: 908-594-4720
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-415-818-8

Query Match 54.0%; Score 10.8; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 4.5e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 2 TTGCGTTGCAGC 15
Db 17 TTGCTCTTGCAGC 4

RESULT 37
US-08-894-236-8/c
Sequence 8, Application US/08894236
Patent No. 5939263
GENERAL INFORMATION:
APPLICANT: Cascleri, Margaret A.
APPLICANT: Linemeyer, David L.
APPLICANT: Macneil, Douglas J.
APPLICANT: Shiao, Lin-Lin
APPLICANT: Strader, Catherine D.
APPLICANT: Tan, Carina P.
APPLICANT: Weinberg, David H.
TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mary A. Appollina
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,236
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/383,746
FILING DATE: 03-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/415,818
FILING DATE: 03-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Appollina, Mary A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19390Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3462
TELEFAX: 908-594-4720
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-894-236-8

Query Match 54.0%; Score 10.8; DB 2; Length 21;
Best Local Similarity 85.7%; Pred. No. 4.5e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 2 TTGCGTTGCAGC 15
Db 17 TTGCTCTTGCAGC 4

RESULT 38
PCT-US96-01444-8/c
Sequence 8, Application PC/TUS9601444
GENERAL INFORMATION:
APPLICANT: Cascleri, Margaret A.
APPLICANT: Linemeyer, David L.

APPLICANT: MacNeill, Douglas J.
APPLICANT: Shiao, Lin-Lin
APPLICANT: Strader, Catherine D.
APPLICANT: Tan, Carina P.
APPLICANT: Weidner, David H.
TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mary A. Appollina
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01444
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/383,746
FILING DATE: 03-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/415,818
FILING DATE: 03-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Appollina, Mary A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19390Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3462
TELEFAX: 908-594-4720
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US96-01444-8

Query Match 54.0%; Score 10.8; DB 5; Length 21;
Best Local Similarity 85.7%; Pred. No. 4.5e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 TTGCTTGCCACT 15
DB 17 TTGCTTGCCACT 4

RESULT 39
US-08-203-198-31/c
Sequence 31, Application US/08203198
Patent No. 5512462
GENERAL INFORMATION:
APPLICANT: Cheng, Suzanne
TITLE OF INVENTION: Methods and Reagents for the Polymerase
TITLE OF INVENTION: Chain Reaction Amplification of Long DNA Sequences
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/203,198
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Percy Ph.D., Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 8894
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-203-198-31

Query Match 54.0%; Score 10.8; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 4.5e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 7 TTGCGCACTCAG 20
DB 21 TTGCGCACTCAG 8

RESULT 40
US-09-358-685-2
Sequence 2, Application US/09358685
Patent No. 6121047
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: ANTISENSE MODULATION OF SHP-1 EXPRESSION
FILE REFERENCE: RTS-0081
CURRENT APPLICATION NUMBER: US/09/358,685
CURRENT FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 2
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Primer
US-09-358-685-2

Query Match 54.0%; Score 10.8; DB 3; Length 22;
Best Local Similarity 85.7%; Pred. No. 4.5e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 GTTGCCACTCAGA 19
DB 7 GTTGCCACTCAGA 20

Search completed: June 7, 2003, 09:45:29
Job time : 53.1818 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 08:51:24 ; Search time 76.3636 Seconds
(Without alignments)
366.546 Million cell updates/sec

Title: US-10-080-959a-2

Perfect score: 20

Sequence: 1 ttctgcttcgcaccacagag 20

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 359952

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	20	100.0	20	9	US-10-080-959a-2	Sequence 2, Appli
2	17	85.0	23	9	US-10-080-959a-4	Sequence 4, Appli
3	13.4	67.0	17	9	US-09-877-478-25	Sequence 25, Appli
4	13.2	66.0	23	10	US-09-972-467-10	Sequence 10, Appli
5	12.2	61.0	17	9	US-09-780-533a-2611	Sequence 2611, Appli
6	12.2	61.0	25	10	US-09-819-097-24	Sequence 24, Appli
7	12	60.0	23	10	US-09-821-821-22	Sequence 22, Appli
8	11.8	59.0	17	9	US-09-780-533a-2000	Sequence 2000, Ap
9	11.8	59.0	22	9	US-09-996-956-14	Sequence 14, Appli
10	11.6	58.0	21	10	US-09-368-834-3	Sequence 3, Appli
11	11.6	58.0	24	9	US-09-940-185-2248	Sequence 2248, Ap
12	11.4	57.0	24	8	US-08-844-215-30	Sequence 30, Appli
13	11.4	57.0	24	9	US-09-913-238-53	Sequence 53, Appli
14	11.4	57.0	25	9	US-10-215-112-10761	Sequence 10761, A
15	11.2	56.0	17	9	US-09-780-533a-505	Sequence 505, App
16	11.2	56.0	17	9	US-09-930-423-1153	Sequence 1153, Ap
17	11.2	56.0	19	9	US-10-206-839-96	Sequence 96, Appli
18	11.2	56.0	20	9	US-10-060-301-158	Sequence 158, App
19	11.2	56.0	20	9	US-10-060-301-160	Sequence 160, App

C	20	11.2	56.0	20	10	US-09-808-680-10	Sequence 10, Appli
C	21	11	55.0	12	9	US-10-117-108a-27	Sequence 27, Appli
C	22	11	55.0	19	9	US-10-175-225-65	Sequence 65, Appli
C	23	11	55.0	20	10	US-09-801-968-5	Sequence 5, Appli
C	24	10.8	54.0	17	9	US-09-780-533a-1366	Sequence 1366, Ap
C	25	10.8	54.0	20	9	US-10-087-082-2	Sequence 2, Appli
C	26	10.8	54.0	20	9	US-09-865-866-22	Sequence 22, Appli
C	27	10.8	54.0	20	9	US-09-865-866-23	Sequence 23, Appli
C	28	10.8	54.0	20	9	US-09-940-925a-68	Sequence 68, Appli
C	29	10.8	54.0	20	9	US-10-001-076-59	Sequence 59, Appli
C	30	10.8	54.0	20	12	US-10-011-119a-6	Sequence 6, Appli
C	31	10.8	54.0	21	9	US-10-135-629-15	Sequence 15, Appli
C	32	10.8	54.0	24	9	US-09-883-152-86	Sequence 86, Appli
C	33	10.8	54.0	24	9	US-09-940-185-2382	Sequence 2382, Ap
C	34	10.8	54.0	25	9	US-10-215-112-665	Sequence 665, App
C	35	10.8	54.0	25	9	US-10-215-112-791	Sequence 791, App
C	36	10.8	54.0	25	9	US-10-215-112-2803	Sequence 2803, Ap
C	37	10.8	54.0	25	9	US-10-215-112-2929	Sequence 2929, Ap
C	38	10.8	54.0	25	9	US-10-215-112-8357	Sequence 8357, Ap
C	39	10.8	54.0	25	9	US-10-215-112-11650	Sequence 11650, A
C	40	10.8	54.0	25	9	US-10-215-112-1458	Sequence 12458, A
C	41	10.6	53.0	20	9	US-09-784-674-1041	Sequence 1041, Ap
C	42	10.6	53.0	20	9	US-09-784-674-1042	Sequence 1042, Ap
C	43	10.6	53.0	20	9	US-09-784-674-1043	Sequence 1043, Ap
C	44	10.6	53.0	20	9	US-09-784-674-1044	Sequence 1044, Ap
C	45	10.6	53.0	20	9	US-09-953-611-82	Sequence 82, Appli
C	46	10.6	53.0	20	10	US-09-808-680-9	Sequence 9, Appli
C	47	10.6	53.0	21	9	US-10-116-949-91	Sequence 91, Appli
C	48	10.6	53.0	21	9	US-10-067-514-53	Sequence 53, Appli
C	49	10.6	53.0	22	10	US-09-804-987-5	Sequence 5, Appli
C	50	10.6	53.0	24	9	US-09-940-185-919	Sequence 919, App
C	51	10.6	53.0	24	9	US-09-940-185-1602	Sequence 1602, Ap
C	52	10.6	53.0	24	10	US-09-771-063-1	Sequence 7, Appli
C	53	10.6	53.0	25	9	US-10-045-631a-13	Sequence 13, Appli
C	54	10.6	53.0	25	9	US-10-215-112-3633	Sequence 3633, Ap
C	55	10.6	53.0	25	9	US-10-215-112-11760	Sequence 11760, A
C	56	10.4	52.0	12	9	US-10-117-108a-28	Sequence 28, Appli
C	57	10.4	52.0	17	9	US-09-848-754a-1238	Sequence 1238, Ap
C	58	10.4	52.0	17	9	US-09-848-754a-1239	Sequence 1239, Ap
C	59	10.4	52.0	17	9	US-09-848-754a-1240	Sequence 1240, Ap
C	60	10.4	52.0	17	9	US-09-848-754a-1241	Sequence 1241, Ap
C	61	10.4	52.0	17	9	US-09-848-754a-1242	Sequence 1242, Ap
C	62	10.4	52.0	19	10	US-09-726-774-107	Sequence 107, App
C	63	10.4	52.0	20	9	US-10-181-177-76	Sequence 76, Appli
C	64	10.4	52.0	20	9	US-10-238-443-24	Sequence 24, Appli
C	65	10.4	52.0	20	9	US-09-741-744a-25	Sequence 25, Appli
C	66	10.4	52.0	20	9	US-09-741-744a-53	Sequence 53, Appli
C	67	10.4	52.0	20	9	US-09-953-047-65	Sequence 65, Appli
C	68	10.4	52.0	20	10	US-09-320-337-18	Sequence 18, Appli
C	69	10.4	52.0	20	10	US-09-800-629a-40	Sequence 40, Appli
C	70	10.4	52.0	20	10	US-09-800-629a-65	Sequence 65, Appli
C	71	10.4	52.0	21	9	US-10-132-652-21	Sequence 21, Appli
C	72	10.4	52.0	21	10	US-09-809-333-75	Sequence 75, Appli
C	73	10.4	52.0	22	9	US-09-881-012-27	Sequence 27, Appli
C	74	10.4	52.0	22	9	US-10-156-610-2	Sequence 2, Appli
C	75	10.4	52.0	22	9	US-10-205-522-108	Sequence 108, App
C	76	10.4	52.0	22	9	US-10-057-833a-57	Sequence 57, Appli
C	77	10.4	52.0	24	9	US-09-940-185-103	Sequence 103, App
C	78	10.4	52.0	24	9	US-09-940-185-1485	Sequence 1485, Ap
C	79	10.4	52.0	24	10	US-09-809-333-74	Sequence 74, Appli
C	80	10.4	52.0	25	9	US-10-202-189-31	Sequence 31, Appli
C	81	10.4	52.0	25	9	US-09-258-113-28	Sequence 28, Appli
C	82	10.4	52.0	25	9	US-10-215-112-3137	Sequence 3137, Ap
C	83	10.4	52.0	25	9	US-10-215-112-8556	Sequence 8556, Ap
C	84	10.4	52.0	25	9	US-10-215-112-10887	Sequence 10887, A
C	85	10.4	52.0	25	9	US-09-940-185-4085	Sequence 4085, Ap
C	86	10.2	51.0	15	9	US-09-997-931-68	Sequence 68, Appli
C	87	10.2	51.0	17	9	US-09-780-533a-504	Sequence 504, App
C	88	10.2	51.0	17	9	US-09-877-478-1789	Sequence 1789, Ap
C	89	10.2	51.0	17	9	US-09-877-478-2454	Sequence 2454, Ap
C	90	10.2	51.0	17	9	US-09-930-423-286	Sequence 286, App
C	91	10.2	51.0	17	9	US-09-930-423-297	Sequence 297, App
C	92	10.2	51.0	18	9	US-10-191-022-13	Sequence 13, Appli

385	9.4	47.0	21	9	US-09-960-244A-7	Sequence 7, Appl	C 458	9.2	46.0	18	9	US-09-907-942-52	Sequence 52, Appl
386	9.4	47.0	21	9	US-09-965-940-14	Sequence 14, Appl	C 459	9.2	46.0	18	9	US-09-952-267-72	Sequence 72, Appl
387	9.4	47.0	21	9	US-10-119-136-62	Sequence 62, Appl	C 460	9.2	46.0	18	9	US-09-904-820-52	Sequence 52, Appl
388	9.4	47.0	21	10	US-09-925-081-88	Sequence 88, Appl	C 461	9.2	46.0	18	9	US-09-904-853-52	Sequence 52, Appl
389	9.4	47.0	21	10	US-09-921-992-66	Sequence 66, Appl	C 462	9.2	46.0	18	9	US-09-909-204-52	Sequence 52, Appl
390	9.4	47.0	21	12	US-10-014-269-50	Sequence 50, Appl	C 463	9.2	46.0	18	9	US-09-904-786-52	Sequence 52, Appl
391	9.4	47.0	22	9	US-09-992-665-87	Sequence 87, Appl	C 464	9.2	46.0	18	9	US-09-906-646-52	Sequence 52, Appl
392	9.4	47.0	22	10	US-09-986-676A-8	Sequence 8, Appl	C 465	9.2	46.0	18	9	US-09-906-700-52	Sequence 52, Appl
393	9.4	47.0	23	9	US-10-005-530-13	Sequence 13, Appl	C 466	9.2	46.0	18	9	US-09-902-900-52	Sequence 52, Appl
394	9.4	47.0	23	9	US-10-084-826-37	Sequence 37, Appl	C 467	9.2	46.0	18	9	US-09-903-742A-52	Sequence 52, Appl
395	9.4	47.0	23	10	US-09-944-508-37	Sequence 37, Appl	C 468	9.2	46.0	18	9	US-09-903-786-52	Sequence 52, Appl
396	9.4	47.0	23	10	US-09-975-579-9	Sequence 9, Appl	C 469	9.2	46.0	18	9	US-09-902-736-52	Sequence 52, Appl
397	9.4	47.0	23	12	US-10-075-579-9	Sequence 9, Appl	C 470	9.2	46.0	18	9	US-09-904-119-52	Sequence 52, Appl
398	9.4	47.0	24	7	US-08-979-847-18	Sequence 18, Appl	C 471	9.2	46.0	18	9	US-09-904-956-52	Sequence 52, Appl
399	9.4	47.0	24	7	US-08-979-847-18	Sequence 34, Appl	C 472	9.2	46.0	18	9	US-09-907-794-52	Sequence 52, Appl
400	9.4	47.0	24	9	US-09-818-991-34	Sequence 160, Appl	C 473	9.2	46.0	18	9	US-09-902-692-52	Sequence 52, Appl
401	9.4	47.0	24	9	US-10-201-386-25	Sequence 25, Appl	C 474	9.2	46.0	18	9	US-09-903-520-52	Sequence 52, Appl
402	9.4	47.0	24	9	US-09-911-904-10	Sequence 10, Appl	C 475	9.2	46.0	18	9	US-09-903-943-52	Sequence 52, Appl
403	9.4	47.0	24	9	US-09-940-185-242	Sequence 242, Appl	C 476	9.2	46.0	18	9	US-09-904-462-52	Sequence 52, Appl
404	9.4	47.0	24	9	US-09-940-185-1002	Sequence 1002, Ap	C 477	9.2	46.0	18	9	US-09-905-056-52	Sequence 52, Appl
405	9.4	47.0	24	9	US-09-940-185-2529	Sequence 2529, Ap	C 478	9.2	46.0	18	9	US-09-907-925-52	Sequence 52, Appl
406	9.4	47.0	24	10	US-09-822-250-37	Sequence 37, Appl	C 479	9.2	46.0	18	9	US-09-904-553-52	Sequence 52, Appl
407	9.4	47.0	24	10	US-09-778-546-7	Sequence 7, Appl	C 480	9.2	46.0	18	9	US-09-905-381-52	Sequence 52, Appl
408	9.4	47.0	25	9	US-10-037-558-12	Sequence 12, Appl	C 481	9.2	46.0	18	9	US-09-909-064-52	Sequence 52, Appl
409	9.4	47.0	25	9	US-09-745-317-46	Sequence 46, Appl	C 482	9.2	46.0	18	9	US-09-905-088-52	Sequence 52, Appl
410	9.4	47.0	25	9	US-10-108-211-4	Sequence 4, Appl	C 483	9.2	46.0	18	9	US-09-907-575-52	Sequence 52, Appl
411	9.4	47.0	25	9	US-09-754-853A-1037	Sequence 1037, Ap	C 484	9.2	46.0	18	9	US-09-902-759-52	Sequence 52, Appl
412	9.4	47.0	25	9	US-10-215-112-300	Sequence 300, App	C 485	9.2	46.0	18	9	US-09-905-075-52	Sequence 52, Appl
413	9.4	47.0	25	9	US-10-215-112-2011	Sequence 3011, Ap	C 486	9.2	46.0	18	9	US-09-902-634-52	Sequence 52, Appl
414	9.4	47.0	25	9	US-10-215-112-6097	Sequence 6097, Ap	C 487	9.2	46.0	18	9	US-09-902-713-52	Sequence 52, Appl
415	9.4	47.0	25	9	US-10-215-112-6959	Sequence 6959, Ap	C 488	9.2	46.0	18	9	US-09-907-979-52	Sequence 52, Appl
416	9.4	47.0	25	9	US-10-215-112-8682	Sequence 8682, Ap	C 489	9.2	46.0	18	9	US-09-902-615-52	Sequence 52, Appl
417	9.4	47.0	25	9	US-10-215-112-9627	Sequence 9627, Ap	C 490	9.2	46.0	18	9	US-09-902-625-52	Sequence 52, Appl
418	9.4	47.0	25	9	US-10-215-112-10409	Sequence 10409, A	C 491	9.2	46.0	18	9	US-09-906-760A-52	Sequence 52, Appl
419	9.4	47.0	25	9	US-10-215-112-12376	Sequence 12376, A	C 492	9.2	46.0	18	10	US-09-828-366-9	Sequence 9, Appl
420	9.4	47.0	25	9	US-09-992-665-357	Sequence 357, App	C 493	9.2	46.0	18	10	US-09-865-018-21	Sequence 21, Appl
421	9.4	47.0	25	9	US-09-940-185-4223	Sequence 4223, Ap	C 494	9.2	46.0	18	10	US-09-909-320-52	Sequence 52, Appl
422	9.4	47.0	25	9	US-09-940-185-4300	Sequence 4300, Ap	C 495	9.2	46.0	18	10	US-09-969-373-4389	Sequence 4389, Ap
423	9.4	47.0	25	9	US-09-940-185-4700	Sequence 4700, Ap	C 496	9.2	46.0	18	10	US-09-809-088B-52	Sequence 52, Appl
424	9.4	47.0	25	10	US-09-804-690-16	Sequence 16, Appl	C 497	9.2	46.0	19	10	US-09-844-493-18	Sequence 18, Appl
425	9.4	47.0	25	10	US-09-827-998-1014	Sequence 1014, Ap	C 498	9.2	46.0	19	10	US-09-844-501-18	Sequence 18, Appl
426	9.4	47.0	25	10	US-09-827-998-1015	Sequence 1015, Ap	C 499	9.2	46.0	19	10	US-09-844-501-18	Sequence 18, Appl
427	9.4	47.0	25	10	US-09-827-998-1016	Sequence 1016, Ap	C 500	9.2	46.0	20	8	US-08-424-550B-107	Sequence 107, App
428	9.4	47.0	25	10	US-09-827-998-1017	Sequence 1017, Ap	C 501	9.2	46.0	20	8	US-08-424-550B-162	Sequence 162, App
429	9.4	47.0	25	10	US-09-827-998-1018	Sequence 1018, Ap	C 502	9.2	46.0	20	9	US-10-125-751-4	Sequence 4, Appl
430	9.4	47.0	25	10	US-09-827-998-1019	Sequence 1019, Ap	C 503	9.2	46.0	20	9	US-10-125-751-4	Sequence 4, Appl
431	9.4	47.0	25	10	US-09-827-998-1020	Sequence 1020, Ap	C 504	9.2	46.0	20	9	US-10-085-108-17	Sequence 17, Appl
432	9.2	46.0	14	9	US-10-146-058-135	Sequence 135, App	C 505	9.2	46.0	20	9	US-09-912-552-4	Sequence 2, Appl
433	9.2	46.0	16	10	US-09-774-021-9	Sequence 9, Appl	C 506	9.2	46.0	20	9	US-09-355-405-2	Sequence 2, Appl
434	9.2	46.0	17	9	US-09-825-805-840	Sequence 840, App	C 507	9.2	46.0	20	9	US-09-881-012-29	Sequence 29, Appl
435	9.2	46.0	17	9	US-09-780-533A-1365	Sequence 1365, Ap	C 508	9.2	46.0	20	9	US-09-863-806-175	Sequence 175, Appl
436	9.2	46.0	17	9	US-09-877-478-1279	Sequence 1279, Ap	C 509	9.2	46.0	20	9	US-09-863-806-183	Sequence 183, App
437	9.2	46.0	17	9	US-09-877-478-1705	Sequence 1705, Ap	C 510	9.2	46.0	20	9	US-09-824-322B-145	Sequence 145, App
438	9.2	46.0	17	9	US-10-213-878-2	Sequence 2, Appl	C 511	9.2	46.0	20	9	US-09-824-322B-146	Sequence 146, App
439	9.2	46.0	17	9	US-10-214-059-2	Sequence 2, Appl	C 512	9.2	46.0	20	9	US-09-935-916A-11	Sequence 11, Appl
440	9.2	46.0	17	10	US-09-310-423-298	Sequence 298, App	C 513	9.2	46.0	20	9	US-09-935-916A-24	Sequence 24, Appl
441	9.2	46.0	17	10	US-09-866-108-9894	Sequence 9894, Ap	C 514	9.2	46.0	20	9	US-10-036-949-43	Sequence 43, Appl
442	9.2	46.0	17	10	US-09-866-108-9895	Sequence 9895, Ap	C 515	9.2	46.0	20	9	US-09-223-785-182	Sequence 182, App
443	9.2	46.0	17	10	US-09-866-108-9896	Sequence 9896, Ap	C 516	9.2	46.0	20	9	US-09-846-430A-3	Sequence 3, Appl
444	9.2	46.0	17	10	US-09-866-108-9897	Sequence 9897, Ap	C 517	9.2	46.0	20	9	US-10-143-122A-7	Sequence 7, Appl
445	9.2	46.0	17	10	US-09-866-108-9898	Sequence 9898, Ap	C 518	9.2	46.0	20	9	US-09-784-674-1039	Sequence 1039, Ap
446	9.2	46.0	18	9	US-09-905-291A-52	Sequence 20, Appl	C 519	9.2	46.0	20	9	US-09-784-674-1039	Sequence 113, App
447	9.2	46.0	18	9	US-09-529-759-7	Sequence 52, Appl	C 520	9.2	46.0	20	9	US-10-238-443-45	Sequence 45, Appl
448	9.2	46.0	18	9	US-09-529-759-11	Sequence 11, Appl	C 521	9.2	46.0	20	9	US-10-238-443-47	Sequence 47, Appl
449	9.2	46.0	18	9	US-09-502-853-52	Sequence 52, Appl	C 522	9.2	46.0	20	9	US-10-271-887-74	Sequence 74, Appl
450	9.2	46.0	18	9	US-09-507-824-52	Sequence 52, Appl	C 523	9.2	46.0	20	9	US-10-271-887-74	Sequence 68, Appl
451	9.2	46.0	18	9	US-09-907-841-52	Sequence 52, Appl	C 524	9.2	46.0	20	9	US-10-145-493B-8	Sequence 38, Appl
452	9.2	46.0	18	9	US-09-904-011-52	Sequence 52, Appl	C 525	9.2	46.0	20	10	US-09-752-983-167	Sequence 167, App
453	9.2	46.0	18	9	US-09-824-322B-164	Sequence 164, App	C 526	9.2	46.0	20	10	US-09-736-863-34	Sequence 34, Appl
454	9.2	46.0	18	9	US-09-824-322B-165	Sequence 165, App	C 527	9.2	46.0	20	10	US-09-179-536B-66	Sequence 66, Appl
455	9.2	46.0	18	9	US-09-906-742-52	Sequence 52, Appl	C 528	9.2	46.0	20	10	US-09-954-695-19	Sequence 19, Appl
456	9.2	46.0	18	9	US-09-906-838-52	Sequence 52, Appl	C 529	9.2	46.0	20	10	US-09-954-695-55	Sequence 55, Appl
457	9.2	46.0	18	9	US-09-907-613-52	Sequence 52, Appl	C 530	9.2	46.0	20	10	US-09-954-695-61	Sequence 61, Appl

C 531	9.2	46.0	20	10	US-09-954-695-67	Sequence 67, Appl	604	9.2	46.0	22	10	US-09-777-732-22	Sequence 26, Appl
C 532	9.2	46.0	20	10	US-09-817-913-23	Sequence 23, Appl	C 605	9.2	46.0	22	10	US-09-909-320-62	Sequence 62, Appl
C 533	9.2	46.0	20	10	US-09-918-029-18	Sequence 4, Appl	C 606	9.2	46.0	22	10	US-09-909-088B-62	Sequence 62, Appl
C 534	9.2	46.0	20	10	US-09-927-668-14	Sequence 16, Appl	C 607	9.2	46.0	23	9	US-09-853-526-172	Sequence 172, Appl
C 535	9.2	46.0	20	10	US-09-900-062-30	Sequence 30, Appl	C 608	9.2	46.0	23	9	US-09-770-107-111	Sequence 111, Appl
C 536	9.2	46.0	20	10	US-09-817-538-23	Sequence 23, Appl	C 609	9.2	46.0	23	9	US-09-964-895-25	Sequence 25, Appl
C 537	9.2	46.0	20	10	US-09-954-586-49	Sequence 49, Appl	C 610	9.2	46.0	23	10	US-09-851-859A-29	Sequence 29, Appl
C 538	9.2	46.0	20	10	US-09-954-586-55	Sequence 55, Appl	C 611	9.2	46.0	23	10	US-09-908-500A-35	Sequence 35, Appl
C 539	9.2	46.0	20	10	US-09-954-586-61	Sequence 61, Appl	C 612	9.2	46.0	23	10	US-09-901-484A-172	Sequence 172, Appl
C 540	9.2	46.0	20	10	US-09-954-586-67	Sequence 67, Appl	C 613	9.2	46.0	23	10	US-09-728-574-3	Sequence 3, Appl
C 541	9.2	46.0	20	10	US-09-954-586-67	Sequence 1053, Ap	C 614	9.2	46.0	23	12	US-10-068-067-1	Sequence 1, Appl
C 542	9.2	46.0	20	12	US-10-038-271-4	Sequence 4, Appl	C 615	9.2	46.0	24	9	US-09-784-674-1	Sequence 1, Appl
C 543	9.2	46.0	21	10	US-10-600-639-14	Sequence 14, Appl	C 616	9.2	46.0	24	9	US-09-940-185-514	Sequence 514, App
C 544	9.2	46.0	21	10	US-09-759-584-53	Sequence 53, Appl	C 617	9.2	46.0	24	9	US-09-940-185-654	Sequence 654, App
C 545	9.2	46.0	21	10	US-09-179-538B-32	Sequence 32, Appl	C 618	9.2	46.0	24	9	US-09-940-185-807	Sequence 807, App
C 546	9.2	46.0	21	10	US-09-726-774-32	Sequence 72, Appl	C 619	9.2	46.0	24	9	US-09-940-185-877	Sequence 877, App
C 547	9.2	46.0	21	10	US-09-848-585-42	Sequence 42, Appl	C 620	9.2	46.0	24	9	US-09-940-185-877	Sequence 1078, App
C 548	9.2	46.0	21	10	US-09-263-959-1165	Sequence 1165, Ap	C 621	9.2	46.0	24	9	US-09-940-185-2109	Sequence 2109, App
C 549	9.2	46.0	22	9	US-09-924-647-4	Sequence 4, Appl	C 622	9.2	46.0	24	9	US-09-940-185-2917	Sequence 2917, App
C 550	9.2	46.0	22	9	US-09-905-291A-62	Sequence 62, Appl	C 623	9.2	46.0	24	9	US-09-940-185-3016	Sequence 3016, App
C 551	9.2	46.0	22	9	US-10-136-517-15	Sequence 15, Appl	C 624	9.2	46.0	24	9	US-09-940-185-3066	Sequence 3066, App
C 552	9.2	46.0	22	9	US-10-066-500-89	Sequence 89, Appl	C 625	9.2	46.0	24	9	US-09-940-185-3409	Sequence 3409, App
C 553	9.2	46.0	22	9	US-09-881-012-22	Sequence 22, Appl	C 626	9.2	46.0	24	9	US-09-940-185-3600	Sequence 3600, App
C 554	9.2	46.0	22	9	US-09-902-853-62	Sequence 62, Appl	C 627	9.2	46.0	24	9	US-10-167-127-25	Sequence 25, Appl
C 555	9.2	46.0	22	9	US-09-907-824-62	Sequence 62, Appl	C 628	9.2	46.0	24	9	US-09-733-151-6	Sequence 6, Appl
C 556	9.2	46.0	22	9	US-09-907-841-62	Sequence 62, Appl	C 629	9.2	46.0	24	10	US-09-758-575-4	Sequence 4, Appl
C 557	9.2	46.0	22	9	US-09-904-011-62	Sequence 62, Appl	C 630	9.2	46.0	24	10	US-09-758-575-4	Sequence 588, App
C 558	9.2	46.0	22	9	US-09-906-742-62	Sequence 62, Appl	C 631	9.2	46.0	25	9	US-09-938-689-1	Sequence 1, Appl
C 559	9.2	46.0	22	9	US-09-906-838-62	Sequence 62, Appl	C 632	9.2	46.0	25	9	US-10-071-370A-12	Sequence 12, Appl
C 560	9.2	46.0	22	9	US-09-907-613-62	Sequence 62, Appl	C 633	9.2	46.0	25	9	US-10-215-112-3046	Sequence 3046, Appl
C 561	9.2	46.0	22	9	US-09-907-642-62	Sequence 62, Appl	C 634	9.2	46.0	25	9	US-10-215-112-4300	Sequence 4300, App
C 562	9.2	46.0	22	9	US-10-002-796-89	Sequence 89, Appl	C 635	9.2	46.0	25	9	US-10-215-112-4594	Sequence 4594, App
C 563	9.2	46.0	22	9	US-10-066-773-89	Sequence 89, Appl	C 636	9.2	46.0	25	9	US-10-215-112-6705	Sequence 6705, App
C 564	9.2	46.0	22	9	US-10-066-773-89	Sequence 89, Appl	C 637	9.2	46.0	25	9	US-10-215-112-6705	Sequence 6831, App
C 565	9.2	46.0	22	9	US-09-904-820-62	Sequence 62, Appl	C 638	9.2	46.0	25	9	US-10-215-112-6835	Sequence 6835, App
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C 567	9.2	46.0	22	9	US-09-909-204-62	Sequence 62, Appl	C 640	9.2	46.0	25	9	US-10-215-112-7502	Sequence 7502, App
C 568	9.2	46.0	22	9	US-09-904-786-62	Sequence 62, Appl	C 641	9.2	46.0	25	9	US-10-215-112-8231	Sequence 8231, App
C 569	9.2	46.0	22	9	US-09-906-646-62	Sequence 62, Appl	C 642	9.2	46.0	25	9	US-10-215-112-8231	Sequence 8231, App
C 570	9.2	46.0	22	9	US-09-906-700-62	Sequence 62, Appl	C 643	9.2	46.0	25	9	US-10-215-112-9112	Sequence 9113, App
C 571	9.2	46.0	22	9	US-10-066-269-89	Sequence 89, Appl	C 644	9.2	46.0	25	9	US-10-215-112-10383	Sequence 10383, A
C 572	9.2	46.0	22	9	US-09-836-439-6	Sequence 6, Appl	C 645	9.2	46.0	25	9	US-10-215-112-10558	Sequence 10558, A
C 573	9.2	46.0	22	9	US-09-902-903-62	Sequence 62, Appl	C 646	9.2	46.0	25	9	US-10-215-112-10888	Sequence 10888, A
C 574	9.2	46.0	22	9	US-09-903-749A-62	Sequence 62, Appl	C 647	9.2	46.0	25	9	US-10-215-112-10963	Sequence 10963, A
C 575	9.2	46.0	22	9	US-09-903-786-62	Sequence 62, Appl	C 648	9.2	46.0	25	9	US-10-215-112-11524	Sequence 11532, A
C 576	9.2	46.0	22	9	US-09-903-786-62	Sequence 89, Appl	C 649	9.2	46.0	25	9	US-10-215-112-12332	Sequence 12365, A
C 577	9.2	46.0	22	9	US-10-066-211-89	Sequence 89, Appl	C 650	9.2	46.0	25	9	US-10-215-112-13265	Sequence 14049, A
C 578	9.2	46.0	22	9	US-09-902-736-62	Sequence 62, Appl	C 651	9.2	46.0	25	9	US-10-215-112-14049	Sequence 14567, A
C 579	9.2	46.0	22	9	US-09-904-119-62	Sequence 62, Appl	C 652	9.2	46.0	25	9	US-10-215-112-14567	Sequence 14567, A
C 580	9.2	46.0	22	9	US-09-904-956-62	Sequence 62, Appl	C 653	9.2	46.0	25	9	US-09-940-185-4484	Sequence 4486, App
C 581	9.2	46.0	22	9	US-09-907-794-62	Sequence 62, Appl	C 654	9.2	46.0	25	10	US-09-866-108-14786	Sequence 14787, A
C 582	9.2	46.0	22	9	US-09-902-692-62	Sequence 62, Appl	C 655	9.2	46.0	25	10	US-09-866-108-14787	Sequence 14788, A
C 583	9.2	46.0	22	9	US-09-903-520-62	Sequence 62, Appl	C 656	9.2	46.0	25	10	US-09-866-108-14788	Sequence 14789, A
C 584	9.2	46.0	22	9	US-09-903-442-62	Sequence 62, Appl	C 657	9.2	46.0	25	10	US-09-866-108-14789	Sequence 14790, A
C 585	9.2	46.0	22	9	US-09-904-462-62	Sequence 62, Appl	C 658	9.2	46.0	25	10	US-09-866-108-14790	Sequence 14791, A
C 586	9.2	46.0	22	9	US-09-905-056-62	Sequence 62, Appl	C 659	9.2	46.0	25	10	US-09-866-108-14791	Sequence 14792, A
C 587	9.2	46.0	22	9	US-09-907-925-62	Sequence 62, Appl	C 660	9.2	46.0	25	10	US-09-866-108-14792	Sequence 14793, A
C 588	9.2	46.0	22	9	US-09-904-553-62	Sequence 62, Appl	C 661	9.2	46.0	25	10	US-09-866-108-14794	Sequence 14795, A
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C 590	9.2	46.0	22	9	US-09-909-064-62	Sequence 62, Appl	C 663	9.2	46.0	25	10	US-09-866-108-14796	Sequence 14797, A
C 591	9.2	46.0	22	9	US-09-905-088-62	Sequence 62, Appl	C 664	9.2	46.0	25	10	US-09-866-108-14797	Sequence 14798, A
C 592	9.2	46.0	22	9	US-09-907-775-62	Sequence 62, Appl	C 665	9.2	46.0	25	10	US-09-866-108-14798	Sequence 14799, A
C 593	9.2	46.0	22	9	US-09-902-759-62	Sequence 62, Appl	C 666	9.2	46.0	25	10	US-09-866-108-14799	Sequence 14800, A
C 594	9.2	46.0	22	9	US-09-905-075-62	Sequence 62, Appl	C 667	9.2	46.0	25	12	US-10-076-900-5	Sequence 5, Appl
C 595	9.2	46.0	22	9	US-09-902-634-62	Sequence 62, Appl	C 668	9.2	46.0	10	12	US-10-033-145-141	Sequence 14, Appl
C 596	9.2	46.0	22	9	US-09-902-713-62	Sequence 62, Appl	C 669	9.2	46.0	12	9	US-10-117-108A-23	Sequence 23, Appl
C 597	9.2	46.0	22	9	US-09-907-979-62	Sequence 62, Appl	C 670	9.2	46.0	15	9	US-09-848-754A-9294	Sequence 9294, App
C 598	9.2	46.0	22	9	US-09-902-615-62	Sequence 62, Appl	C 671	9.2	46.0	15	10	US-09-504-231A-873	Sequence 873, App
C 599	9.2	46.0	22	9	US-09-903-925-62	Sequence 62, Appl	C 672	9.2	46.0	15	10	US-09-274-553D-873	Sequence 873, App
C 600	9.2	46.0	22	9	US-09-906-760A-62	Sequence 62, Appl	C 673	9.2	46.0	17	9	US-09-864-785-414	Sequence 414, App
C 601	9.2	46.0	22	10	US-09-426-548-132	Sequence 132, App	C 674	9.2	46.0	17	9	US-10-023-407-5	Sequence 517, App
C 602	9.2	46.0	22	10	US-09-284-663A-18	Sequence 18, Appl	C 675	9.2	46.0	17	9	US-09-825-835-517	Sequence 517, App
C 603	9.2	46.0	22	10	US-09-767-609-4	Sequence 4, Appl	C 676	9.2	46.0	17	9	US-09-780-533A-1130	Sequence 1130, App

C 823	9	45.0	24	9	US-09-978-1192A-116	Sequence 116, App	C 896	9	45.0	25	9	US-09-997-601-237	Sequence 237, App
C 824	9	45.0	24	9	US-09-999-832A-116	Sequence 116, App	C 897	9	45.0	25	9	US-09-989-729A-237	Sequence 237, App
C 825	9	45.0	24	9	US-09-738-62E-7046	Sequence 7046, App	C 898	9	45.0	25	9	US-09-990-440-237	Sequence 237, App
C 826	9	45.0	24	9	US-09-978-189-116	Sequence 116, App	C 899	9	45.0	25	9	US-09-991-854-237	Sequence 237, App
C 827	9	45.0	24	9	US-09-977-418-58	Sequence 58, App1	C 900	9	45.0	25	9	US-09-997-348-237	Sequence 237, App
C 828	9	45.0	24	9	US-09-978-608A-116	Sequence 116, App	C 901	9	45.0	25	9	US-09-997-440-237	Sequence 237, App
C 829	9	45.0	24	9	US-09-978-191A-116	Sequence 116, App	C 902	9	45.0	25	9	US-09-997-628-237	Sequence 237, App
C 830	9	45.0	24	9	US-09-978-403A-116	Sequence 116, App	C 903	9	45.0	25	9	US-09-997-683-237	Sequence 237, App
C 831	9	45.0	24	9	US-09-978-564A-116	Sequence 116, App	C 904	9	45.0	25	9	US-09-993-469-237	Sequence 237, App
C 832	9	45.0	24	9	US-09-978-585A-116	Sequence 116, App	C 905	9	45.0	25	9	US-09-993-748-237	Sequence 237, App
C 833	9	45.0	24	9	US-10-017-081A-116	Sequence 116, App	C 906	9	45.0	25	9	US-09-997-542-237	Sequence 237, App
C 834	9	45.0	24	9	US-09-978-824-116	Sequence 116, App	C 907	9	45.0	25	9	US-09-990-427-237	Sequence 237, App
C 835	9	45.0	24	9	US-09-981-915A-116	Sequence 116, App	C 908	9	45.0	25	9	US-09-990-439-237	Sequence 237, App
C 836	9	45.0	24	9	US-09-989-833A-116	Sequence 116, App	C 909	9	45.0	25	9	US-09-989-328-237	Sequence 237, App
C 837	9	45.0	24	9	US-10-047-403-30	Sequence 30, App1	C 910	9	45.0	25	9	US-09-993-583-237	Sequence 237, App
C 838	9	45.0	24	9	US-10-167-749-116	Sequence 116, App	C 911	9	45.0	25	9	US-09-941-992-237	Sequence 237, App
C 839	9	45.0	24	9	US-09-918-585A-116	Sequence 116, App	C 912	9	45.0	25	9	US-09-992-521-237	Sequence 237, App
C 840	9	45.0	24	9	US-09-978-423A-116	Sequence 116, App	C 913	9	45.0	25	9	US-10-215-112-1694	Sequence 1694, App
C 841	9	45.0	24	9	US-10-013-923A-116	Sequence 116, App	C 914	9	45.0	25	9	US-10-215-112-1830	Sequence 1830, App
C 842	9	45.0	24	9	US-09-878-193A-116	Sequence 116, App	C 915	9	45.0	25	9	US-10-215-112-12871	Sequence 12871, App
C 843	9	45.0	24	9	US-10-013-923A-116	Sequence 116, App	C 916	9	45.0	25	9	US-10-215-112-3827	Sequence 3827, App
C 844	9	45.0	24	9	US-10-016-177A-116	Sequence 116, App	C 917	9	45.0	25	9	US-10-215-112-3827	Sequence 3827, App
C 845	9	45.0	24	9	US-09-999-830A-116	Sequence 116, App	C 918	9	45.0	25	9	US-10-215-112-5055	Sequence 5055, App
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C 847	9	45.0	24	9	US-09-978-757A-116	Sequence 116, App	C 920	9	45.0	25	9	US-10-215-112-7883	Sequence 7883, App
C 848	9	45.0	24	9	US-09-940-185-55	Sequence 55, App1	C 921	9	45.0	25	9	US-10-215-112-7925	Sequence 7925, App
C 849	9	45.0	24	9	US-09-940-185-144	Sequence 144, App	C 922	9	45.0	25	9	US-10-215-112-8511	Sequence 8511, App
C 850	9	45.0	24	9	US-09-940-185-322	Sequence 322, App	C 923	9	45.0	25	9	US-10-215-112-8637	Sequence 8637, App
C 851	9	45.0	24	9	US-09-940-185-324	Sequence 324, App	C 924	9	45.0	25	9	US-10-215-112-9183	Sequence 9183, App
C 852	9	45.0	24	9	US-09-940-185-684	Sequence 684, App	C 925	9	45.0	25	9	US-10-215-112-11025	Sequence 11025, App
C 853	9	45.0	24	9	US-09-940-185-1089	Sequence 1089, App	C 926	9	45.0	25	9	US-10-215-112-11676	Sequence 11676, App
C 854	9	45.0	24	9	US-09-940-185-2768	Sequence 2768, App	C 927	9	45.0	25	9	US-10-215-112-11886	Sequence 11886, App
C 855	9	45.0	24	9	US-09-940-185-3433	Sequence 3433, App	C 928	9	45.0	25	9	US-09-997-333-237	Sequence 237, App
C 856	9	45.0	24	9	US-09-940-185-3539	Sequence 3539, App	C 929	9	45.0	25	9	US-09-997-384-237	Sequence 237, App
C 857	9	45.0	24	9	US-09-940-185-3641	Sequence 3641, App	C 930	9	45.0	25	9	US-09-992-665-243	Sequence 243, App
C 858	9	45.0	24	9	US-09-878-187B-116	Sequence 116, App	C 931	9	45.0	25	9	US-09-940-185-4325	Sequence 4325, App
C 859	9	45.0	24	10	US-09-216-393-360	Sequence 360, App	C 932	9	45.0	25	9	US-09-940-185-4326	Sequence 4326, App
C 860	9	45.0	24	10	US-09-102-831-11	Sequence 11, App1	C 933	9	45.0	25	9	US-09-307-331A-14	Sequence 14, App1
C 861	9	45.0	24	10	US-09-931-700-12	Sequence 12, App1	C 934	9	45.0	25	10	US-09-866-108-11696	Sequence 11696, App
C 862	9	45.0	24	10	US-09-896-096A-14	Sequence 14, App1	C 935	9	45.0	25	10	US-09-866-108-11697	Sequence 11697, App
C 863	9	45.0	24	10	US-09-894-924-14	Sequence 14, App1	C 936	9	45.0	25	10	US-09-866-108-11698	Sequence 11698, App
C 864	9	45.0	25	9	US-09-992-598-237	Sequence 237, App1	C 937	9	45.0	25	10	US-09-866-108-11699	Sequence 11699, App
C 865	9	45.0	25	9	US-10-005-057A-25	Sequence 25, App1	C 938	9	45.0	25	10	US-09-866-108-11699	Sequence 11699, App
C 866	9	45.0	25	9	US-09-989-293A-237	Sequence 237, App	C 939	9	45.0	25	10	US-09-866-108-11700	Sequence 11700, App
C 867	9	45.0	25	9	US-09-989-733-237	Sequence 237, App	C 940	9	45.0	25	10	US-09-866-108-11701	Sequence 11701, App
C 868	9	45.0	25	9	US-09-989-733-237	Sequence 237, App	C 941	9	45.0	25	10	US-09-866-108-11702	Sequence 11702, App
C 869	9	45.0	25	9	US-09-990-444-237	Sequence 237, App	C 942	9	45.0	25	10	US-09-866-108-11703	Sequence 11703, App
C 870	9	45.0	25	9	US-09-989-730-237	Sequence 237, App	C 943	9	45.0	25	10	US-09-866-108-11704	Sequence 11704, App
C 871	9	45.0	25	9	US-09-990-436-237	Sequence 237, App	C 944	9	45.0	25	10	US-09-866-108-11398	Sequence 11398, App
C 872	9	45.0	25	9	US-09-991-181-237	Sequence 237, App	C 945	9	45.0	25	10	US-09-866-108-11399	Sequence 11399, App
C 873	9	45.0	25	9	US-09-993-687-237	Sequence 237, App	C 946	9	45.0	25	10	US-09-866-108-11399	Sequence 11399, App
C 874	9	45.0	25	9	US-09-993-687-237	Sequence 237, App	C 947	9	45.0	25	10	US-09-866-108-11399	Sequence 11399, App
C 875	9	45.0	25	9	US-09-754-853A-687	Sequence 687, App	C 948	9	45.0	25	10	US-09-866-108-11399	Sequence 11399, App
C 876	9	45.0	25	9	US-09-754-853A-720	Sequence 720, App	C 949	9	45.0	25	10	US-09-866-108-11399	Sequence 11399, App
C 877	9	45.0	25	9	US-09-754-853A-824	Sequence 824, App	C 950	9	45.0	25	10	US-09-866-108-11399	Sequence 11399, App
C 878	9	45.0	25	9	US-09-989-734-237	Sequence 237, App	C 951	9	45.0	25	10	US-09-866-108-11399	Sequence 11399, App
C 879	9	45.0	25	9	US-09-997-653-237	Sequence 237, App	C 952	9	45.0	25	10	US-09-866-108-11397	Sequence 11397, App
C 880	9	45.0	25	9	US-09-993-667-237	Sequence 237, App	C 953	9	45.0	25	10	US-09-866-108-11397	Sequence 11397, App
C 881	9	45.0	25	9	US-09-990-438-237	Sequence 237, App	C 954	9	45.0	25	10	US-09-866-108-11812	Sequence 11812, App
C 882	9	45.0	25	9	US-09-990-562-237	Sequence 237, App	C 955	9	45.0	25	10	US-09-866-108-11812	Sequence 11812, App
C 883	9	45.0	25	9	US-09-997-428-237	Sequence 237, App	C 956	9	45.0	25	10	US-09-866-108-11814	Sequence 11814, App
C 884	9	45.0	25	9	US-09-997-666-237	Sequence 237, App	C 957	9	45.0	25	10	US-09-866-108-11815	Sequence 11815, App
C 885	9	45.0	25	9	US-09-990-711-237	Sequence 237, App	C 958	9	45.0	25	10	US-09-866-108-11816	Sequence 11816, App
C 886	9	45.0	25	9	US-09-989-726-237	Sequence 237, App	C 959	9	45.0	25	10	US-09-866-108-11817	Sequence 11817, App
C 887	9	45.0	25	9	US-09-990-437-237	Sequence 237, App	C 960	9	45.0	25	10	US-09-866-108-11818	Sequence 11818, App
C 888	9	45.0	25	9	US-09-998-156-237	Sequence 237, App	C 961	9	45.0	25	10	US-09-866-108-11819	Sequence 11819, App
C 889	9	45.0	25	9	US-10-071-370A-112	Sequence 12, App1	C 962	9	45.0	25	10	US-09-866-108-11820	Sequence 11820, App
C 890	9	45.0	25	9	US-09-991-157-237	Sequence 237, App	C 963	9	45.0	25	10	US-09-989-723-237	Sequence 237, App
C 891	9	45.0	25	9	US-09-991-172-237	Sequence 237, App	C 964	9	45.0	25	10	US-09-989-723-237	Sequence 237, App
C 892	9	45.0	25	9	US-09-997-514-237	Sequence 237, App	C 965	9	45.0	25	10	US-09-989-727-237	Sequence 237, App
C 893	9	45.0	25	9	US-09-997-573-237	Sequence 237, App	C 966	9	45.0	25	10	US-09-915-593-15	Sequence 15, App1
C 894	9	45.0	25	9	US-09-990-443-237	Sequence 237, App	C 967	9	45.0	25	10	US-09-827-996-1573	Sequence 1573, App
C 895	9	45.0	25	9	US-09-990-726-237	Sequence 237, App	C 968	9	45.0	25	10	US-09-827-998-1574	Sequence 1574, App

969 9 45.0 25 10 US-09-827-998-1575 Sequence 1575, Ap
970 9 45.0 25 10 US-09-827-998-1576 Sequence 1576, Ap
971 9 45.0 25 10 US-09-827-998-1577 Sequence 1577, Ap
972 9 45.0 25 10 US-09-827-998-1578 Sequence 1578, Ap
973 9 45.0 25 10 US-09-827-998-1579 Sequence 1579, Ap
974 9 45.0 25 10 US-09-827-998-1580 Sequence 1580, Ap
975 9 45.0 25 10 US-09-827-998-1581 Sequence 1581, Ap
976 9 45.0 25 10 US-09-827-998-1582 Sequence 1582, Ap
977 9 45.0 25 10 US-09-827-998-1583 Sequence 1583, Ap
978 9 45.0 25 10 US-09-827-998-1584 Sequence 1584, Ap
979 9 45.0 25 10 US-09-827-998-1585 Sequence 1585, Ap
980 9 45.0 25 10 US-09-827-998-1586 Sequence 1586, Ap
981 9 45.0 25 10 US-09-827-998-1587 Sequence 1587, Ap
982 9 45.0 25 10 US-09-827-998-1588 Sequence 1588, Ap
983 9 45.0 25 10 US-09-827-998-1589 Sequence 1589, Ap
984 9 45.0 25 10 US-09-827-998-1590 Sequence 1590, Ap
985 9 45.0 25 10 US-09-827-998-1591 Sequence 1591, Ap
986 9 45.0 25 10 US-09-827-998-1592 Sequence 1592, Ap
987 9 45.0 25 10 US-09-827-998-1593 Sequence 1593, Ap
988 9 45.0 25 10 US-09-827-998-1594 Sequence 1594, Ap
989 9 45.0 25 10 US-09-827-998-1595 Sequence 1595, Ap
990 9 45.0 25 10 US-09-827-998-1596 Sequence 1596, Ap
991 9 45.0 25 10 US-09-827-998-1597 Sequence 1597, Ap
992 9 45.0 25 10 US-09-827-998-1598 Sequence 1598, Ap
993 9 45.0 25 10 US-09-827-998-1599 Sequence 1599, Ap
994 9 45.0 25 10 US-09-827-998-1600 Sequence 1600, Ap
995 9 45.0 25 10 US-09-827-998-1601 Sequence 1601, Ap
996 9 45.0 25 10 US-09-827-998-1602 Sequence 1602, Ap
997 9 45.0 25 10 US-09-827-998-1603 Sequence 1603, Ap
998 9 45.0 25 10 US-09-827-998-1604 Sequence 1604, Ap
999 9 45.0 25 10 US-09-827-998-1605 Sequence 1605, Ap
1000 9 45.0 25 10 US-09-827-998-1606 Sequence 1606, Ap

ALIGNMENTS

RESULT 1
US-10-080-959A-2
Sequence 2, Application US/10080959A
Publication No. US20030054369A1
GENERAL INFORMATION:
APPLICANT: Cruz-Perez, Patricia
APPLICANT: Buttner, Mark P.
TITLE OF INVENTION: Method for Detection of Stachybotrys chartarum in Pure Culture an
FILE REFERENCE: 0001-00001
CURRENT APPLICATION NUMBER: US/10/080,959A
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: US 60/280,712
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 2
LENGTH: 20
TYPE: DNA
ORGANISM: Stachybotrys chartarum
FEATURE:
NAME/KEY:
LOCATION:
OTHER INFORMATION:
US-10-080-959A-2

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.29; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCGTTGGCCACTCAGAG 20
DB 1 TTTCGTTGGCCACTCAGAG 20

RESULT 2
US-10-080-959A-4

Sequence 4, Application US/10080959A
Publication No. US20030054369A1
GENERAL INFORMATION:
APPLICANT: Cruz-Perez, Patricia
APPLICANT: Buttner, Mark P.
TITLE OF INVENTION: Method for Detection of Stachybotrys chartarum in Pure Culture an
FILE REFERENCE: 0001-00001
CURRENT APPLICATION NUMBER: US/10/080,959A
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: US 60/280,712
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 4
LENGTH: 23
TYPE: DNA
ORGANISM: Stachybotrys chartarum
FEATURE:
NAME/KEY:
LOCATION:
OTHER INFORMATION:
US-10-080-959A-4

Query Match 85.0%; Score 17; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCGTTGGCCACTCAGAG 20
DB 1 GCGTTGGCCACTCAGAG 17

RESULT 3
US-09-877-478-25/c
Sequence 25, Application US/09877478
Publication No. US20030068301A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: Blact, Larry
APPLICANT: McSwigen, Jim
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: MBH00-845-H (400/029)
CURRENT APPLICATION NUMBER: US/09/877,478
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 08/433,993
PRIOR FILING DATE: 1995-05-04
PRIOR APPLICATION NUMBER: US 08/434,504
PRIOR FILING DATE: 1995-05-04
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6586
SOFTWARE: PatentIn version 3.0
SEQ ID NO 25
LENGTH: 17
TYPE: RNA
ORGANISM: Hepatitis B virus
US-09-877-478-25

Query Match 67.0%; Score 13.4; DB 9; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCCTTGCCACTCAG 18
DB 15 GAGTTGCCACTCAG 1

RESULT 4

US-09-972-467-10/c
Sequence 10, Application US/09972467
Patent No. US20020090373A1
GENERAL INFORMATION:
APPLICANT: PFIZER INC.
TITLE OF INVENTION: ADAMTS POLYPEPTIDES, NUCLEIC ACIDS ENCODING THEM, AND
FILE REFERENCE: PC10850A
CURRENT APPLICATION NUMBER: US/09/972,467
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 23
SEQ ID NO 10
TYPE: DNA
ORGANISM: Human
US-09-972-467-10

Query Match 66.0%; Score 13.2; DB 10; Length 23;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGGCTTGCCACTCAG 20
DB 19 TGGCTTGCCACTCAGTG 2

RESULT 5

US-09-780-533A-2611
Sequence 2611, Application US/09780533A
Publication No. US20030060611A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Chowrira, Bharat
APPLICANT: Heberli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NCO Gene
FILE REFERENCE: MHB00.878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2611
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-780-533A-2611

Query Match 61.0%; Score 12.2; DB 9; Length 17;
Best Local Similarity 52.9%; Pred. No. 4.1e+03;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTGGCTTGCCACTCA 17
DB 1 UCUGCUUGGCCACUCA 17

RESULT 6

US-09-819-097-24/c
Sequence 24, Application US/09819097
Patent No. US20020106347A1
GENERAL INFORMATION:
APPLICANT: Douglae, Andrea M.

APPLICANT: Beqley, Colin G.
TITLE OF INVENTION: CYTOKINES AND THEIR USE IN TREATMENT AND/OR PROPHYLAXIS
FILE REFERENCE: 113752
CURRENT APPLICATION NUMBER: US/09/819,097
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 09/051,939
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: IL-3R (OTHER INFORMATION: oligonucleotide probe
US-09-819-097-24

Query Match 61.0%; Score 12.2; DB 10; Length 25;
Best Local Similarity 83.4%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGGCTTGCCACTCAGA 19
DB 20 TGGCTTGCCACTCGGA 4

RESULT 7

US-09-821-821-22/c
Sequence 22, Application US/09821821
Patent No. US20020064823A1
GENERAL INFORMATION:
APPLICANT: Welcher, Andrew A.
APPLICANT: Calzone, Frank J.
TITLE OF INVENTION: CD20/19E-Receptor Like Molecules and Uses Thereof
FILE REFERENCE: 01017/36938A
CURRENT APPLICATION NUMBER: US/09/821,821
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: US 09/723,258
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: US 60/193,728
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: Primer 2323-70
US-09-821-821-22

Query Match 60.0%; Score 12; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGGCACTCAGAG 20
DB 23 TGGCACTCAGAG 12

RESULT 8

US-09-780-533A-2000
Sequence 2000, Application US/09780533A
Publication No. US20030060611A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Chowrira, Bharat
APPLICANT: Heberli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NCO Gene

```
FILE REFERENCE: MEHBO0,878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 66/9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2000
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-780-533A-2000

Query Match
Best Local Similarity 59.0%; Score 11.8; DB 9; Length 17;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGCCTTGGCCACTCA 17
Db 2 UGCUUGGCCACUCA 16

RESULT 9
US-09-996-956-14
Sequence 14, Application US/09996956
Patent No. US20020155463A1
GENERAL INFORMATION:
APPLICANT: Origene Technologies, Inc
TITLE OF INVENTION: Prostate Polynucleotides and Uses
FILE REFERENCE: 9U 301 R1
CURRENT APPLICATION NUMBER: US/09/996,956
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/250,354
PRIOR FILING DATE: 2001-12-01
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 22
TYPE: DNA
ORGANISM: Homo sapiens
US-09-996-956-14

Query Match
Best Local Similarity 59.0%; Score 11.8; DB 9; Length 22;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGCCTTGGCCACTCA 17
Db 5 TGCCTTGGCCACTCA 19

RESULT 10
US-09-368-834-3
Sequence 3, Application US/09368834
Patent No. US20020068317A1
GENERAL INFORMATION:
APPLICANT: Mundschien, David
Smith, Leonard
TITLE OF INVENTION: Polypeptide Compositions and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Fredrikson & Byron, P.A.
STREET: 900 Second Avenue South
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402-3397
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows-95
SOFTWARE: ASCII files
CURRENT APPLICATION DATA:
```

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APPLICATION NUMBER: US/09/368,834
FILING DATE: 05-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/908,212
FILING DATE: 07 August 1997
APPLICATION NUMBER: 08/644,399
FILING DATE: 10 May 1996
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Philip M.
REGISTRATION NUMBER: 31,162
REFERENCE/DOCKET NUMBER: 15050.1,2,2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 347-7088
TELEFAX: (612) 347-7077
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-368-834-3

Query Match
Best Local Similarity 58.0%; Score 11.6; DB 10; Length 21;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTCCTTGGCCACTCAG 18
Db 2 TTTCCTTGGCCACTCAG 19

RESULT 11
US-09-940-185-2248/c
Sequence 2248, Application US/09940185
Publication No. US20030096239A1
GENERAL INFORMATION:
APPLICANT: Gunderson, Kevin
Chee, Mark
TITLE OF INVENTION: Probes and Decoder Oligonucleotides
FILE REFERENCE: A-69605-1
CURRENT APPLICATION NUMBER: US/09/940,185
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: US 60/227,948
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/228,854
PRIOR FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 4768
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2248
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-2248

Query Match
Best Local Similarity 58.0%; Score 11.6; DB 9; Length 24;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTCCTTGGCCACTCAG 18
Db 18 TTTCCTTGGCCACTCAG 1

RESULT 12
US-08-844-215-30
Sequence 30, Application US/08844215
Patent No. US20020016445A1
GENERAL INFORMATION:
APPLICANT: PERSSON, MATS AXEL
```

APPLICANT: ALLANDER, TOBIAS ERIK
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,215
FILING DATE: 17-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/635,109
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 80146.002
TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7823
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-844-215-30

Query Match 57.0%; Score 11.4; DB 8; Length 24;
Best Local Similarity 92.3%; Pred. No. 1.1e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGCGTTGCCA 13
DB 10 TTAGCGTTGCCA 22

RESULT 13
US-09-913-238-53
Sequence 53, Application US/09913238
Publication No. US20030049251A1
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
APPLICANT: Steinberger, Peter
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR
TITLE OF INVENTION: INHIBITING CCR5-DEPENDENT INFECTION OF CELLS BY HIV-1
FILE REFERENCE: TSRI 728.1
CURRENT APPLICATION NUMBER: US/09/913,238
CURRENT FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: PCT/EPO 0/12419
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: US 60/169,653
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 53
LENGTH: 24
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Synthesized
US-09-913-238-53

Query Match 57.0%; Score 11.4; DB 9; Length 24;
Best Local Similarity 92.3%; Pred. No. 1.1e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGCGTTGCCA 13
DB 10 TTAGCGTTGCCA 22

RESULT 14
US-10-215-112-10761
Sequence 10761, Application US/10215112
Publication No. US20030082596A1
GENERAL INFORMATION:
APPLICANT: Michael Miltman
TITLE OF INVENTION: Method of Genetic Analysis of Probes:
FILE REFERENCE: 3119
CURRENT APPLICATION NUMBER: US/10/215,112
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 14936
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10761
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-10761

Query Match 57.0%; Score 11.4; DB 9; Length 25;
Best Local Similarity 92.3%; Pred. No. 1.1e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TTGCCACTCAGAG 20
DB 13 TTGCCGCTCAGAG 25

RESULT 15
US-09-780-533A-505
Sequence 505, Application US/09780533A
Publication No. US20030060611A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwigen, Jim
APPLICANT: Chowdhry, Bharat
APPLICANT: Haebertl, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MBH00, 878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: Patentin version 3.0
SEQ ID NO 505
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-780-533A-505

Query Match 56.0%; Score 11.2; DB 9; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.4e+04;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTGGCTTGGCACTC 16
DB 2 UUGGCUUGGCCACUC 17


```

RESULT 16
US-09-930-423-1153/c
; Sequence 1153, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blact, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MHH00, 918-A, 400/027
; CURRENT APPLICATION NUMBER: US/09/930, 423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1153
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1153

Query Match      56.0%; Score 11.2; DB 9; Length 17;
Best Local Similarity 81.2%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 TGGCTTGGCCACTCAG 18
      |||||
DB      17 TGGCTTGGCTGCTCAG 2

RESULT 17
US-10-206-839-96
; Sequence 96, Application US/10206839
; Publication No. US2003009997A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Kurth, Janice
; TITLE OF INVENTION: Genotyping Human Phenol Sulfotransferase
; FILE REFERENCE: 4389-6 (formerly SEQ-16P)
; CURRENT APPLICATION NUMBER: US/10/206, 839
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 09/328,174
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 96
; LENGTH: 19
; TYPE: DNA
; ORGANISM: H. sapiens
US-10-206-839-96

Query Match      56.0%; Score 11.2; DB 9; Length 19;
Best Local Similarity 81.2%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5 CGTTGGCCACTCAG 20
      |||||
DB      1 CTTTGGCCCAAG 16

RESULT 18
US-10-060-301-158
; Sequence 158, Application US/10060301
; Publication No. US20020182622A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, Yusuke et al.
; TITLE OF INVENTION: A METHOD FOR SNP (SINGLE NUCLEOTIDE POLYMORPHISM) TYPING
; FILE REFERENCE: 1254-0195D
; CURRENT APPLICATION NUMBER: US/10/060,301
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: JP 2001-25700
; PRIOR FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 200

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 158
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Reverse Primer for SNP ID 79
US-10-060-301-158

Query Match      56.0%; Score 11.2; DB 9; Length 20;
Best Local Similarity 81.2%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 TGGCTTGGCCACTCAG 18
      |||||
DB      5 TGGCTTGGCCACTCAG 20

RESULT 19
US-10-060-301-160
; Sequence 160, Application US/10060301
; Publication No. US20020182622A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, Yusuke et al.
; TITLE OF INVENTION: A METHOD FOR SNP (SINGLE NUCLEOTIDE POLYMORPHISM) TYPING
; FILE REFERENCE: 1254-0195D
; CURRENT APPLICATION NUMBER: US/10/060,301
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: JP 2001-25700
; PRIOR FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 160
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Reverse Primer for SNP ID 80
US-10-060-301-160

Query Match      56.0%; Score 11.2; DB 9; Length 20;
Best Local Similarity 81.2%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 TGGCTTGGCCACTCAG 18
      |||||
DB      5 TGGCTTGGCCACTCAG 20

RESULT 20
US-09-808-680-10/c
; Sequence 10, Application US/09808680
; Patent No. US20020052331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F
; APPLICANT: Bennett, C. Frank
; APPLICANT: Anderson, Kevin P
; APPLICANT: Condon, Thomas P
; TITLE OF INVENTION: Compositions and Methods for Antisense Inhibition of
; FILE REFERENCE: ISPH-0557
; CURRENT APPLICATION NUMBER: US/09/808,680
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/194,230
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: PCT/US97/07132
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: 08/653,653
; PRIOR FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: 08/440,740
; PRIOR FILING DATE: 1995-05-12

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PRIOR APPLICATION NUMBER: 08/063,167
PRIOR FILING DATE: 1993-05-17
PRIOR APPLICATION NUMBER: 08/007,997
PRIOR FILING DATE: 1993-01-21
PRIOR APPLICATION NUMBER: 07/939,855
PRIOR FILING DATE: 1992-09-02
PRIOR APPLICATION NUMBER: 07/567,286
PRIOR FILING DATE: 1990-08-14
PRIOR APPLICATION NUMBER: 07/927,506
PRIOR FILING DATE: 1992-11-19
PRIOR APPLICATION NUMBER: 07/568,366
PRIOR FILING DATE: 1990-08-16
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-808-680-10

Query Match 56.0%; Score 11.2; DB 10; Length 20;
Best Local Similarity 81.2%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CGTTGCCACTCAGAG 20
DB 20 CCTCTGCTACTCAGAG 5

RESULT 21
US-10-117-108A-27
Sequence 27, Application US/10117108A
Publication No. US20030082571A1
GENERAL INFORMATION:
APPLICANT: KACHAB, Edward H.
TITLE OF INVENTION: LINEAR NUCLEIC ACID AND SEQUENCE THEREFOR
FILE REFERENCE: 37955-0004
CURRENT APPLICATION NUMBER: US/10/117,108A
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 60/282,491
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
NAME/KEY: misc feature
LOCATION: (1)-(6)
OTHER INFORMATION: The monomer ttgcgc may be repeated from 2-20 times
US-10-117-108A-27

Query Match 55.0%; Score 11; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCGCTTTC 11
DB 1 TTTCGCTTTC 11

RESULT 22
US-10-175-225-65
Sequence 65, Application US/10175225
Publication No. US20030082582A1
GENERAL INFORMATION:
APPLICANT: Richard A. Gatti

TITLE OF INVENTION: METHODS FOR DETECTION OF ATAXIA
TITLE OF INVENTION: TELANGIECTASIA MUTATIONS
FILE REFERENCE: UC078.001DVI
CURRENT APPLICATION NUMBER: US/10/175,225
CURRENT FILING DATE: 2002-08-23
PRIOR APPLICATION NUMBER: US 09/360,416
PRIOR FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 143
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 65
LENGTH: 19
TYPE: DNA
ORGANISM: Human
US-10-175-225-65

Query Match 55.0%; Score 11; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGCCACTCAGA 19
DB 2 TGCCACTCAGA 12

RESULT 23
US-09-801-968-5
Sequence 5, Application US/09801968
Patent No. US20020082205A1
GENERAL INFORMATION:
APPLICANT: Itch, No. US20020082205A1uyuk1
TITLE OF INVENTION: HUMAN RGF-23 GENE AND GENE EXPRESSION
FILE REFERENCE: PP-17150.001/201130.40901
CURRENT APPLICATION NUMBER: US/09/801,968
CURRENT FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sense PCR primer
US-09-801-968-5

Query Match 55.0%; Score 11; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GCCACTCAGAG 20
DB 8 GCCACTCAGAG 18

RESULT 24
US-09-780-533A-1366
Sequence 1366, Application US/09780533A
Publication No. US20030060611A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blate, Larry
APPLICANT: McSwigen, Jim
APPLICANT: Chowitra, Bharat
APPLICANT: Haebertl, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MBH00.878-A(400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: PatentIn version 3.0

SEQ ID NO 1366
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-780-533A-1366

Query Match 54.0%; Score 10.8; DB 9; Length 17;
Best Local Similarity 64.3%; Pred. No. 2.3e+04;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 4 GCGTTGGCCTCA 17
1 GCUUGGCCACUCA 14

RESULT 25
US-10-087-082-2/c
Sequence 2, Application US/10087082
Patent No. US2002016040A1
GENERAL INFORMATION:
APPLICANT: Diemaler, Wolfgang
APPLICANT: Ruschoff, Josef
TITLE OF INVENTION: IMPROVED METHOD OF PRIMER-EXTENSION PREAMPLIFICATION PCR
FILE REFERENCE: 4802
CURRENT APPLICATION NUMBER: US/10/087,082
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: DE 198 13 317.0
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Description of artificial sequence: Primer for Human genomic sequ
US-10-087-082-2

Query Match 54.0%; Score 10.8; DB 9; Length 20;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TTGGCACTCAGAG 20
DB 19 TTGGCACACTGAG 6

RESULT 26
US-09-865-866-22
Sequence 22, Application US/09865866
Publication No. US20030045487A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
FILE REFERENCE: RTS-0221
CURRENT APPLICATION NUMBER: US/09/865,866
CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 173
SEQ ID NO 22
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-865-866-22

Query Match 54.0%; Score 10.8; DB 9; Length 20;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TTGGCACTCAGAG 20
DB 19 TTGGCACACTGAG 6

Db 4 TTACTCTCAGAG 17

RESULT 27
US-09-865-866-23
Sequence 23, Application US/09865866
Publication No. US20030045487A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) E
FILE REFERENCE: RTS-0221
CURRENT APPLICATION NUMBER: US/09/865,866
CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 173
SEQ ID NO 23
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-865-866-23

Query Match 54.0%; Score 10.8; DB 9; Length 20;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TTGGCACTCAGAG 20
DB 7 TTACTCTCAGAG 20

RESULT 28
US-09-940-925A-68/c
Sequence 68, Application US/09940925A
Publication No. US20030054338A1
GENERAL INFORMATION:
APPLICANT: BROW, MARY ANN D.
APPLICANT: LYAMICHEV, VICTOR I.
OLIVE, DAVID M.
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
PATHOGENS
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/940,925A
FILING DATE: 10-Jun-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-09-940-925A-68

Query Match 54.0%; Score 10.8; DB 9; Length 20;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TTTGCCACTCAG 20
DB 19 TTTGCCACTCAG 6

RESULT 29
US-10-001-076-59
Sequence 59, Application US/10001076
Publication No. US20030096775A1
GENERAL INFORMATION:
APPLICANT: Mark J. Graham
TITLE OF INVENTION: ANTISENSE MODULATION OF COMPLEMENT COMPONENT C3 EXPRESSION
FILE REFERENCE: RTS-0329
CURRENT APPLICATION NUMBER: US/10/001,076
PRIORITY FILING DATE: 2001-10-23
NUMBER OF SEQ ID NOS: 179
SEQ ID NO 59
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-076-59

Query Match 54.0%; Score 10.8; DB 9; Length 20;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GTTGCACACTGAGA 19
DB 2 GTTGCACACTGAGA 15

RESULT 30
US-10-011-119A-6/c
Sequence 6, Application US/10011119A
Patent No. US20020150928A1
GENERAL INFORMATION:
APPLICANT: Lundin, Tomas
TITLE OF INVENTION: DNA-EMBEDDING MEDIUM AND METHOD OF USE
FILE REFERENCE: P/2432-45
CURRENT APPLICATION NUMBER: US/10/011,119A
PRIORITY FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/605,611
PRIORITY FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 6
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-011-119A-6

Query Match 54.0%; Score 10.8; DB 12; Length 20;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TTTGCCACTCAGAG 20
DB 19 TTTGCCACTCAGAG 6

RESULT 31
US-10-135-629-15

Sequence 15, Application US/10135629
Publication No. US20030073657A1
GENERAL INFORMATION:
APPLICANT: Halle, Jorn-Peter
APPLICANT: Goppelt, Andreas
APPLICANT: Hof, Peter
TITLE OF INVENTION: Use of Alpha 1-Antichymotrypsin
TITLE OF INVENTION: Polypeptides, or Nucleic Acids Encoding Them, or of a Cell
TITLE OF INVENTION: Which is Expressing an ACT Polypeptide, or a Nucleic Acid
TITLE OF INVENTION: Encoding It, for Treatment and/or Prevention of
TITLE OF INVENTION: Diabetes-Associated and/or Arterial Poorly Healing Wounds
TITLE OF INVENTION: and for Identifying Pharmacologically Active Substances
FILE REFERENCE: 50125/033002
CURRENT APPLICATION NUMBER: US/10/135,629
PRIORITY FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: DE 10121225.0
PRIOR FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: US 60/323,348
PRIOR FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-10-135-629-15

Query Match 54.0%; Score 10.8; DB 9; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCGTTGCCACTCA 17
DB 3 GCGTTGCCACTCA 16

RESULT 32
US-09-883-152-86
Sequence 86, Application US/09883152
Publication No. US2003008284A1
GENERAL INFORMATION:
APPLICANT: Kennedy, Giulia
APPLICANT: Kang, Sanmao
APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne Bennett
TITLE OF INVENTION: POLYNUCLEOTIDES RELATED TO COLON CANCER
FILE REFERENCE: 2300-1663
CURRENT APPLICATION NUMBER: US/09/883,152
PRIORITY FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/211,835
PRIORITY FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 127
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 86
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-09-883-152-86

Query Match 54.0%; Score 10.8; DB 9; Length 24;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGCCTTGCCTC 16
DB 3 TGCCTTGCCTC 16

```
RESULT 33
US-09-940-185-2382
; Sequence 2382, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940.185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2382
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-2382

Query Match          54.0%; Score 10.8; DB 9; Length 24;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 3 TGGCTTGGCACTC 16
Db 2 TGTGTTGCCAGC 15

RESULT 34
US-10-215-112-665
; Sequence 665, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215.112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 665
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-665

Query Match          54.0%; Score 10.8; DB 9; Length 25;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 4 GCGTTGGCACTCA 17
Db 5 GCATTGGCTACTCA 18

RESULT 35
US-10-215-112-791
; Sequence 791, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-791

Query Match          54.0%; Score 10.8; DB 9; Length 25;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 4 GCGTTGGCACTCA 17
Db 5 GCATTGGCTACTCA 18

RESULT 36
US-10-215-112-2803/c
; Sequence 2803, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215.112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2803
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-2803

Query Match          54.0%; Score 10.8; DB 9; Length 25;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 4 GCGTTGGCACTCA 17
Db 21 GCATTGGCTACTCA 8

RESULT 37
US-10-215-112-2929/c
; Sequence 2929, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215.112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2929
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-2929

Query Match          54.0%; Score 10.8; DB 9; Length 25;
```

```
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCGTTGCCACTCA 17
   |||||
   21 GCATTGCCACTCA 8

RESULT 38
US-10-215-112-8357
; Sequence 8357, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittman
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8357
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-8357

Query Match 54.0%; Score 10.8; DB 9; Length 25;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGTGGCCACTCAG 18
   |||||
   2 CTTTGTCTCTCAG 15

Db 2 CTTTGTCTCTCAG 15

RESULT 39
US-10-215-112-11650/c
; Sequence 11650, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittman
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11650
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-11650

Query Match 54.0%; Score 10.8; DB 9; Length 25;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGTGGCCACTCAG 18
   |||||
   24 CTTTGTCTCTCAG 11

Db 24 CTTTGTCTCTCAG 11

RESULT 40
US-10-215-112-12458
; Sequence 12458, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Michael Mittman
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12458
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-12458

Query Match 54.0%; Score 10.8; DB 9; Length 25;
Best Local Similarity 85.7%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGCGTTGCCAC 14
   |||||
   2 TTGTGTTGTCTAC 15

Db 2 TTGTGTTGTCTAC 15
```

Search completed: June 7, 2003, 11:39:08
Job time : 89.3636 secs

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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 08:05:49 / Search time 1145.09 Seconds
(without alignments)
282.868 Million cell updates/sec

Title: US-10-080-959A-2
Perfect score: 20
Sequence: 1 ttgcgttcgcacccagag 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 18144

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: em_esa:db:*
2: em_esa:db:*
3: em_esa:db:*
4: em_esa:db:*
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6: em_esa:db:*
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8: em_esa:db:*
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27: em_esa:db:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match length	ID	Description
C 1	11.6	58.0	20	9	AU256704	AU256704 AU256704
C 2	11.2	56.0	25	9	AU189662	AU189662 qd18n06.x
C 3	11	55.0	24	9	AU257541	AU257541 AU257541
C 4	10.8	54.0	20	14	D18747	D18747 MUSGS01809
C 5	10.6	53.0	22	17	AZ779532	AZ779532 2M0016K03
C 6	10	50.0	19	17	AZ655339	AZ655339 1M0464F13

C 7	10	50.0	21	9	AU254819	AU254819 AU254819
C 8	10	50.0	21	17	AZ785704	AZ785704 2M0029C21
C 9	10	50.0	24	17	BH813511	BH813511 SALK_0643
C 10	9.8	49.0	24	17	AZ762000	AZ762000 1M0556F08
C 11	9.8	49.0	24	17	TA259C080	TA259C080 T. brucei
C 12	9.6	48.0	22	9	AA916047	AA916047 og3d01.b
C 13	9.6	48.0	22	17	AZ592068	AZ592068 1M0402H08
C 14	9.6	48.0	22	17	TA271198	TA271198 1M0573M08
C 15	9.6	48.0	22	17	TA223E07P	TA223E07P T. brucei
C 16	9.6	48.0	23	17	TA202H11Q	TA202H11Q T. brucei
C 17	9.6	48.0	25	17	BH864166	BH864166 SALK_0954
C 18	9.6	48.0	25	17	BH864216	BH864216 SALK_0955
C 19	9.4	47.0	20	17	AZ589990	AZ589990 1M0399016
C 20	9.4	47.0	21	17	AZ812038	AZ812038 2M0078022
C 21	9.4	47.0	22	17	AZ662093	AZ662093 1M0541C05
C 22	9.4	47.0	22	17	AZ612609	AZ612609 1M0439P23
C 23	9.4	47.0	24	17	TA186D08P	TA186D08P T. brucei
C 24	9.2	46.0	21	17	AZ405188	AZ405188 1M0173G15
C 25	9.2	46.0	21	17	AZ427688	AZ427688 1M0209G15
C 26	9.2	46.0	21	17	AZ948720	AZ948720 2M0211D23
C 27	9.2	46.0	22	17	AZ583690	AZ583690 1M0378E16
C 28	9.2	46.0	23	17	AZ634674	AZ634674 1M0490A11
C 29	9.2	46.0	23	17	AZ646716	AZ646716 1M0512D23
C 30	9.2	46.0	24	17	AZ418103	AZ418103 1M0194L03
C 31	9.2	46.0	24	17	AZ829689	AZ829689 2M0107C22
C 32	9.2	46.0	25	17	AZ379234	AZ379234 1M0134P16
C 33	9.2	46.0	25	17	BH759341	BH759341 KG02510-3
C 34	9.2	46.0	25	17	AZ954781	AZ954781 2M0220C07
C 35	9.2	46.0	20	17	AZ435809	AZ435809 1M0223L03
C 36	9.2	46.0	20	17	AZ991405	AZ991405 2M0275004
C 37	9.2	46.0	20	17	TA361F06P	TA361F06P T. brucei
C 38	9.2	46.0	21	17	TA62B07P	TA62B07P T. brucei
C 39	9.2	46.0	22	17	AT186405	AT186405 qd20e05.x
C 40	9.2	46.0	22	17	AZ367707	AZ367707 1M0117N08
C 41	9.2	46.0	23	17	TA101C01Q	TA101C01Q T. brucei
C 42	9.2	46.0	24	17	AZ612609	AZ612609 1M0439P23
C 43	9.2	46.0	25	17	AQ0073480	AQ0073480 EP(2)2310
C 44	9.2	46.0	25	17	AZ514617	AZ514617 1M0361N23
C 45	9.2	46.0	19	17	AZ737052	AZ737052 1M0584C20
C 46	9.2	46.0	21	17	AZ307601	AZ307601 1M0009C16
C 47	9.2	46.0	21	17	AZ375290	AZ375290 1M0128N01
C 48	9.2	46.0	22	9	A1804482	A1804482 uc71909.x
C 49	9.2	46.0	22	9	A1804482	A1804482 uc71909.x
C 50	9.2	46.0	23	17	AZ335754	AZ335754 1M0065P22
C 51	9.2	46.0	23	17	AZ335754	AZ335754 1M0065P22
C 52	9.2	46.0	24	17	AZ957958	AZ957958 2M0225G04
C 53	9.2	46.0	25	17	AZ588895	AZ588895 1M0397R04
C 54	9.2	46.0	25	17	TA263F03Q	TA263F03Q T. brucei
C 55	9.2	46.0	20	9	AU254453	AU254453 AU254453
C 56	9.2	46.0	20	9	AU267884	AU267884 AU267884
C 57	9.2	46.0	20	17	AZ395013	AZ395013 1M0158M18
C 58	9.2	46.0	20	17	AZ793050	AZ793050 2M0045M15
C 59	9.2	46.0	20	17	AZ992248	AZ992248 2M0076N17
C 60	9.2	46.0	21	14	D20000	D20000 HUMGS00970
C 61	9.2	46.0	21	17	AZ472579	AZ472579 1M0287R21
C 62	9.2	46.0	21	17	AZ949072	AZ949072 2M0212D19
C 63	9.2	46.0	21	17	AZ991096	AZ991096 2M0275C09
C 64	9.2	46.0	22	9	A1120642	A1120642 ub71a05.x
C 65	9.2	46.0	22	17	TA43D08P	TA43D08P T. brucei
C 66	9.2	46.0	24	17	AZ502375	AZ502375 1M041R08
C 67	9.2	46.0	24	17	AZ662752	AZ662752 1M0542G05
C 68	9.2	46.0	24	17	AZ805590	AZ805590 2M0067L05
C 69	9.2	46.0	24	17	TA100C01Q	TA100C01Q T. brucei
C 70	9.2	46.0	25	14	BH840574	BH840574 KG05441-5
C 71	9.2	46.0	15	14	L76129	L76129 SCRAPO223
C 72	9.2	46.0	19	17	AZ807609	AZ807609 1M0121R18
C 73	9.2	46.0	19	17	AZ807609	AZ807609 2M0070M03
C 74	9.2	46.0	20	17	AZ782243	AZ782243 2M0022B21
C 75	9.2	46.0	20	17	TA359F10Q	TA359F10Q T. brucei
C 76	9.2	46.0	21	17	AZ610564	AZ610564 1M0435U23
C 77	9.2	46.0	21	17	TA23D03P	TA23D03P T. brucei
C 78	9.2	46.0	22	17	AZ309687	AZ309687 1M0016R17
C 79	9.2	46.0	22	17	AZ442914	AZ442914 1M0237A24

C 80	8.4	42.0	22	17	AZ476175	AZ476175	1M0294E14	C 153	8	40.0	25	9	A1143800	A1143800 qc01C03.x
C 81	8.4	42.0	22	17	AZ844290	AZ844290	2M0143A10	C 154	8	40.0	25	9	A1539240	A1539240 cp64B08.x
C 82	8.4	42.0	23	17	AZ447907	AZ447907	1M0245I18	C 155	8	40.0	25	9	AU254451	AU254451
C 83	8.4	42.0	23	17	AZ789956	AZ789956	2M0038L05	C 156	8	40.0	25	13	BC924523	BC924523 HNC27-1-G
C 84	8.4	42.0	23	17	TA111H02Q	TA111H02Q	AL460694 T. brucei	C 157	8	40.0	25	17	A2368070	A2368070 1M0118A01
C 85	8.4	42.0	23	17	TA144D04Q	TA144D04Q	AL466870 T. brucei	C 158	8	40.0	25	17	A2621173	A2621173 1M0454B17
C 86	8.4	42.0	23	17	TA380G08Q	TA380G08Q	AL497844 T. brucei	C 159	8	40.0	25	17	A2780039	A2780039 2M0016P21
C 87	8.4	42.0	23	17	TA78E03P	TA78E03P	AL461956 T. brucei	C 160	8	40.0	25	17	A2806433	A2806433 2M0068P24
C 88	8.4	42.0	24	17	AW248929	AW248929	AW248929 2819212.3	C 161	8	40.0	25	17	A2806897	A2806897 2M0068P13
C 89	8.4	42.0	24	17	AZ307682	AZ307682	AZ307682 1M0009P21	C 162	8	40.0	25	17	A2829742	A2829742 2M0107M02
C 90	8.4	42.0	24	17	AZ309981	AZ309981	AZ309981 1M0018H06	C 163	8	40.0	25	17	TA20D01P	TA20D01P
C 91	8.4	42.0	24	17	AZ476560	AZ476560	AZ476560 1M0295C03	C 164	8	40.0	19	17	A2610584	A2610584 1M0335C23
C 92	8.4	42.0	24	17	AZ585729	AZ585729	AZ585729 1M0391A08	C 165	8	39.0	19	17	A2780992	A2780992
C 93	8.4	42.0	24	17	AZ819874	AZ819874	AZ819874 2M0091F13	C 166	8	39.0	19	17	AZ839642	AZ839642
C 94	8.4	42.0	25	9	A1181643	A1181643	AL181643 ub79h08.x	C 167	8	39.0	20	17	A2485309	A2485309
C 95	8.4	42.0	25	17	AZ312923	AZ312923	AZ312923 1M0029L01	C 168	8	39.0	20	17	A2485309	A2485309
C 96	8.4	42.0	25	17	AZ818404	AZ818404	AZ818404 2M0088I22	C 169	8	39.0	20	17	A2489135	A2489135
C 97	8.4	42.0	25	17	TA208E01Q	TA208E01Q	AL479320 T. brucei	C 170	8	39.0	20	17	A2615164	A2615164
C 98	8.4	42.0	25	17	TA26G100	TA26G100	AL452958 T. brucei	C 171	8	39.0	20	17	A2780925	A2780925
C 99	8.2	41.0	19	17	AZ441752	AZ441752	AZ441752 1M0234K06	C 172	8	39.0	20	17	A2824749	A2824749
C 100	8.2	41.0	19	17	AZ509071	AZ509071	AZ509071 1M0351A21	C 173	8	39.0	20	17	A2824749	A2824749
C 101	8.2	41.0	20	17	AZ390214	AZ390214	AZ390214 1M0151O21	C 174	8	39.0	21	17	A2341842	A2341842
C 102	8.2	41.0	22	17	AZ456534	AZ456534	AZ456534 1M0259L13	C 175	8	39.0	21	17	A2443639	A2443639
C 103	8.2	41.0	22	17	D18746	D18746	D18746 M0SGS01808	C 176	8	39.0	21	17	A2486694	A2486694
C 104	8.2	41.0	22	17	AZ444633	AZ444633	AZ444633 1M0214M24	C 177	8	39.0	21	17	A2784525	A2784525
C 105	8.2	41.0	22	17	AZ620271	AZ620271	AZ620271 1M0239I22	C 178	8	39.0	21	17	A2784525	A2784525
C 106	8.2	41.0	22	17	AZ623308	AZ623308	AZ623308 1M0460P21	C 179	8	39.0	21	17	A2784525	A2784525
C 107	8.2	41.0	22	17	TA184A12P	TA184A12P	AL474131 T. brucei	C 180	8	39.0	21	17	A2784525	A2784525
C 108	8.2	41.0	23	9	AU255370	AU255370	AU255370	C 181	8	39.0	22	9	AU254611	AU254611
C 109	8.2	41.0	23	17	AZ665877	AZ665877	AZ665877 1M0547L01	C 182	8	39.0	22	17	A2360276	A2360276
C 110	8.2	41.0	23	17	AZ781989	AZ781989	AZ781989 2M0021P18	C 183	8	39.0	22	17	A2476175	A2476175
C 111	8.2	41.0	23	17	TA201F03Q	TA201F03Q	AL477466 T. brucei	C 184	8	39.0	22	17	A2588797	A2588797
C 112	8.2	41.0	23	17	TA314B11Q	TA314B11Q	AL489852 T. brucei	C 185	8	39.0	22	17	A2623402	A2623402
C 113	8.2	41.0	23	17	TA3164P07P	TA3164P07P	AL494487 T. brucei	C 186	8	39.0	22	17	A2794867	A2794867
C 114	8.2	41.0	23	17	AZ812679	AZ812679	AZ812679 2M0079H03	C 187	8	39.0	22	17	A2863707	A2863707
C 115	8.2	41.0	24	17	BH848943	BH848943	BH848943 SALK 0690	C 188	8	39.0	22	17	TA8C02P	TA8C02P
C 116	8.2	41.0	25	9	A1049424	A1049424	AL453202 T. brucei	C 189	8	39.0	23	17	A2309657	A2309657
C 117	8.2	41.0	25	17	AU025409	AU025409	AU025409 EP(X)1348	C 190	8	39.0	23	17	A2345606	A2345606
C 118	8.2	41.0	25	17	AZ310966	AZ310966	AZ310966 1M0026K08	C 191	8	39.0	23	17	A2387861	A2387861
C 119	8.2	41.0	25	17	AZ328535	AZ328535	AZ328535 1M0052B21	C 192	8	39.0	23	17	A2488263	A2488263
C 120	8.2	41.0	25	17	AZ818404	AZ818404	AZ818404 2M0088I22	C 193	8	39.0	23	17	A2785466	A2785466
C 121	8.2	41.0	25	17	AZ809111	AZ809111	AZ809111 2M0072P23	C 194	8	39.0	23	17	A2806458	A2806458
C 122	8.2	41.0	25	17	BH866379	BH866379	BH866379 SALK 1012	C 195	8	39.0	23	17	A2859707	A2859707
C 123	8.2	41.0	25	17	AZ608537	AZ608537	AZ608537 1M0432N14	C 196	8	39.0	23	17	A2991622	A2991622
C 124	8.2	41.0	19	17	AZ627654	AZ627654	AZ627654 2M0104O12	C 197	8	39.0	23	17	TA129F12P	TA129F12P
C 125	8.2	41.0	20	17	AZ588000	AZ588000	AZ588000 1M0396I06	C 198	8	39.0	23	17	TA242D06P	TA242D06P
C 126	8.2	41.0	20	17	AZ761543	AZ761543	AZ761543 1M0355J23	C 199	8	39.0	23	17	TA30F09P	TA30F09P
C 127	8.2	41.0	20	17	AZ809111	AZ809111	AZ809111 2M0215O12	C 200	8	39.0	24	14	L32034	L32034
C 128	8.2	41.0	20	17	AZ951314	AZ951314	AZ951314 2M0215O12	C 201	8	39.0	24	17	A2304717	A2304717
C 129	8.2	41.0	20	17	TA30G04Q	TA30G04Q	AL453202 T. brucei	C 202	8	39.0	24	17	A2341147	A2341147
C 130	8.2	41.0	21	9	AU256158	AU256158	AL453202 T. brucei	C 203	8	39.0	24	17	A2626098	A2626098
C 131	8.2	41.0	21	10	AW248836	AW248836	AW248836 2821108.3	C 204	8	39.0	24	17	A2626098	A2626098
C 132	8.2	41.0	21	17	AZ486932	AZ486932	AZ486932 1M0316F14	C 205	8	39.0	24	17	A2795736	A2795736
C 133	8.2	41.0	21	17	AA907590	AA907590	AA907590 cm29e05.s	C 206	8	39.0	24	17	AZ809979	AZ809979
C 134	8.2	41.0	22	9	A1723256	A1723256	A1723256 fc34g02.x	C 207	8	39.0	24	17	AZ813287	AZ813287
C 135	8.2	41.0	22	17	AZ334245	AZ334245	AZ334245 1M0063K01	C 208	8	39.0	24	17	AZ893498	AZ893498
C 136	8.2	41.0	22	17	AZ334245	AZ334245	AZ334245 1M0063K01	C 209	8	39.0	24	17	TA110D11P	TA110D11P
C 137	8.2	41.0	22	17	TA129B01P	TA129B01P	AL463979 T. brucei	C 210	8	39.0	24	17	TA38B04Q	TA38B04Q
C 138	8.2	41.0	23	17	AZ621487	AZ621487	AZ621487 1M0037N21	C 211	8	39.0	24	17	TA5F09P	TA5F09P
C 139	8.2	41.0	23	17	AZ658085	AZ658085	AZ658085 1M053J07	C 212	8	39.0	25	9	A136779	A136779
C 140	8.2	41.0	23	17	AZ800080	AZ800080	AZ800080 2M0057I22	C 213	8	39.0	25	9	AU254198	AU254198
C 141	8.2	41.0	23	17	AZ826455	AZ826455	AZ826455 2M0102P09	C 214	8	39.0	25	9	AA469268	AA469268
C 142	8.2	41.0	23	17	TA114F03Q	TA114F03Q	AL462961 T. brucei	C 215	8	39.0	25	17	A2445454	A2445454
C 143	8.2	41.0	23	17	D18741	D18741	D18741 M0SGS01803	C 216	8	39.0	25	17	AZ483632	AZ483632
C 144	8.2	41.0	24	14	AZ617463	AZ617463	AZ617463 1M0448F15	C 217	8	39.0	25	17	AZ786392	AZ786392
C 145	8.2	41.0	24	17	AZ655394	AZ655394	AZ655394 1M0530C05	C 218	8	39.0	25	17	AZ786392	AZ786392
C 146	8.2	41.0	24	17	AZ762011	AZ762011	AZ762011 1M0556P09	C 219	8	39.0	25	17	AZ786392	AZ786392
C 147	8.2	41.0	24	17	AZ805440	AZ805440	AZ805440 2M0066F15	C 220	8	39.0	25	17	AZ786392	AZ786392
C 148	8.2	41.0	24	17	AZ817941	AZ817941	AZ817941 2M0087M09	C 221	8	39.0	25	17	AZ786392	AZ786392
C 149	8.2	41.0	24	17	AZ833716	AZ833716	AZ833716 2M0116D02	C 222	8	39.0	25	17	BH614917	BH614917
C 150	8.2	41.0	24	17	TA200H11P	TA200H11P	AL475521 T. brucei	C 223	8	39.0	25	17	BH789461	BH789461
C 151	8.2	41.0	24	17	TA20E11P	TA20E11P	AL454537 T. brucei	C 224	8	39.0	25	17	BH846552	BH846552
C 152	8.2	41.0	24	17	TA20E11P	TA20E11P	AL454537 T. brucei	C 225	8	39.0	25	17	AW246520	AW246520

C 226	7.6	38.0	19	17	AZ345359	AZ345159	1M0079P23	C 299	7.4	37.0	20	17	AZ787173	AZ781173	2M0033006
C 227	7.6	38.0	19	17	AZ411255	AZ411355	1M0184C18	C 300	7.4	37.0	21	17	AZ818067	AZ818067	2M0083E20
C 228	7.6	38.0	19	17	AZ413276	AZ413776	1M0197L07	C 301	7.4	37.0	20	19	AU060547	AU060547	AU060547
C 229	7.6	38.0	19	17	AZ785324	AZ785324	2M0029G11	C 302	7.4	37.0	21	17	AZ344683	AZ344683	1M0046C13
C 230	7.6	38.0	20	17	AZ316884	AZ316884	1M0035106	C 303	7.4	37.0	21	17	AZ330777	AZ330777	1M0056P08
C 231	7.6	38.0	20	17	AZ435809	AZ435809	1M0223L03	C 304	7.4	37.0	21	17	AZ453588	AZ453588	1M0255M02
C 232	7.6	38.0	20	17	AZ438858	AZ438858	1M0229T10	C 305	7.4	37.0	21	17	AZ463806	AZ463806	1M0272G19
C 233	7.6	38.0	20	17	AZ478502	AZ478502	1M0298B09	C 306	7.4	37.0	21	17	AZ613931	AZ613931	1M0442P01
C 234	7.6	38.0	20	17	AZ651194	AZ651194	1M0521E18	C 307	7.4	37.0	21	17	AZ628010	AZ628010	1M0476K09
C 235	7.6	38.0	20	17	AZ658035	AZ658035	1M0534P03	C 308	7.4	37.0	21	17	AZ664326	AZ664326	1M0506C18
C 236	7.6	38.0	21	9	AU258664	AU258664	AU258664	C 309	7.4	37.0	21	17	AZ800303	AZ800303	2M0058B14
C 237	7.6	38.0	21	9	AZ377507	AZ377507	1M0131G21	C 310	7.4	37.0	21	17	AZ829064	AZ829064	2M0106G01
C 238	7.6	38.0	21	17	AZ595078	AZ595078	1M0407M03	C 311	7.4	37.0	21	17	AZ834643	AZ834643	2M0130B15
C 239	7.6	38.0	21	17	AZ813392	AZ813392	2M0080T08	C 312	7.4	37.0	21	17	AZ836111	AZ836111	2M0130B15
C 240	7.6	38.0	21	17	AZ833301	AZ833301	2M0112T10	C 313	7.4	37.0	22	9	AZ938474	AZ938474	1M0550Z18
C 241	7.6	38.0	21	17	AZ965F030	AZ965F030	T. brucei	C 314	7.4	37.0	22	9	AU015745	AU015745	0U71D12.8
C 242	7.6	38.0	22	17	AZ419130	AZ419130	1M0195P03	C 315	7.4	37.0	22	9	AU016967	AU016967	0U71D12.8
C 243	7.6	38.0	22	17	AZ603366	AZ603366	1M0422L17	C 316	7.4	37.0	22	9	AU685766	AU685766	0U71D12.8
C 244	7.6	38.0	22	17	AZ822991	AZ822991	2M0096C13	C 317	7.4	37.0	22	9	AU708831	AU708831	0U71D12.8
C 245	7.6	38.0	22	17	AZ991196	AZ991196	2M0275F13	C 318	7.4	37.0	22	9	AU915487	AU915487	0U71D12.8
C 246	7.6	38.0	22	17	TA330G090	TA330G090	T. brucei	C 319	7.4	37.0	22	17	AZ342148	AZ342148	1M0075L01
C 247	7.6	38.0	23	9	HSW004394	HSW004394	1M0399L18	C 320	7.4	37.0	22	17	AZ376795	AZ376795	1M0130N14
C 248	7.6	38.0	23	9	AU256581	AU256581	AU256581	C 321	7.4	37.0	22	17	AZ442121	AZ442121	1M0234M07
C 249	7.6	38.0	23	9	AU271099	AU271099	AU271099	C 322	7.4	37.0	22	17	AZ442529	AZ442529	1M0236H10
C 250	7.6	38.0	23	14	D45826	D45826	1M0503046	C 323	7.4	37.0	22	17	AZ482536	AZ482536	1M0307D12
C 251	7.6	38.0	23	17	AZ307616	AZ307616	1M0009H17	C 324	7.4	37.0	22	17	AZ663539	AZ663539	1M0543A15
C 252	7.6	38.0	23	17	AZ309458	AZ309458	1M0013F14	C 325	7.4	37.0	22	17	AZ761211	AZ761211	1M0555I22
C 253	7.6	38.0	23	17	AZ372664	AZ372664	1M0124E09	C 326	7.4	37.0	22	17	AZ794203	AZ794203	2M0047E20
C 254	7.6	38.0	23	17	AZ483352	AZ483352	1M0246M06	C 327	7.4	37.0	22	17	AZ801266	AZ801266	2M0059I07
C 255	7.6	38.0	23	17	AZ514463	AZ514463	1M0361A19	C 328	7.4	37.0	22	17	AZ809838	AZ809838	2M0074G04
C 256	7.6	38.0	23	17	AZ808551	AZ808551	2M0072G08	C 329	7.4	37.0	22	17	AZ810608	AZ810608	2M0076D15
C 257	7.6	38.0	23	17	AZ822271	AZ822271	2M0095C18	C 330	7.4	37.0	22	17	AZ819824	AZ819824	2M0091K07
C 258	7.6	38.0	23	17	AZ824868	AZ824868	2M0099C15	C 331	7.4	37.0	22	17	AZ829430	AZ829430	2M0107A08
C 259	7.6	38.0	23	17	AZ858813	AZ858813	2M0164H10	C 332	7.4	37.0	22	17	AZ936470	AZ936470	2M0193J08
C 260	7.6	38.0	23	17	AZ973344	AZ973344	2M0247H06	C 333	7.4	37.0	22	17	TA200B03P	TA200B03P	T. brucei
C 261	7.6	38.0	23	17	BH811375	BH811375	SALX. 0585	C 334	7.4	37.0	22	17	TA361H12P	TA361H12P	T. brucei
C 262	7.6	38.0	23	17	TA270E010	TA270E010	T. brucei	C 335	7.4	37.0	22	17	TA71G05P	TA71G05P	T. brucei
C 263	7.6	38.0	23	17	TA369A110	TA369A110	T. brucei	C 336	7.4	37.0	22	17	TA80B09P	TA80B09P	T. brucei
C 264	7.6	38.0	24	17	AZ441888	AZ441888	1M0234K14	C 337	7.4	37.0	22	13	BG927951	BG927951	1M0555I22
C 265	7.6	38.0	24	17	AZ476937	AZ476937	1M0296G12	C 338	7.4	37.0	23	17	AZ309458	AZ309458	1M0013F14
C 266	7.6	38.0	24	17	AZ786547	AZ786547	2M0032B10	C 339	7.4	37.0	23	17	AZ376108	AZ376108	1M0129N14
C 267	7.6	38.0	24	17	AZ822664	AZ822664	2M0096M07	C 340	7.4	37.0	23	17	AZ434508	AZ434508	1M0220K22
C 268	7.6	38.0	25	9	AA881443	AA881443	vx19a01.r	C 341	7.4	37.0	23	17	AZ458587	AZ458587	1M0331P21
C 269	7.6	38.0	25	9	A1631952	A1631952	QY37E02.x	C 342	7.4	37.0	23	17	AZ617124	AZ617124	1M0448B15
C 270	7.6	38.0	25	9	A1635253	A1635253	tz79G05.x	C 343	7.4	37.0	23	17	AZ784247	AZ784247	2M0026D20
C 271	7.6	38.0	25	10	AV740046	AV740046	AV740046	C 344	7.4	37.0	23	17	AZ785027	AZ785027	2M0026D20
C 272	7.6	38.0	25	17	AZ802490	AZ802490	2M0061I12	C 345	7.4	37.0	23	17	AZ788088	AZ788088	2M0034P19
C 273	7.6	38.0	25	17	AZ809292	AZ809292	2M0073A17	C 346	7.4	37.0	23	17	AZ796147	AZ796147	2M0053F06
C 274	7.6	38.0	25	17	AZ827658	AZ827658	2M0104P12	C 347	7.4	37.0	23	17	AZ797023	AZ797023	2M0053F06
C 275	7.6	38.0	25	17	AZ979867	AZ979867	2M0256K11	C 348	7.4	37.0	23	17	AZ800080	AZ800080	2M0057I22
C 276	7.6	38.0	25	17	BH851330	BH851330	SALX. 0728	C 349	7.4	37.0	23	17	AZ808416	AZ808416	2M0071M22
C 277	7.6	38.0	25	17	TA486070	TA486070	T. brucei	C 350	7.4	37.0	23	17	AZ863841	AZ863841	2M0173F09
C 278	7.4	37.0	15	13	BM658732	BM658732	LZV602768	C 351	7.4	37.0	23	17	TA25D04P	TA25D04P	T. brucei
C 279	7.4	37.0	15	14	R41075	R41075	HK082-f. Adu	C 352	7.4	37.0	23	17	TA66H11P	TA66H11P	T. brucei
C 280	7.4	37.0	19	9	AT241100	AT241100	QK05D10.x	C 353	7.4	37.0	24	10	AM064435	AM064435	SP1032.KR
C 281	7.4	37.0	19	9	A1524591	A1524591	tz43F09.x	C 354	7.4	37.0	24	17	AZ345465	AZ345465	1M0080N09
C 282	7.4	37.0	19	14	C00646	C00646	HMG5000819	C 355	7.4	37.0	24	17	AZ345509	AZ345509	1M0080N09
C 283	7.4	37.0	19	17	AZ342555	AZ342555	1M0075K11	C 356	7.4	37.0	24	17	AZ445467	AZ445467	1M0248L17
C 284	7.4	37.0	19	17	AZ386064	AZ386064	1M0145C04	C 357	7.4	37.0	24	17	AZ490697	AZ490697	1M0323O16
C 285	7.4	37.0	19	17	AZ423190	AZ423190	1M0202L11	C 358	7.4	37.0	24	17	AZ491111	AZ491111	1M0324D03
C 286	7.4	37.0	19	17	AZ465132	AZ465132	1M0274D24	C 359	7.4	37.0	24	17	AZ493317	AZ493317	1M0327L24
C 287	7.4	37.0	19	17	AZ489350	AZ489350	1M0321K14	C 360	7.4	37.0	24	17	AZ579593	AZ579593	1M0367O09
C 288	7.4	37.0	19	17	BH000474	BH000474	2M0288B20	C 361	7.4	37.0	24	17	AZ582169	AZ582169	1M0374F20
C 289	7.4	37.0	20	17	AZ309121	AZ309121	1M0018G24	C 362	7.4	37.0	24	17	AZ586687	AZ586687	1M0392K16
C 290	7.4	37.0	20	17	AZ331630	AZ331630	1M0059N08	C 363	7.4	37.0	24	17	AZ621109	AZ621109	1M0454D12
C 291	7.4	37.0	20	17	AZ451921	AZ451921	1M0251C05	C 364	7.4	37.0	24	17	AZ776570	AZ776570	2M0010L14
C 292	7.4	37.0	20	17	AZ479222	AZ479222	1M0299A13	C 365	7.4	37.0	24	17	AZ799324	AZ799324	2M0056B11
C 293	7.4	37.0	20	17	AZ510137	AZ510137	1M0354O19	C 366	7.4	37.0	24	17	AZ819888	AZ819888	2M0091H18
C 294	7.4	37.0	20	17	AZ588658	AZ588658	1M0397F08	C 367	7.4	37.0	24	17	AZ966858	AZ966858	2M0283L08
C 295	7.4	37.0	20	17	AZ601843	AZ601843	1M0420M13	C 368	7.4	37.0	24	17	TA114801P	TA114801P	T. brucei
C 296	7.4	37.0	20	17	AZ632650	AZ632650	1M0487H23	C 369	7.4	37.0	24	17	TA144805P	TA144805P	T. brucei
C 297	7.4	37.0	20	17	AZ759840	AZ759840	1M0553B05	C 370	7.4	37.0	24	17	TA306B12P	TA306B12P	T. brucei
C 298	7.4	37.0	20	17	AZ766876	AZ766876	1M0568D08	C 371	7.4	37.0	24	17	TA80A11P	TA80A11P	T. brucei

C 372	7.4	37.0	25	9	A1327424	A1327424	MG45B06.x	445	7.2	36.0	23	17	A2476931	A2476931	1M0296F09
C 373	7.4	37.0	25	9	A1589311	A1589311	CE58B04.x	446	7.2	36.0	23	17	A2784247	A2784247	2M0026D20
C 374	7.4	37.0	25	9	A1633471	A1633471	EH62B09.x	447	7.2	36.0	23	17	A2785027	A2785027	2M0028H03
C 375	7.4	37.0	25	9	A1971185	A1971185	WR26B10.x	448	7.2	36.0	23	17	A2785578	A2785578	2M0029M01
C 376	7.4	37.0	25	10	AW245275	AW245275	2819969.3	449	7.2	36.0	23	17	A2863968	A2863968	2M0173M17
C 377	7.4	37.0	25	10	AW247153	AW247153	2819969.3	450	7.2	36.0	23	17	A2954682	A2954682	2M0220P23
C 378	7.4	37.0	25	14	H26073	H26073	Y156a12.r1	451	7.2	36.0	23	17	BH792497	BH792497	SALK_0646
C 379	7.4	37.0	25	14	A2593511	A2593511	1M0156B07	452	7.2	36.0	23	17	TA133E1P	TA133E1P	1M0237C0P
C 380	7.4	37.0	25	17	A2427752	A2427752	1M0209N21	453	7.2	36.0	23	17	TA175H02P	TA175H02P	1M0238A0P
C 381	7.4	37.0	25	17	A2442576	A2442576	1M0236K13	454	7.2	36.0	23	17	TA233E1P	TA233E1P	1M0239C0P
C 382	7.4	37.0	25	17	A2513056	A2513056	1M0359E05	455	7.2	36.0	23	17	TA268C02P	TA268C02P	1M0242B19
C 383	7.4	37.0	25	17	A2580365	A2580365	1M0368002	456	7.2	36.0	23	17	TA354H05O	TA354H05O	1M0242B19
C 384	7.4	37.0	25	17	A2586010	A2586010	1M0391D12	457	7.2	36.0	23	17	TA354H05O	TA354H05O	1M0242B19
C 385	7.4	37.0	25	17	A2606311	A2606311	1M0428G09	458	7.2	36.0	24	9	AU270898	AU270898	1M0327B10
C 386	7.4	37.0	25	17	A2611849	A2611849	1M0438M21	459	7.2	36.0	24	14	D45825	D45825	1M0327B10
C 387	7.4	37.0	25	17	A2781720	A2781720	2M0021G16	461	7.2	36.0	24	17	A2354113	A2354113	1M0293F15
C 388	7.4	37.0	25	17	A2792292	A2792292	2M0043H11	462	7.2	36.0	24	17	A2443047	A2443047	1M0237I06
C 389	7.4	37.0	25	17	A2798748	A2798748	2M0055P12	463	7.2	36.0	24	17	A2443113	A2443113	1M0237C08
C 390	7.4	37.0	25	17	A2808849	A2808849	2M0273B24	464	7.2	36.0	24	17	A2444127	A2444127	1M0242B19
C 391	7.4	37.0	25	17	A2890228	A2890228	2M0273B24	465	7.2	36.0	24	17	A2460288	A2460288	1M0255P06
C 392	7.4	37.0	25	17	BH812755	BH812755	SALK_0630	466	7.2	36.0	24	17	A2467278	A2467278	1M0278K02
C 393	7.4	37.0	25	17	BH848553	BH848553	SALK_0685	467	7.2	36.0	24	17	A2476673	A2476673	1M0298J20
C 394	7.4	37.0	25	17	BH865973	BH865973	SALK_1001	468	7.2	36.0	24	17	A2486450	A2486450	1M0314A06
C 395	7.4	37.0	25	17	TA334H10Q	TA334H10Q	1M0391D12	469	7.2	36.0	24	17	A2492799	A2492799	1M0327B10
C 396	7.2	36.0	19	9	A1174345	A1174345	an17f09.8	470	7.2	36.0	24	17	A2505251	A2505251	1M0327B10
C 397	7.2	36.0	19	12	BG869649	BG869649	HOA59-1.C	471	7.2	36.0	24	17	A2505251	A2505251	1M0327B10
C 398	7.2	36.0	19	12	A2309531	A2309531	1M0013X06	472	7.2	36.0	24	17	A2523508	A2523508	1M0552D02
C 399	7.2	36.0	19	17	A2775273	A2775273	2M0007F04	473	7.2	36.0	24	17	A2759639	A2759639	1M0552D02
C 400	7.2	36.0	19	17	A2779085	A2779085	2M0015B01	474	7.2	36.0	24	17	A2761320	A2761320	1M0553A02
C 401	7.2	36.0	19	17	A2799057	A2799057	2M0056B20	475	7.2	36.0	24	17	A2771365	A2771365	1M0573A03
C 402	7.2	36.0	19	17	A2822385	A2822385	2M0095F09	476	7.2	36.0	24	17	A2807619	A2807619	2M0070001
C 403	7.2	36.0	19	17	A2822713	A2822713	2M0096M08	477	7.2	36.0	24	17	A2817310	A2817310	2M0093C13
C 404	7.2	36.0	19	17	A2842166	A2842166	2M0103M22	478	7.2	36.0	24	17	A2820794	A2820794	2M0093C13
C 405	7.2	36.0	19	17	A2842166	A2842166	2M0103M22	479	7.2	36.0	24	17	TA20811P	TA20811P	1M0327B10
C 406	7.2	36.0	20	17	A2329547	A2329547	1M0053P17	480	7.2	36.0	25	9	AA877944	AA877944	0101B01.8
C 407	7.2	36.0	20	17	A2346702	A2346702	1M0082L01	481	7.2	36.0	25	9	AA877944	AA877944	0101B01.8
C 408	7.2	36.0	20	17	A2407675	A2407675	1M0178B04	482	7.2	36.0	25	9	AA877944	AA877944	0101B01.8
C 409	7.2	36.0	20	17	A2433830	A2433830	1M0219I22	483	7.2	36.0	25	9	AA877944	AA877944	0101B01.8
C 410	7.2	36.0	20	17	A2445436	A2445436	1M0241B15	484	7.2	36.0	25	9	AA877944	AA877944	0101B01.8
C 411	7.2	36.0	20	17	A2486007	A2486007	1M0313E17	485	7.2	36.0	25	9	AA877944	AA877944	0101B01.8
C 412	7.2	36.0	20	17	A2581146	A2581146	1M0313E17	486	7.2	36.0	25	9	AA877944	AA877944	0101B01.8
C 413	7.2	36.0	20	17	A2587020	A2587020	1M0394B19	487	7.2	36.0	25	14	H93534	H93534	1M0029L01
C 414	7.2	36.0	20	17	A2662848	A2662848	1M0542K07	488	7.2	36.0	25	17	A2312923	A2312923	1M0029L01
C 415	7.2	36.0	20	17	A2775705	A2775705	2M0008P11	489	7.2	36.0	25	17	A2404619	A2404619	1M0173L20
C 416	7.2	36.0	20	17	A2859065	A2859065	2M0164F06	490	7.2	36.0	25	17	A2606849	A2606849	1M0429A06
C 417	7.2	36.0	20	17	TA18A08P	TA18A08P	1M0459S2.T. bruce1	491	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 418	7.2	36.0	20	17	TA207B03O	TA207B03O	1M0459S2.T. bruce1	492	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 419	7.2	36.0	20	17	TA345E06Q	TA345E06Q	1M0459S2.T. bruce1	493	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 420	7.2	36.0	20	17	A2341757	A2341757	1M0074P18	494	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 421	7.2	36.0	21	17	A2342282	A2342282	1M0075H14	495	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 422	7.2	36.0	21	17	A2345496	A2345496	1M0080F03	496	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 423	7.2	36.0	21	17	A2462647	A2462647	1M0269N08	497	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 424	7.2	36.0	21	17	A2626965	A2626965	1M0467E15	498	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 425	7.2	36.0	21	17	A26633083	A26633083	1M0504H14	499	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 426	7.2	36.0	21	17	A2767674	A2767674	2M0034H14	500	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 427	7.2	36.0	22	9	A1032023	A1032023	OW68A04.x	501	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 428	7.2	36.0	22	13	BG928486	BG928486	HNC48-1.H	502	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 429	7.2	36.0	22	14	C21207	C21207	HUMGS000223	503	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 430	7.2	36.0	22	17	A2314013	A2314013	1M0030C08	504	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 431	7.2	36.0	22	17	A2341756	A2341756	1M0074P17	505	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 432	7.2	36.0	22	17	A2396435	A2396435	1M0161C03	506	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 433	7.2	36.0	22	17	A2447653	A2447653	1M0238C08	507	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 434	7.2	36.0	22	17	A2488753	A2488753	1M0319M12	508	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 435	7.2	36.0	22	17	A2598225	A2598225	1M0412K22	509	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 436	7.2	36.0	22	17	A2772718	A2772718	1M0583O13	510	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 437	7.2	36.0	22	17	A2864903	A2864903	2M0174E13	511	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 438	7.2	36.0	22	17	TA119B07P	TA119B07P	1M0467E15	512	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 439	7.2	36.0	22	17	TA197A04Q	TA197A04Q	1M0467E15	513	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 440	7.2	36.0	23	14	D18240	D18240	MUGSG00520	514	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 441	7.2	36.0	23	14	D19998	D19998	HUMGS00968	515	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 442	7.2	36.0	23	17	A2307555	A2307555	1M0009M19	516	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 443	7.2	36.0	23	17	A2387178	A2387178	1M0146K19	517	7.2	36.0	25	17	A2641910	A2641910	1M0504N09
C 444	7.2	36.0	23	17	A2393604	A2393604	1M0156C14	517	7.2	36.0	25	17	A2641910	A2641910	1M0504N09

518	7	35.0	19	17	A2991531	A2991531	2M0275K15	591	7	35.0	24	17	A2864947	A2864947	2M0174N14
519	7	35.0	20	10	AM246466	AM246466	2821777.3	592	7	35.0	24	17	A2866692	A2866692	2M0177P18
520	7	35.0	20	17	A2307088	A2307088	1M0008M23	593	7	35.0	24	17	BH790798	BH790798	AL790798
521	7	35.0	20	17	A2339957	A2339957	1M0071K07	594	7	35.0	24	17	TA161D07P	TA161D07P	AL761D07P
522	7	35.0	20	17	A2445437	A2445437	1M0241B16	595	7	35.0	24	17	TA245F07P	TA245F07P	AL745F07P
523	7	35.0	20	17	A2456534	A2456534	1M0259L03	596	7	35.0	25	9	AA918137	AA918137	on46502.8
524	7	35.0	20	17	A2478502	A2478502	1M0298B09	597	7	35.0	25	9	AA1127762	AA1127762	CG31d01.x
525	7	35.0	20	17	A2479732	A2479732	1M0300A09	598	7	35.0	25	9	AA1181406	AA1181406	UC59404.x
526	7	35.0	20	17	A2479985	A2479985	1M0301C08	599	7	35.0	25	9	AA1181643	AA1181643	UB79408.x
527	7	35.0	20	17	A2588882	A2588882	1M03397D02	600	7	35.0	25	9	AA199484	AA199484	CO02609.x
528	7	35.0	20	17	A2654725	A2654725	1M0497D02	601	7	35.0	25	13	BM400178	BM400178	5009-0.68
529	7	35.0	20	17	A2653794	A2653794	1M05290C3	602	7	35.0	25	14	CO1243	CO1243	HUMG500796
530	7	35.0	20	17	A2660921	A2660921	1M0539E18	603	7	35.0	25	17	A2307549	A2307549	1M0009J24
531	7	35.0	20	17	A2776807	A2776807	2M0010H14	604	7	35.0	25	17	A2324338	A2324338	1M0046D14
532	7	35.0	20	17	A2809111	A2809111	2M0072P23	605	7	35.0	25	17	A2336975	A2336975	1M0067A03
533	7	35.0	20	17	A2827842	A2827842	2M0104F03	606	7	35.0	25	17	A2391004	A2391004	1M0152U17
534	7	35.0	20	17	A2891405	A2891405	2M0275004	607	7	35.0	25	17	A2654166	A2654166	1M0528M12
535	7	35.0	21	9	AU112051	AU112051	AU112051	608	7	35.0	25	17	A2785568	A2785568	2M0029K02
536	7	35.0	21	9	AU112155	AU112155	AU112155	609	7	35.0	25	17	A2809149	A2809149	2M0073G05
537	7	35.0	21	17	A2312710	A2312710	1M0028P04	610	7	35.0	25	17	A2816517	A2816517	2M0085N20
538	7	35.0	21	17	A2823340	A2823340	1M0460021	611	7	35.0	25	17	A2984054	A2984054	2M0272H13
539	7	35.0	21	17	A2860221	A2860221	1M0538M09	612	7	35.0	25	17	A2993079	A2993079	2M0277P20
540	7	35.0	21	17	A2795028	A2795028	2M0049L03	613	7	35.0	25	17	A2998093	A2998093	2M0284D21
541	7	35.0	21	17	A2806440	A2806440	2M0068B05	614	7	35.0	25	17	BH759548	BH759548	KG04960-5
542	7	35.0	21	17	TA185E09P	TA185E09P	AL474070 T. Brucei	615	7	35.0	25	17	BH789667	BH789667	SALK_0423
543	7	35.0	22	9	AA928512	AA928512	on17G11.8	616	7	35.0	25	17	BH855488	BH855488	SALK_0850
544	7	35.0	22	9	AA978189	AA978189	OP33C10.8	617	7	35.0	25	17	TA185D02P	TA185D02P	T. Brucei
545	7	35.0	22	9	AI016967	AI016967	ou27H03.x	618	7	35.0	25	17	AM059513	AM059513	HUTR.BaBe
546	7	35.0	22	9	AI080445	AI080445	ox82d10.8	619	7	35.0	25	17	BH754332	BH754332	AL154875
547	7	35.0	22	9	AI226666	AI226666	uj13C01.Y	620	7	35.0	25	17	AI154875	AI154875	u80E0F4.x
548	7	35.0	22	13	BG927952	BG927952	HNCA5-1-F	621	7	35.0	25	17	AI695666	AI695666	cx60F06.x
549	7	35.0	22	13	BG928008	BG928008	HNCA5-1-H	622	7	35.0	25	17	BG900981	BG900981	HOA52-1-D
550	7	35.0	22	13	BG928097	BG928097	HNCA6-1-C	623	7	35.0	25	17	BG928060	BG928060	HNCA1-1-G
551	7	35.0	22	17	A2346298	A2346298	1M0081B18	624	7	35.0	25	17	A249856	A249856	2821566.3
552	7	35.0	22	17	A2407386	A2407386	1M0178K06	625	7	35.0	25	17	AM250449	AM250449	AM250449
553	7	35.0	22	17	A248244	A248244	1M0245M15	626	7	35.0	25	17	AA916934	AA916934	on14A09.8
554	7	35.0	22	17	A2483833	A2483833	1M0310H03	627	7	35.0	25	17	AA934303	AA934303	SMOVL3CAN
555	7	35.0	22	17	A2582417	A2582417	1M0374N13	628	7	35.0	25	17	AA934303	AA934303	SMOVL3CAN
556	7	35.0	22	17	A2590903	A2590903	1M0400B15	629	7	35.0	25	17	AA977115	AA977115	OG24C08.8
557	7	35.0	22	17	A2623338	A2623338	1M0460019	630	7	35.0	25	17	AI004427	AI004427	OG26D01.8
558	7	35.0	22	17	A2761113	A2761113	1M0555G13	631	7	35.0	25	17	AI120725	AI120725	UB72B11.x
559	7	35.0	22	17	A2812224	A2812224	2M0078G13	632	7	35.0	25	17	A2309987	A2309987	AM063940
560	7	35.0	22	17	A2854429	A2854429	2M0157C14	633	7	35.0	25	17	A2323986	A2323986	DP0975 KR
561	7	35.0	22	17	TA118E05P	TA118E05P	AL463374 T. Brucei	634	7	35.0	25	17	A2338061	A2338061	AM0018K04
562	7	35.0	22	17	TA215E06P	TA215E06P	AL479258 T. Brucei	635	7	35.0	25	17	A2375581	A2375581	AM0045P09
563	7	35.0	22	17	TA245C11P	TA245C11P	AL483574 T. Brucei	636	7	35.0	25	17	A2439162	A2439162	AM0534C03
564	7	35.0	23	9	AU254983	AU254983	AU254983	637	7	35.0	25	17	A2449942	A2449942	AM0543D15
565	7	35.0	23	9	AU264172	AU264172	AU264172	638	7	35.0	25	17	A2450047	A2450047	AM0659N12
566	7	35.0	23	17	A2341368	A2341368	1M0073L05	639	7	35.0	25	17	A2617087	A2617087	AM0048M12
567	7	35.0	23	17	A2357282	A2357282	1M0098A16	640	7	35.0	25	17	A2635086	A2635086	AM0491P17
568	7	35.0	23	17	A2417030	A2417030	1M0192H05	641	7	35.0	25	17	A2635848	A2635848	AM0529C20
569	7	35.0	23	17	A2418429	A2418429	1M0194F02	642	7	35.0	25	17	A2657651	A2657651	AM0543C03
570	7	35.0	23	17	A2479801	A2479801	1M0300G16	643	7	35.0	25	17	A2663881	A2663881	AM0543D15
571	7	35.0	23	17	A2613963	A2613963	1M0442K06	644	7	35.0	25	17	A2769244	A2769244	AM0659N12
572	7	35.0	23	17	A2634998	A2634998	1M0491B10	645	7	35.0	25	17	A2777644	A2777644	AM0012M24
573	7	35.0	23	17	A2655243	A2655243	1M0530D07	646	7	35.0	25	17	A2784639	A2784639	2M00927B10
574	7	35.0	23	17	A2762870	A2762870	1M0558C14	647	7	35.0	25	17	A2805949	A2805949	2M0067F07
575	7	35.0	23	17	A2768060	A2768060	1M0567P13	648	7	35.0	25	17	A2805995	A2805995	2M0067F13
576	7	35.0	23	17	A2772591	A2772591	1M0583P03	649	7	35.0	25	17	A2818421	A2818421	2M0088M19
577	7	35.0	23	17	A2779607	A2779607	1M0501E18	650	7	35.0	25	17	A28130578	A28130578	2M0109H23
578	7	35.0	23	17	A2807926	A2807926	2M0071C09	651	7	35.0	25	17	A2865832	A2865832	2M0176D09
579	7	35.0	23	17	A2824304	A2824304	2M0098N17	652	7	35.0	25	17	A2865832	A2865832	2M0176D09
580	7	35.0	23	17	BH792865	BH792865	SALK_0651	653	7	35.0	25	9	AL695159	AL695159	AL695159
581	7	35.0	23	17	TA122H08P	TA122H08P	AL462672 T. Brucei	654	7	35.0	25	9	AU257355	AU257355	AU257355
582	7	35.0	24	17	A2316663	A2316663	1M0034G22	655	7	35.0	25	9	AU257355	AU257355	AU257355
583	7	35.0	24	17	A2324350	A2324350	1M0046F14	656	7	35.0	25	14	BO789787	BO789787	hag6002AB
584	7	35.0	24	17	A2331594	A2331594	1M0059D12	657	7	35.0	25	17	A2345926	A2345926	1M0009T16
585	7	35.0	24	17	A2351302	A2351302	1M0089T17	658	7	35.0	25	17	A2345926	A2345926	1M0080T23
586	7	35.0	24	17	A2411813	A2411813	1M0185H03	659	7	35.0	25	17	A2366205	A2366205	1M0118L07
587	7	35.0	24	17	A2440877	A2440877	1M0232K11	660	7	35.0	25	17	A2404469	A2404469	1M0172A15
588	7	35.0	24	17	A2505865	A2505865	1M0346C18	661	7	35.0	25	17	A2436106	A2436106	1M0233H07
589	7	35.0	24	17	A2586934	A2586934	1M0394B13	662	7	35.0	25	17	A2448577	A2448577	1M0245A22
590	7	35.0	24	17	A2760063	A2760063	1M0553A04	663	7	35.0	25	17	A2449127	A2449127	1M0247A17

C 664	6.8	34.0	20	17	AZ467382	AZ467332	1M0278C14	737	6.8	34.0	22	17	AZ806598	AZ806598	2M0068G16
C 665	6.8	34.0	20	17	AZ468701	AZ468712	1M0281A18	738	6.8	34.0	22	17	AZ824702	AZ824702	2M0099P20
C 666	6.8	34.0	20	17	AZ469472	AZ469472	1M0283A06	739	6.8	34.0	22	17	AZ829109	AZ829109	2M0106L03
C 667	6.8	34.0	20	17	AZ490187	AZ490187	1M0323E06	740	6.8	34.0	22	17	AZ831937	AZ831937	2M0111P22
C 668	6.8	34.0	20	17	AZ514794	AZ514794	1M0361C13	741	6.8	34.0	22	17	BH852180	BH852180	SA1K 0742
C 669	6.8	34.0	20	17	AZ611386	AZ611386	1M0437N08	742	6.8	34.0	22	17	TA175C05P	TA175C05P	AL475133 T. brucei
C 670	6.8	34.0	20	17	AZ622553	AZ622553	1M0459C04	743	6.8	34.0	22	17	TA259N06P	TA259N06P	AL484347 T. brucei
C 671	6.8	34.0	20	17	AZ654458	AZ654458	1M0528G10	744	6.8	34.0	22	17	TA28BD10	TA28BD10	AL453252 T. brucei
C 672	6.8	34.0	20	17	AZ660043	AZ660043	1M0537E20	745	6.8	34.0	22	17	TA327G01Q	TA327G01Q	AL493268 T. brucei
C 673	6.8	34.0	20	17	AZ660124	AZ660124	1M0538F03	746	6.8	34.0	22	17	TA348C12Q	TA348C12Q	AL496112 T. brucei
C 674	6.8	34.0	20	17	AZ759844	AZ759844	1M0553C04	747	6.8	34.0	23	17	AZ333226	1M0662P12	AZ333226 1M0662P12
C 675	6.8	34.0	20	17	AZ769811	AZ769811	1M0570B23	748	6.8	34.0	23	17	AZ335717	AZ335717	AZ335717 1M0665J20
C 676	6.8	34.0	20	17	AZ785549	AZ785549	2M0029F01	749	6.8	34.0	23	17	AZ398730	AZ398730	1M0164F15
C 677	6.8	34.0	20	17	AZ788116	AZ788116	2M0035E06	750	6.8	34.0	23	17	AZ442542	AZ442542	1M0226P11
C 678	6.8	34.0	20	17	AZ795472	AZ795472	2M0049A14	751	6.8	34.0	23	17	AZ460491	AZ460491	1M0265A21
C 679	6.8	34.0	20	17	AZ795800	AZ795800	2M0051P08	752	6.8	34.0	23	17	AZ468097	AZ468097	1M0279K22
C 680	6.8	34.0	20	17	AZ799305	AZ799305	2M0056N05	753	6.8	34.0	23	17	AZ480535	1M0302E10	AZ480535 1M0302E10
C 681	6.8	34.0	20	17	AZ816496	AZ816496	2M0085G16	754	6.8	34.0	23	17	AZ493087	1M0327L24	AZ493087 1M0327L24
C 682	6.8	34.0	20	17	AZ828544	AZ828544	2M0105O04	755	6.8	34.0	23	17	AZ495857	1M0331P21	AZ495857 1M0331P21
C 683	6.8	34.0	20	17	AZ845673	AZ845673	2M0145N04	756	6.8	34.0	23	17	AZ582153	1M0374B24	AZ582153 1M0374B24
C 684	6.8	34.0	20	17	AZ946089	AZ946089	2M0207A13	757	6.8	34.0	23	17	AZ584523	1M0389C10	AZ584523 1M0389C10
C 685	6.8	34.0	20	17	TA339D11Q	TA339D11Q	AL492597 T. brucei	758	6.8	34.0	23	17	AZ609822	1M0434J13	AZ609822 1M0434J13
C 686	6.8	34.0	21	17	AZ375798	AZ375798	1M0203E03	759	6.8	34.0	23	17	AZ622923	1M0460J05	AZ622923 1M0460J05
C 687	6.8	34.0	21	17	AZ440095	AZ440095	1M0212C02	760	6.8	34.0	23	17	AZ659339	1M0536I07	AZ659339 1M0536I07
C 688	6.8	34.0	21	17	AZ433959	AZ433959	1M0230B12	761	6.8	34.0	23	17	AZ666452	1M0548A07	AZ666452 1M0548A07
C 689	6.8	34.0	21	17	AZ452622	AZ452622	1M0259C08	762	6.8	34.0	23	17	AZ771926	1M0574P20	AZ771926 1M0574P20
C 690	6.8	34.0	21	17	AZ471259	AZ471259	1M0287F21	763	6.8	34.0	23	17	AZ775677	2M0008F10	AZ775677 2M0008F10
C 691	6.8	34.0	21	17	AZ482019	AZ482019	1M0306I17	764	6.8	34.0	23	17	AZ783377	2M0025I04	AZ783377 2M0025I04
C 692	6.8	34.0	21	17	AZ483617	AZ483617	1M0309A05	765	6.8	34.0	23	17	AZ785098	2M0028N07	AZ785098 2M0028N07
C 693	6.8	34.0	21	17	AZ490638	AZ490638	1M0323B13	766	6.8	34.0	23	17	AZ785926	2M0030X08	AZ785926 2M0030X08
C 694	6.8	34.0	21	17	AZ521072	AZ521072	1M0454M05	767	6.8	34.0	23	17	AZ789371	2M0033L01	AZ789371 2M0033L01
C 695	6.8	34.0	21	17	AZ623540	AZ623540	1M0461G23	768	6.8	34.0	23	17	AZ800969	2M0059D17	AZ800969 2M0059D17
C 696	6.8	34.0	21	17	AZ657958	AZ657958	1M0534B02	769	6.8	34.0	23	17	AZ807263	2M0070C02	AZ807263 2M0070C02
C 697	6.8	34.0	21	17	AZ665302	AZ665302	1M0546J09	770	6.8	34.0	23	17	AZ807926	2M0071C09	AZ807926 2M0071C09
C 698	6.8	34.0	21	17	AZ781467	AZ781467	2M0019F23	771	6.8	34.0	23	17	AZ808894	2M0072G09	AZ808894 2M0072G09
C 699	6.8	34.0	21	17	AZ782494	AZ782494	2M0022I23	772	6.8	34.0	23	17	AZ834916	2M0177C22	AZ834916 2M0177C22
C 700	6.8	34.0	21	17	AZ796355	AZ796355	2M0052I06	773	6.8	34.0	23	17	AZ840308	2M0136H12	AZ840308 2M0136H12
C 701	6.8	34.0	21	17	AZ799765	AZ799765	2M0057I20	774	6.8	34.0	23	17	AZ844206	2M0143I11	AZ844206 2M0143I11
C 702	6.8	34.0	21	17	AZ800744	AZ800744	2M0058K24	775	6.8	34.0	23	17	AZ844951	2M0144H22	AZ844951 2M0144H22
C 703	6.8	34.0	21	17	AZ806440	AZ806440	2M0068B05	776	6.8	34.0	23	17	AZ853913	2M0219D19	AZ853913 2M0219D19
C 704	6.8	34.0	21	17	AZ812038	AZ812038	2M0078C22	777	6.8	34.0	23	17	AZ891550	2M0275O18	AZ891550 2M0275O18
C 705	6.8	34.0	21	17	AZ821784	AZ821784	2M0094N09	778	6.8	34.0	23	17	BH846974	SA1K 0122	BH846974 SA1K 0122
C 706	6.8	34.0	21	17	AZ933804	AZ933804	2M0279D05	779	6.8	34.0	23	17	TA164G12Q	AL463175 T. brucei	TA164G12Q AL463175 T. brucei
C 707	6.8	34.0	22	9	AA885905	AA885905	oj19h02.8	780	6.8	34.0	23	17	TA251E06Q	AL482245 T. brucei	TA251E06Q AL482245 T. brucei
C 708	6.8	34.0	22	9	AA931331	AA931331	o06c03.8	781	6.8	34.0	23	17	TA260H01P	AL485135 T. brucei	TA260H01P AL485135 T. brucei
C 709	6.8	34.0	22	9	AA998033	AA998033	o0a1d04.8	782	6.8	34.0	23	17	TA338B01P	AL493153 T. brucei	TA338B01P AL493153 T. brucei
C 710	6.8	34.0	22	9	AI021002	AI021002	ua98e09.x	783	6.8	34.0	23	17	TA88A08P	AL495996 T. brucei	TA88A08P AL495996 T. brucei
C 711	6.8	34.0	22	9	AI057600	AI057600	ov31d12.x	784	6.8	34.0	23	9	AL047412	DKFZP586E	AL047412 DKFZP586E
C 712	6.8	34.0	22	9	AI174110	AI174110	v287d11.x	785	6.8	34.0	24	9	AL585768	AL585768	AL585768 AL585768
C 713	6.8	34.0	22	9	AI569444	AI569444	cn86n06.x	786	6.8	34.0	24	9	AU257684	AU257684	AU257684 AU257684
C 714	6.8	34.0	22	9	AI687266	AI687266	cp94d10.x	787	6.8	34.0	24	13	BM3599103	BM3599103	BM3599103 5009-0-53
C 715	6.8	34.0	22	9	AU259732	AU259732	AU259732	788	6.8	34.0	24	14	D18741	D18741	D18741 MUSGS01803
C 716	6.8	34.0	22	17	AZ310074	AZ310074	1M0018I15	789	6.8	34.0	24	17	AZ308225	1M0011B06	AZ308225 1M0011B06
C 717	6.8	34.0	22	17	AZ345644	AZ345644	1M0080J22	790	6.8	34.0	24	17	AZ314798	1M0031G16	AZ314798 1M0031G16
C 718	6.8	34.0	22	17	AZ462988	AZ462988	1M0080B18	791	6.8	34.0	24	17	AZ338159	1M0069C11	AZ338159 1M0069C11
C 719	6.8	34.0	22	17	AZ407386	AZ407386	1M0178K06	792	6.8	34.0	24	17	AZ374821	1M0127G19	AZ374821 1M0127G19
C 720	6.8	34.0	22	17	AZ459715	AZ459715	1M0264E13	793	6.8	34.0	24	17	AZ510127	1M0354L21	AZ510127 1M0354L21
C 721	6.8	34.0	22	17	AZ468023	AZ468023	1M0279L15	794	6.8	34.0	24	17	AZ514486	1M0361F23	AZ514486 1M0361F23
C 722	6.8	34.0	22	17	AZ468023	AZ468023	1M0279L15	795	6.8	34.0	24	17	AZ514503	1M0361J19	AZ514503 1M0361J19
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C 731	6.8	34.0	22	17	AZ655943	AZ655943	1M0531M12	804	6.8	34.0	24	17	AZ807619	2M0070001	AZ807619 2M0070001
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C 988	6.6	33.0	25	17	Ta131D07P	A146356 T. brucei	
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ALIGNMENTS

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; mRNA sequence.
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KEYWORDS EST.
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ORGANISM Homo sapiens
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REFERENCE 1 (bases 1 to 25)
AUTHORS   NCIC-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
COMMENT   Unpublished (1997)
            Contact: Robert Straubeberg, Ph.D.
            Email: cgabs-remail.nih.gov.
            This clone is available royalty-free through LNLN ; contact the
            IMAGE Consortium (info@image.lnl.gov) for further information.
            Trace considered overall poor quality
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RESULT 1
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AU256704
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EST.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Kato, K. and Maroba, R.
Generation of expressed sequence tags from mouse brain
Unpublished (2002)
Contact: Kikuya Kato

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
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Fax: 81-743-72-5589
Email: kkatc@bs.nist-nara.ac.jp

BASE COUNT	2	a	4	c	5	g	14	t
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ACCESSION BBD0010829 3', mRNA sequence.
VERSION AU257541
KEYWORDS AU257541.1 GI:20322263
SOURCE EST.
ORGANISM house mouse.
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Kato, K. and Matsuba, R.
Generation of expressed sequence tags from mouse brain.
Unpublished (2002)
Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkatob@nara.ac.jp
URL: http://love2.alst-nara.ac.jp/BBD/index.html.
Location/Qualifiers

FEATURES
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ACCESSION md0270 3', mRNA sequence.
VERSION D18747
KEYWORDS D18747.1 GI:1100716
SOURCE EST.
ORGANISM western European house mouse.
Mus musculus domesticus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Kawamoto, S., Okubo, K., Yoshii, J., Katsuki, M. and Matsubara, K.
Analysis of gene expression in mouse embryogenesis by 3'-directed cDNA sequencing
Unpublished (1995)
Contact: Kawamoto, S., Okubo, K., Yoshii, J., Katsuki, M. and Matsubara, K.
Institute for Cellular and Molecular Biology
Osaka University
3-1 Yamada-oka, Suita, Osaka 565, Japan.
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20 TTTGCTTTGACAC 7

RESULT 5
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ACCESSION AZ779522
VERSION AZ779522.1 GI:12910259
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, F., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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/db_xref="taxon:10090"
/clone="UUCG2M0016K03"
/clone_lib="Mouse 10kb plasmid UUCGM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/note="Vector: PMD42uv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnarep/). The DNA was hydronically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF19072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 10 a 6 c 3 g 3 t

Query Match 53.0%; Score 10.6; DB 17; Length 22;
Best Local Similarity 76.5%; Pred. No. 3e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 TTTCGCTTGCACCTCA 17
19 TTTCGCTTGCACCTCA 3

RESULT 6
LOCUS A2625339 19 bp DNA linear GSS 13-DEC-2000
DEFINITION M0464F13R Mouse 10kb plasmid UGCM library Mus musculus genomic
clone UGCM0464F13 R, DNA sequence.

ACCESSION A2625339 GI:11747529
VERSION A2625339.1
KEYWORDS GSS.

SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Kelly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weis, R.
COMMENT Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0464 row: F column: 13
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES
source

1..19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM0464F13"
/clone_1lb="Mouse 10kb plasmid UGCM library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114[g14732114]g14732114), a copy-number inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 2 c 6 g 7 t

Query Match 50.0%; Score 10; DB 17; Length 19;
Best Local Similarity 72.2%; Pred. No. 5.6e+05;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 3 TTTCGCTTGCACCTCAGAG 20
2 TTTCGCTTGCACCTCAGAG 19

RESULT 7
LOCUS AU254819 21 bp mRNA linear EST 25-APR-2002
DEFINITION AU254819 3'-directed mouse cDNA library Mus musculus cDNA clone BED0003462 3', mRNA sequence.

ACCESSION AU254819 GI:20316963
VERSION AU254819.1
KEYWORDS EST.

SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)
AUTHORS Kato, K. and Matoba, R.
TITLE Generation of expressed sequence tags from mouse brain
JOURNAL Unpublished (2002)
COMMENT Contact: Rikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takeyama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkatobds.aist-nara.ac.jp, BED/index.html.
URL: http://love2.aist-nara.ac.jp/BED/index.html.
Location/Qualifiers

FEATURES
source

1..21
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="BED0003462"
/clone_1lb="3'-directed mouse cDNA library"
/tissue type="brain"
/note="Vector: pGEM-T-easy"
BASE COUNT 12 a 3 c 3 g 2 t 1 others
ORIGIN

Query Match 50.0%; Score 10; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTTCGCTTGG 10
13 TTTCGCTTGG 4

RESULT 8
LOCUS A2785704 21 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0029C21R Mouse 10kb plasmid UGCM library Mus musculus genomic clone UGCM2M0029C21 R, DNA sequence.

ACCESSION A2785704 GI:12922730
VERSION A2785704.1
KEYWORDS GSS.

SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weis
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0029 row: C column: 21
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers
 1..21
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U06C2M029C21"
 /clone_id="Mouse 10kb plasmid U06C1M library"
 /sex="Male"
 /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 4 c 7 g 6 t
 ORIGIN
 Query Match 50.0%; Score 10; DB 17; Length 21;
 Best Local Similarity 72.2%; Pred. No. 5.8e+05;
 Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 TGGCTTGGCACTCAGAG 20
 |||||
 1 TGGGTTTACACACCGAG 18
 Db
 RESULT 9
 BH813511 24 bp DNA linear GSS 02-MAY-2002
 LOCUS SALK_064374 Arabidopsis thaliana TDNA insertion lines Arabidopsis
 DEFINITION thaliana genomic clone SALK_064374, DNA sequence.
 ACCESSION BH813511
 VERSION BH813511.1 GI:20392116
 KEYWORDS GSS.
 SOURCE chae cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE 1 (bases 1 to 24)
 AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadtrind,C., Jeske,E.A., Kanes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J., and Becker,J.R.
 TITLE A Sequence-indexed library of Insertion Mutations in the Arabidopsis Genome
 JOURNAL Unpublished (2001)
 COMMENT Contact: Joseph R. Becker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At1g60590.
 Class: TDNA tagged.
 Location/Qualifiers
 1..24
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_064374"
 /clone_id="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html.

BASE COUNT 7 a 4 c 3 g 10 t
 ORIGIN
 Query Match 50.0%; Score 10; DB 17; Length 24;
 Best Local Similarity 72.2%; Pred. No. 6e+05;
 Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 TGGCTTGGCACTCAGAG 20
 |||||
 3 TGGTTTACACACTGAGT 20
 Db
 RESULT 10
 A2762000 24 bp DNA linear GSS 16-FEB-2001
 LOCUS 1M0556F08R Mouse 10kb plasmid U06C1M library Mus musculus genomic
 DEFINITION clone U06C1M0556F08 R, DNA sequence.
 ACCESSION A2762000
 VERSION A2762000.1 GI:12871547
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 24)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weis
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0556 row: F column: 08

Seq primer: CACACAGGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers

FEATURES

source

1..24
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0556F08"
 /clone_1ib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: FMD2mv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD22 (G1473214|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

7 a 7 c 5 g 5 t

Query Match 49.0%; Score 9.8; DB 17; Length 24;
 Best Local Similarity 84.6%; Pred. No. 7.6e+05;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TTGGCCTTGCAC 19
 |||||
 DB 9 TCTGCCACACAGA 21

RESULT 11

TA259G080/c 24 bp DNA linear GSS 13-DEC-2000
 DEFINITION T. brucei sheared genomic DNA clone 259G08, reverse sequence.

ACCESSION AL488403
 VERSION AL488403.1 GI:11863797

KEYWORDS GSS
 SOURCE Trypanosoma brucei.
 ORGANISM Trypanosoma brucei
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE 1 (bases 1 to 24)
 Hall N., Bowman S., Lennard N.J., Doggett J., Atkin R.,
 Chillingworth C., Ormond D., Harris B., El-Sayed N., Hou L.,
 Melville S.E., Rajandream M.A. and Barrett B.G.

TITLE Direct SubMISSION
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nhls@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vardín and B.
 Barrell, Oxford University Press, 1999).

Email: neilsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES

source

1..24
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="259G08"

BASE COUNT

9 a 5 c 7 g 3 t

Query Match 49.0%; Score 9.8; DB 17; Length 24;
 Best Local Similarity 84.6%; Pred. No. 7.6e+05;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGGCCTTGCAC 14
 |||||
 DB 19 TCGCGTTGACTC 7

RESULT 12

AA916047/c 22 bp mRNA linear EST 29-APR-1998
 LOCUS AA916047
 DEFINITION OG30d01.s1 NCI CGAP Br7 Homo sapiens CDNA clone IMAGE:1441345 3'
 similar to SW:RL34_HUMAN P49207 60S RIBOSOMAL PROTEIN L34. ;, mRNA
 sequence.

ACCESSION AA916047
 VERSION AA916047.1 GI:3055439
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 22)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 unknown library type
 Insert Length: 502
 Insert Length: 502
 Std Error: 0.00
 Seg primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 1.

FEATURES

source

1..22
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1441345"
 /clone_1ib="NCI CGAP Br7"
 /lab_host="DH10B"
 /note="Organ: breast; Vector: pCMV-SPORT4; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.2 kb. Life Technologies catalog
 #:10985-018"

BASE COUNT 5 a 5 c 7 g 5 t

ORIGIN

Query Match 48.0%; Score 9.6; DB 9; Length 22;
 Best Local Similarity 75.0%; Pred. No. 9.3e+05;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GCGTTGGCCTCACA 19
 |||||
 DB 17 GCGTTGACATACGA 2

RESULT 13

AZ592068 22 bp DNA linear GSS 13-DEC-2000
 LOCUS AZ592068
 DEFINITION IM0402H08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0402H08 R, DNA sequence.

ACCESSION	A2592068
VERSION	A2592068.1
KEYWORDS	GI:11714258
SOURCE	
ORGANISM	house mouse.
REFERENCE	Mus musculus.
AUTHORS	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus. 1 (bases 1 to 22)
TITLE	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: dunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0402 row: H column: 08 Seq primer: CACACAGCAACACCTATGACC Class: plasmid end High quality sequence stop: 22. Location/Qualifiers 1..22
FEATURES	
SOURCE	

/organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U06C1M0402H08"
 /clone_id="Mouse 10kb plasmid U06C1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repated with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g11473114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ACCESSION	AZ771198
VERSION	AZ771198.1
KEYWORDS	GI:12893200
SOURCE	GSS.
ORGANISM	house mouse.
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingy,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL	Plasmid inserts
COMMENT	Unpublished (2000)
	Contact: Robert B. Weiss
	University of Utah Genome Center
	University of Utah
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT 84112, USA
	Tel: 801 585 5606
	Fax: 801 585 7177
	Email: ddunn@genetics.utah.edu
	Insert Length: 10000
	Std Error: 0.00
	Plate: 0573
	row: M
	column: 08
	Seq primer: CGTTGTAACGACGCGCCACT
	Class: plasmid ends
FEATURES	High quality sequence stop: 22.
source	Location/Qualifiers
	1..22

```

BASE COUNT
ORIGIN
1
a
9
c
2
g
10
t
c
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0573M08"
/clone_1b="UUGC1M0573M08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PMD42ny. Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14f22114[gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

ACCESSION AL480269
 VERSION AL480269.1 GI:11846049
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei.
 ORGANISM Trypanosoma brucei
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 REFERENCE 1 (bases 1 to 22)
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
 COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nh@sanger.ac.uk
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers
 FEATURES
 source
 1..22
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="223e07"
 BASE COUNT 9 a 1 c 12 g 0 t
 ORIGIN
 Query Match 48.0%; Score 9.6; DB 17; Length 22;
 Best Local Similarity 75.0%; Pred. No. 9.3e+05;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 TTGGCTTGCCACTC 16
 |||||
 16 TTTCCTTTTCCCTC 1
 RESULT 16
 TA202H10/c
 LOCUS 23 bp DNA linear GSS 13-DEC-2000
 DEFINITION T. brucei sheared genomic DNA clone 202h11, reverse sequence,
 genomic survey sequence.
 ACCESSION AL477083
 VERSION AL477083.1 GI:11843538
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei.
 ORGANISM Trypanosoma brucei
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 REFERENCE 1 (bases 1 to 23).
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
 COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small

Insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nh@sanger.ac.uk
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers
 FEATURES
 source
 1..23
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="202h11"
 BASE COUNT 9 a 8 c 4 g 2 t
 ORIGIN
 Query Match 48.0%; Score 9.6; DB 17; Length 23;
 Best Local Similarity 75.0%; Pred. No. 9.4e+05;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 TTGGCTTGCCACTC 16
 |||||
 21 TTGGGATGCCATTC 6
 RESULT 17
 BH64166
 LOCUS 25 bp DNA linear GSS 05-AUG-2002
 DEFINITION SALK_095483 Arabidopsis thaliana TDNA insertion lines Arabidopsis
 thaliana genomic clone SALK_095483, DNA sequence.
 ACCESSION BH64166
 VERSION BH64166.1 GI:22100064
 KEYWORDS GSS.
 SOURCE Thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 1 (bases 1 to 25)
 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadriab,
 C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.,
 Zimmerman, J., and Ecker, J.R.
 A Sequence-indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.
 Class: TDNA tagged.
 Location/Qualifiers
 FEATURES
 source
 1..25
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_095483"
 /note="Arabidopsis thaliana TDNA insertion lines"
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html
 BASE COUNT 6 a 3 c 3 g 13 t
 ORIGIN
 Query Match 48.0%; Score 9.6; DB 17; Length 25;
 Best Local Similarity 75.0%; Pred. No. 9.7e+05;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	1	TTTGGCGTTGCCACTC	16
Db	5	TTTCCGTTTGAATTC	20

RESULT 18	LOCUS	DEFINITION
BH864216	25 bp DNA	linear GSS 05-AUG-2002
BH864216	Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_095576, DNA sequence.	

REFERENCE	1 (bases 1 to 25)
AUTHORS	Alonso, J. M., Lejse, T. J., Barajas, P., Chen, H., Cheuk, R., Gadri nab

Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckers@salik.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.

BASE COUNT	ORIGIN
6 a	3 c
3 g	13 e

Query Match	48.0%	Score 9.6	DB 17	Length 25
Best Local Similarity	75.0%	Pred. No. 9.7e+05		
Matches	12	Conservative	0	Mismatches 4
				Indels 0
				Gaps 0
QY	1	TTTGGCTTGGCACTC	16	
Db	5	TTTCGGTTGGAATTC	20	

RESULT	19
AZ589990/c	
LOCUS	
DEFINITION	AZ589990 20 bp DNA linear GSS 13-DEC-2000 IM039016t Mouse 10kb plasmid UOUC1M library Mus musculus genomic clone UOUC1M039016 P, DNA sequence.
ACCESSION	AZ589990
VERSION	AZ589990.1 GI:11712180
KEYWORDS	GSS.
SOURCE	house mouse.
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE AUTHORS	
1 (bases 1 to 20)	
Dunn, D., Aoyagi, A.	

FEATURES	Location/Qualifiers
source	1. .20

BASE COUNT	3 a	5 c	7 g	5 t
ORIGIN				

Query March	47.0%;	Score 9.4;	DB 17;	Length 20;
Best Local Similarity	90.9%;	Pred. No. 1, 1e+06;		
Matches 10; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
OY	10	GCACCTCAGAG	20	
b	14	GCACCTCAGAG	4	

[illegible]

REFERENCE 1 (bases 1 to 21)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0078 row: O column: 22
 Seq primer: CGTTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers
 1..21
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCGM0078022"
 /clone_lib="Mouse 10kb plasmid UUCGM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1[4732114]bp[AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 7 c 6 g 5 t
 ORIGIN
 Query Match 47.0%; Score 9.4; DB 17; Length 21;
 Best Local Similarity 90.9%; Pred. No. 1.2e+06;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 10 GCCACTCAGAG 20
 14 GCCACTCAGAG 4
 RESULT 21
 AZ662093/c 22 bp DNA linear GSS 14-DEC-2000
 LOCUS IM0541C05F Mouse 10kb plasmid UUCGM library Mus musculus genomic
 DEFINITION clone UUCGM0541C05 F, DNA sequence.
 ACCESSION AZ662093
 VERSION AZ662093.1 GI:11799239
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0541 row: C column: 05
 Seq primer: CGTTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers
 1..22
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCGM0541C05"
 /clone_lib="Mouse 10kb plasmid UUCGM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1[4732114]bp[AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 6 c 7 g 8 t
 ORIGIN
 Query Match 47.0%; Score 9.4; DB 17; Length 22;
 Best Local Similarity 90.9%; Pred. No. 1.2e+06;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 10 GCCACTCAGAG 20
 22 GCCACTCAGAG 12
 RESULT 22
 AZ612609 24 bp DNA linear GSS 13-DEC-2000
 LOCUS AZ612609
 DEFINITION IM0439P23F Mouse 10kb plasmid UUCGM library Mus musculus genomic
 clone UUCGM0439P23 F, DNA sequence.
 ACCESSION AZ612609
 VERSION AZ612609.1 GI:11734715
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Baecorn, T., Duval, B., Hamil, C., Ismail, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A., and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0439 row: P column: 23
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1. .24
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0439P23"
/clone_11b="Mouse 10kb plasmid UUCG1M 1library"
/sex="Male"
/lab_host="E. Coli strain X110-Gold, T1-resistant, F-"
/note="vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnars/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerases and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 8 g 6 t
ORIGIN 7 c

Query Match 47.0%; Score 9.4; DB 17; Length 24;
Best Local Similarity 90.9%; Pred. No. 1.2e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 10 GCCACTCAGAG 20
|||||
Db 3 GCCACTCAG 13

RESULT 23
TA186D08P 24 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 186d08, forward sequence,
DEFINITION
ACCESSION AL475706
VERSION AL475706.1 GI:11841017
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE	1 (bases 1 to 24)
AUTHORS	Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., McVillie,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE	Direct Submision
JOURNAL	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhls@sanger.ac.uk
COMMENT	Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds M. Vaubin and B. Barrell, Oxford University Press, 1999).
FEATURES	Email: nels@edc.tigr.org Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/. Location/Qualifiers
SOURCE	1..24 /organism="Trypanosoma brucei" /strain="TREU927" /db_xref="taxon:5691" /clone="186d08"
BASE COUNT	g a 7 c 3 g 5 t
ORIGIN	
Query Match	47.0% Score 9.4; DB 17; Length 24;
Best Local Similarity	60.4%; Pred. No. 1.2e+06;
Matches	1; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Oy	2 TTGGCTTGCCACTCAGAC 20 6 TTGCGCAAAACACTCATRG 24
Db	
RESULT 24	
AZ405188	21 bp DNA linear GSS 03-OCT-2000
LOCUS	IM0173GISR Mouse 10kb plasmid UOUCIM libray Mus musculus genomic clone UOUCIM0173IS R, DNA sequence.
DEFINITION	AZ405188
ACCESSION	AZ405188.1 GI:10529201
VERSION	GSS.
KEYWORDS	house mouse. Mus musculus
SOURCE	Eukaryote; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ORGANISM	1 (bases 1 to 21) Dunn.D., Ayvagi,A., Barber.M., Beacorn,T., Duval.B., Hamil.C., Islam.H., Longacre.S., Mahmoud.M., Meenen,E., Pedersen.T., Reilly.M., Rose.M., Rose.R., Stokes.R., Tingey.A., von Niederhausern.A. and Wright,D., Weiss,R.
REFERENCE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
AUTHORS	Unpublished (2000)
TITLE	Contact: Robert B. Weiss
JOURNAL	University of Utah Genome Center
COMMENT	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5506 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0173 row: G column: 15 Seq primer: CACACGAGAACAAGCTATGACC Class: plasmid ends High quality sequence stop: 21. Location/Qualifiers
FEATURES	

source
1. .21
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGM0211D23"
/clone_1lb="Mouse 10kb plasmid UUCGM library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|gblAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 5 a 5 c 3 g 8 t
ORIGIN

Query Match 46.0%; Score 9.2; DB 17; Length 21;
Best Local Similarity 78.6%; Pred. No. 1.5e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 GTTTCCTGCTCAGA 19
|||||
4 GTTTCCTGCTCATA 17

Db 4 GTTTCCTGCTCATA 17

RESULT 27
A2583690 22 bp DNA linear GSS 13-DEC-2000
LOCUS A2583690
DEFINITION IM0378E1R Mouse 10kb plasmid UUCGM library Mus musculus genomic
clone UUCGM0378E16 R, DNA sequence.
ACCESSION A2583690
VERSION A2583690.1 GI:11703825
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
TITILE Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0378 row: E column: 16
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES

source
1. .22
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGM0378E16"
/clone_1lb="Mouse 10kb plasmid UUCGM library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|gblAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 10 a 2 c 7 g 3 t
ORIGIN

Query Match 46.0%; Score 9.2; DB 17; Length 22;
Best Local Similarity 78.6%; Pred. No. 1.5e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTCCTTTCCTC 14
|||||
22 TTTCCTTTCCTC 9

Db 22 TTTCCTTTCCTC 9

RESULT 28
A2634674 23 bp DNA linear GSS 13-DEC-2000
LOCUS A2634674
DEFINITION IM040A11R Mouse 10kb plasmid UUCGM library Mus musculus genomic
clone UUCGM040A11 R, DNA sequence.
ACCESSION A2634674
VERSION A2634674.1 GI:11756864
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
TITILE Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0490 row: A column: 11
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES

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source
1. .23
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C1M0490A11"
/clone_1lb="Mouse 10kb plasmid U06C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT      2 a      7 c      3 g      11 t
ORIGIN

Query Match      46.0%; Score 9.2; DB 17; Length 23;
Best Local Similarity 78.6%; Pred. No. 1.5e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 TTTGGCTTGGCCAC 14
Db      9 TTGAGTTTCTCTC 22

RESULT 29
LOCUS      AZ646716      23 bp      DNA      linear      GSS 14-DEC-2000
DEFINITION      IM0512D3R Mouse 10kb plasmid U06C1M library Mus musculus genomic
ACCESSION      AZ646716
VERSION      AZ646716.1 GI:11777462
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0512 row: D column: 23
Seq primer: CACACGGAACGCTATAC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
FEATURES

```

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source
1. .23
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C1M0512D3"
/clone_1lb="Mouse 10kb plasmid U06C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT      6 a      4 c      4 g      7 t
ORIGIN

Query Match      46.0%; Score 9.2; DB 17; Length 23;
Best Local Similarity 78.6%; Pred. No. 1.5e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      7 TTTGGCACTCAGAG 20
Db      3 TTACACACACAGAG 16

RESULT 30
LOCUS      A2418103      24 bp      DNA      linear      GSS 03-OCT-2000
DEFINITION      IM0194L03R Mouse 10kb plasmid U06C1M library Mus musculus genomic
ACCESSION      A2418103
VERSION      A2418103.1 GI:10542116
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0194 row: L column: 03
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
FEATURES

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source

1. 24

/organism="Mus musculus"

/strain="C57BL/6J"

/db xref="taxon:10090"

/clone="UUCGM0194L03"

/clone_1lb="Mouse 10kb plasmid UUCGM library"

/sex="Male"

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 10 a 4 c 4 g 6 t

ORIGIN

Query Match 46.0%; Score 9.2; DB 17; Length 24;

Best Local Similarity 78.6%; Pred. No. 1.5e+06;

Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 TTGGCCTCTGAG 20

Db 23 TCTGCCATTAGAG 10

RESULT 31

AZ829689

LOCUS 24 bp DNA linear GSS 30-FEB-2001

DEFINITION 2M0107222P Mouse 10kb plasmid UUCGM library Mus musculus genomic

ACCESSION AZ829689

VERSION AZ829689.1 GI:12999513

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weis

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0107 row: C column: 22

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 24.

Location/Qualifiers

source

1. 24

/organism="Mus musculus"

/strain="C57BL/6J"

/db xref="taxon:10090"

/clone="UUCGM0107C22"

/clone_1lb="Mouse 10kb plasmid UUCGM library"

/sex="Male"

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 7 c 6 g 5 t

ORIGIN

Query Match 46.0%; Score 9.2; DB 17; Length 24;

Best Local Similarity 78.6%; Pred. No. 1.5e+06;

Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 TTGGCCTCTGAG 20

Db 8 TTAGACACTGAG 21

RESULT 32

AZ379234/c

LOCUS 25 bp DNA linear GSS 02-OCT-2000

DEFINITION 1M0134P16F Mouse 10kb plasmid UUCGM library Mus musculus genomic

ACCESSION AZ379234

VERSION AZ379234.1 GI:10492934

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 25)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weis

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0134 row: P column: 16

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 25.

Location/Qualifiers

FEATURES

FEATURES

```

source
1. .25
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="U0610134P16"
/clone_lib="Mouse 10kb plasmid U0610134P16"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, Ti-resistant, F-."
/notes="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT      10 a      4 c      5 g      6 t
ORIGIN
Query Match      46.0%; Score 9.2; DB 17; Length 25;
Best Local Similarity 78.6%; Pred. No. 1.5e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      7 TTTGCCACTCAGAG 20
      |||||
      22 TTGCTCTCAGAG 9

RESULT 33
BH759341      25 bp      DNA      linear      GSS 12-MAR-2002
LOCUS      KG02510-3prime Drosophila melanogaster P[SUPOR-P] P element
DEFINITION      insertion lines Drosophila melanogaster genomic Sequence recovered
      from 3' end of P element, DNA sequence.
ACCESSION      BH759341
VERSION      BH759341.1 GI:19352580
KEYWORDS      GSS.
SOURCE      fruit fly.
      Drosophila melanogaster
      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
      Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
      Ephydroidea; Drosophilidae; Drosophila.
      1 (bases 1 to 25)
AUTHORS      Leiva, R., Hoskins, R., Liao, G., Morzen, N., Tsang, G., He, Y., Karpen
      G., Belter, H., Rubin, G. and Spradling, A.
      The Berkeley Drosophila Genome Project Gene Disruption Project
      Unpublished (2001)
TITLE      Contact: Gerald Rubin
      Berkeley Drosophila Genome Project
      University of California, Berkeley
      LSA Building, Berkeley, CA 94720-3200, USA
      Fax: 5106433947
      Email: gerry@fruitfly.berkeley.edu
      Sequence recovery method was inverse PCR.
      Sequence orientation is forward strand relative to 5' end of P
      element
      The P element insertion position is base 1 in the 25 bases. This
      insertion position refers to the first base of the 8 base target
      recognition sequence.
      Class: transposon-tagged.
      Location/Qualifiers
1. .25

```

```

/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="Drosophila melanogaster P[SUPOR-P] P element
insertion lines"
/notes="Inverse PCR was performed on Drosophila
melanogaster strains each of which contains one or more
P[SUPOR-P] P-element transposon insertion. The resultant
fragment for each strain was directly sequenced to
determine the genomic sequence at the site of insertion.
Details of the protocols used can be found at
http://www.fruitfly.org/about/methods/inverse.pcr.html."

BASE COUNT      1 a      9 c      6 g      9 t
ORIGIN
Query Match      46.0%; Score 9.2; DB 17; Length 25;
Best Local Similarity 78.6%; Pred. No. 1.5e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 GCGTTGCCACTCA 17
      |||||
      7 GGGTTCCCTCTCA 20

RESULT 34
A2954781      19 bp      DNA      linear      GSS 27-APR-2001
LOCUS      2M0220C07R Mouse 10kb plasmid U062M library Mus musculus genomic
DEFINITION      clone U062M2020C07 R, DNA sequence.
ACCESSION      A2954781
VERSION      A2954781.1 GI:13826008
KEYWORDS      GSS.
SOURCE      house mouse.
      Mus musculus
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
      1 (bases 1 to 19)
AUTHORS      Dunn, D., Aoyagi, A., Barber, M., Bascorn, T., Duval, B., Hamill, C.,
      Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
      M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
      and Wright, D., Weiss, R.
      Mouse whole genome scaffolding with paired end reads from 10kb
      plasmid inserts
      Unpublished (2000)
TITLE      Contact: Robert B. Weiss
      University of Utah Genome Center
      University of Utah
      Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
      84112, USA
      Tel: 801 585 5606
      Fax: 801 585 7177
      Email: ddunn@genetics.utah.edu
      Insert Length: 1000 Std. Error: 0.00
      Plate: 0220 Row: C Column: 07
      Seq primer: CACACGAGAAACAGCTATGAC
      Class: plasmid ends
      High quality sequence strop: 19.
      Location/Qualifiers
1. .19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="U062M2020C07"
/clone_lib="Mouse 10kb plasmid U062M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Ti-resistant, F-."
/notes="Vector: PMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were

```

ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptor complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E.coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN

8 a 6 c 4 g 1 t

Query Match 45.0%; Score 9; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGCGTTTG 10
|||||
Db 11 TTGCGTTTG 3

RESULT 35
AZ435809 20 bp DNA linear GSS 03-OCT-2000
LOCUS M0223103F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0223103 F, DNA sequence.
ACCESSION AZ435809
VERSION AZ435809.1 GI:10559822
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Relliy
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0223 row: L column: 03
Seq primer: CGTTGTAACGACGCGCAGCT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source1. 20
Location/Qualifiers

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0223103"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptor complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E.coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN

6 a 6 c 3 g 5 t

Query Match 45.0%; Score 9; DB 17; Length 20;
Best Local Similarity 70.6%; Pred. No. 1.8e+06;
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 TGGGTTGGCAGTCA 19
|||||
Db 2 TACGATGCTCTCA 18

RESULT 36
AZ991405 20 bp DNA linear GSS 27-APR-2001
LOCUS M0275004R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION clone UUGC2M0275004 R, DNA sequence.
ACCESSION AZ991405
VERSION AZ991405.1 GI:13862632
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Relliy
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0275 row: O column: 04
Seq primer: CACACAGAAACACCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source1. 20
Location/Qualifiers

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0275004"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (G114732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent *E. coli* XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 7 a 6 c 2 g 5 t

Query Match 45.0%; Score 9; DB 17; Length 20;
 Best Local Similarity 70.6%; Pred. No. 1.8e+06;
 Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TGGCTTGCACCTCAGA 19
 Db 3 TGGCATTCACCAACTA 19

RESULT 37
 TA361F06P/c 20 bp DNA linear GSS 13-DEC-2000
 LOCUS T brucei sheared genomic DNA clone 361f06, forward sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AL494520
 VERSION AL494520.1 GI:11870977
 KEYWORDS GSS.

SOURCE Trypanosoma brucei.
 ORGANISM Trypanosoma brucei
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 20)
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
 source Location/Qualifiers

1..20
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="361f06"

BASE COUNT 6 a 9 c 3 g 2 t

ORIGIN
 Query Match 45.0%; Score 9; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGGCTTGC 11
 Db 17 TGGCTTGC 9

RESULT 38
 TA62B07P/c 21 bp DNA linear GSS 16-DEC-2000
 LOCUS T. brucei sheared genomic DNA clone 62b07, forward sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AL465023
 VERSION AL465023.1 GI:11877508
 KEYWORDS GSS.

SOURCE Trypanosoma brucei.
 ORGANISM Trypanosoma brucei
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 21)
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
 source Location/Qualifiers

1..21
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="62b07"

BASE COUNT 7 a 5 c 4 g 5 t

ORIGIN
 Query Match 45.0%; Score 9; DB 17; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TTGGCACT 15
 Db 19 TTGGCACT 11

RESULT 39
 A1186405/c 22 bp mRNA linear EST 28-OCT-1998
 LOCUS qd20605.x1 Soareg placentae 8to9weeks_2NBH8B8c9w Homo sapiens CDNA
 clone IMAGE:1724288 3' similar to TR:015726 Q15726 MALIGNANT
 MELANOMA METASTASIS-SUPPRESSOR.1, mRNA sequence.
 ACCESSION A1186405
 VERSION A1186405.1 GI:3737043
 KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 22)
 AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph. D.
 Email: cga@bbs-remail.nih.gov

This clone is available royalty-free through LNL; contact the

FEATURES

SOURCE

IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 759 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers

BASE COUNT

8 a 4 c 8 g 2 t

ORIGIN

/clone="UUGC1M0117A08"
/clone.lib="Mouse 10kb plasmid UUGC1M 1library"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity 45.0%; Score 9; DB 9; Length 22;
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 TTGGCTTGGCCTCA 17

22 TTTCCTGTGCACCCA 6

2 TTGGCTTGGCCTCAG 18

18 TTTCCTGTGCCTCTG 2

DB

Search completed: June 7, 2003, 09:44:13
Job time: 1175.09 secs

RESULT 40

A2367707/c

LOCUS

1M0117A08R Mouse 10kb plasmid UUGC1M 1library Mus musculus genomic
clone UUGC1M0117A08 R, DNA sequence.

ACCESSION

A2367707

VERSION

A2367707.1 GI:10481503

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

AUTHORS

1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A.
and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Unpublished (2000)

CONTACT

Contact: Robert B. Weiss

UNIVERSITY

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84112, USA

TELEPHONE

Tel: 801 585 5606

FAX

Fax: 801 585 7177

EMAIL

Email: ddunn@genetics.utah.edu

INSERT LENGTH

Insert Length: 10000 Std Error: 0.00

PLATE

Plate: 0117 row: A column: 08

SEQ PRIMER

Seq primer: CACACGAGAAACAGCTATGACC

CLASS

Class: plasmid ends

HIGH QUALITY

High quality sequence stop: 22.

LOCATION/QUALIFIERS

Location/Qualifiers

1. 22

/organism="Mus musculus"

/strain

/strain="C57BL/6J"

/db_xref

/db_xref="taxon:10090"

FEATURES

FEATURES

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 07:20:34 ; Search time 391.418 Seconds

(without alignments)
1338.340 Million cell updates/sec

Title: US-10-080-959A-5

Sequence: 18
1 ctgcgccgcgaccagc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 521186

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: gb_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pac:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlg_mus:*
34: em_hlg_pln:*
35: em_hlg_rdd:*
36: em_hlg_mam:*
37: em_hlg_vrt:*
38: em_ey:*
39: em_higo_hum:*
40: em_higo_mus:*
41: em_higo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6	AR210276
2	18	100.0	18	6	AX402704
3	13	72.2	21	6	AR159747
4	12.8	71.1	17	6	AR210194
5	12.8	71.1	17	6	AX402622
6	12.4	68.9	18	6	104828
7	12.4	68.9	22	6	171353
8	12.2	67.8	21	6	AX404363
9	12.2	67.8	21	6	AX404364
10	12	66.7	18	6	104832
11	12	66.7	21	6	AX096029
12	12	66.7	25	6	AR139910
13	12	66.7	25	6	AR167554
14	11.8	65.6	18	6	A38123
15	11.8	65.6	18	6	A42267
16	11.8	65.6	18	6	AR000469
17	11.8	65.6	18	6	AR044543
18	11.8	65.6	18	6	AR098234
19	11.8	65.6	18	6	AR127034
20	11.8	65.6	18	6	189306
21	11.8	65.6	18	6	189318
22	11.8	65.6	18	6	193614
23	11.8	65.6	24	6	A32651
24	11.8	65.6	24	6	A32652
25	11.8	65.6	24	6	AR097798
26	11.8	65.6	24	6	AR097799
27	11.8	65.6	24	6	191779
28	11.8	65.6	25	6	A75774
29	11.8	65.6	19	6	AR085110
30	11.6	64.4	21	6	AX322593
31	11.6	64.4	21	6	AR021129
32	11.6	64.4	21	6	AX404361
33	11.6	64.4	21	6	AX404362
34	11.6	64.4	21	6	AX404365
35	11.6	64.4	21	6	AX404366
36	11.6	64.4	22	6	AR021109
37	11.6	64.4	22	6	AR021110
38	11.6	64.4	22	6	AR036253
39	11.6	64.4	22	6	AR036254
40	11.6	64.4	24	6	AX031299
41	11.6	64.4	24	13	AX031325
42	11.4	63.3	15	6	A15500
43	11.4	63.3	15	6	A15500
44	11.4	63.3	15	6	A15501
45	11.4	63.3	15	6	A15501
46	11.4	63.3	15	6	A32421
47	11.4	63.3	19	6	BD011931
48	11.4	63.3	19	6	BD011987
49	11.4	63.3	19	6	BD012048
50	11.4	63.3	19	6	BD012935
51	11.4	63.3	19	6	E23331
52	11.4	63.3	19	6	E27100
53	11.4	63.3	19	23	BD004411
54	11.4	63.3	19	23	BD004467
55	11.4	63.3	19	23	BD004528
56	11.4	63.3	19	23	BD008361
57	11.4	63.3	20	6	A81367
58	11.4	63.3	20	6	AR163730
59	11.4	63.3	20	6	AX001587
60	11.4	63.3	22	6	AR023933
61	11.4	63.3	22	6	AR182249
62	11.4	63.3	24	6	A24897
63	11.4	63.3	24	6	AR032196
64	11.2	62.2	16	6	AR196066
65	11.2	62.2	16	6	AX317642

Pred. No. is the number of results predicted by chance to have a

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C	68	11.2	62.2	19	6	AI210182	AI210182 Sequence	141	10.4	57.8	12	6	E08683	E08683 BamHI linker
C	69	11.2	62.2	19	6	AX026210	AX026210 Sequence	142	10.4	57.8	12	6	104862	104862 Sequence 2
C	70	11.2	62.2	20	6	AX296221	AX296221 Sequence	143	10.4	57.8	12	6	104862	104862 Sequence 2
C	71	11.2	62.2	21	6	AI138848	AI138848 Sequence	144	10.4	57.8	12	6	128840	128840 Sequence 78
C	72	11.2	62.2	22	6	AI317639	AI317639 Sequence	145	10.4	57.8	12	6	128840	128840 Sequence 78
C	73	11.2	62.2	23	6	AI144354	AI144354 Sequence	146	10.4	57.8	13	6	AI15498	AI15498 oligonucleo
C	74	11.2	62.2	24	6	AX291588	AX291588 Sequence	147	10.4	57.8	13	6	AI15498	AI15498 oligonucleo
C	75	11.2	62.2	24	6	AX095225	AX095225 Sequence	148	10.4	57.8	13	6	AI15499	AI15499 oligonucleo
C	76	11.2	62.2	24	6	AX342721	AX342721 Sequence	149	10.4	57.8	13	6	AI15499	AI15499 oligonucleo
C	77	11.2	62.2	24	6	AX031302	AX031302 Sequence	150	10.4	57.8	18	6	AR069001	AR069001 Sequence
C	78	11.2	62.2	24	13	AX031328	AX031328 Sequence	151	10.4	57.8	18	6	AR069001	AR069001 Sequence
C	79	11.2	62.2	25	6	AR068845	AR068845 Sequence	152	10.4	57.8	18	6	AR065514	AR065514 Sequence
C	80	11.2	62.2	25	6	AR070145	AR070145 Sequence	153	10.4	57.8	18	6	E05746	E05746 PCR primer
C	81	11.2	62.2	25	6	AR102902	AR102902 Sequence	154	10.4	57.8	19	6	AR009255	AR009255 Sequence
C	82	11.2	62.2	25	6	AR108081	AR108081 Sequence	155	10.4	57.8	19	6	AX259683	AX259683 Sequence
C	83	11.2	62.2	25	6	AR134729	AR134729 Sequence	156	10.4	57.8	19	6	178495	178495 Sequence 6
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C	95	10.8	60.0	20	6	AR212475	AR212475 Sequence	168	10.4	57.8	23	6	166696	166696 Sequence 36
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C	108	10.8	60.0	24	6	127884	127884 Sequence 12	181	10.4	57.8	24	6	AR125661	AR125661 Sequence
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C	119	10.8	60.0	20	6	AX459982	AX459982 Sequence	192	10.4	57.8	24	6	144740	144740 Sequence 3
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C	125	10.6	58.9	24	6	AR025330	AR025330 Sequence	198	10.4	57.8	24	6	145669	145669 Sequence 3
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C	137	10.6	58.9	24	6	186341	186341 Sequence 76	210	10.4	57.8	25	6	A65270	A65270 Sequence 1
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c 213	10.2	56.7	17	6	AR195708	AR195708 Sequence	285	10.2	56.7	21	6	I21311	I21311 Sequence 5
c 214	10.2	56.7	17	6	AR210194	AR210194 Sequence	287	10.2	56.7	21	6	I84721	I84721 Sequence 9
c 215	10.2	56.7	17	6	AX092740	AX092740 Sequence	288	10.2	56.7	22	6	AR066396	AR066396 Sequence
c 216	10.2	56.7	17	6	AX272862	AX272862 Sequence	288	10.2	56.7	22	6	AR200656	AR200656 Sequence
c 217	10.2	56.7	17	6	AX273293	AX273293 Sequence	290	10.2	56.7	22	6	AX188736	AX188736 Sequence
c 218	10.2	56.7	17	6	AX273294	AX273294 Sequence	291	10.2	56.7	22	6	AX188744	AX188744 Sequence
c 219	10.2	56.7	17	6	AX316104	AX316104 Sequence	292	10.2	56.7	24	6	A04371	A04371 Sequence fo
c 220	10.2	56.7	17	6	AX356933	AX356933 Sequence	293	10.2	56.7	24	6	A04371	A04371 Sequence fo
c 221	10.2	56.7	17	6	AX402622	AX402622 Sequence	294	10.2	56.7	24	6	A11769	A11769 Sequence fo
c 222	10.2	56.7	18	6	A87862	A87862 Sequence 10	295	10.2	56.7	24	6	AR019471	AR019471 Sequence
c 223	10.2	56.7	18	6	A89829	A89829 Sequence 10	296	10.2	56.7	24	6	AR028994	AR028994 Sequence
c 224	10.2	56.7	19	6	A70729	A70729 Sequence 50	297	10.2	56.7	24	6	AR065932	AR065932 Sequence
c 225	10.2	56.7	19	6	A79213	A79213 Sequence 50	298	10.2	56.7	24	6	AR065932	AR065932 Sequence
c 226	10.2	56.7	19	6	A93435	A93435 Sequence 1	298	10.2	56.7	24	6	AR095367	AR095367 Sequence
c 227	10.2	56.7	19	6	A96984	A96984 Sequence 62	300	10.2	56.7	24	6	AR176111	AR176111 Sequence
c 228	10.2	56.7	19	6	AR049021	AR049021 Sequence	301	10.2	56.7	24	6	AR201753	AR201753 Sequence
c 229	10.2	56.7	19	6	AR124122	AR124122 Sequence	302	10.2	56.7	24	6	AX289512	AX289512 Sequence
c 230	10.2	56.7	19	6	AR129881	AR129881 Sequence	302	10.2	56.7	24	6	AX290919	AX290919 Sequence
c 231	10.2	56.7	19	6	AR203412	AR203412 Sequence	303	10.2	56.7	24	6	AX291102	AX291102 Sequence
c 232	10.2	56.7	19	6	AX147709	AX147709 Sequence	304	10.2	56.7	24	6	AX292453	AX292453 Sequence
c 233	10.2	56.7	19	6	AX358553	AX358553 Sequence	305	10.2	56.7	24	6	AX406704	AX406704 Sequence
c 234	10.2	56.7	19	6	BD003443	BD003443 A Gene re	306	10.2	56.7	24	6	AX445821	AX445821 Sequence
c 235	10.2	56.7	19	6	AR012172	AR012172 Sequence	307	10.2	56.7	24	6	AX447168	AX447168 Sequence
c 236	10.2	56.7	20	6	AR012174	AR012174 Sequence	308	10.2	56.7	24	6	A00431	A00431 Nucleotide
c 237	10.2	56.7	20	6	AR062072	AR062072 Sequence	309	10.2	56.7	25	6	AR051207	AR051207 Sequence
c 238	10.2	56.7	20	6	AR066430	AR066430 Sequence	310	10.2	56.7	25	6	AR139910	AR139910 Sequence
c 239	10.2	56.7	20	6	AR093755	AR093755 Sequence	311	10.2	56.7	25	6	AR154075	AR154075 Sequence
c 240	10.2	56.7	20	6	AR093757	AR093757 Sequence	312	10.2	56.7	25	6	AR167554	AR167554 Sequence
c 241	10.2	56.7	20	6	AR093757	AR093757 Sequence	313	10.2	56.7	25	6	AX339699	AX339699 Sequence
c 242	10.2	56.7	20	6	AR104951	AR104951 Sequence	314	10.2	56.7	25	6	E28833	E28833 Human CC ty
c 243	10.2	56.7	20	6	AR147480	AR147480 Sequence	315	10.2	56.7	25	6	AR049483	AR049483 Sequence
c 244	10.2	56.7	20	6	AR162416	AR162416 Sequence	316	10.2	56.7	25	6	AR051634	AR051634 Sequence
c 245	10.2	56.7	20	6	AR163924	AR163924 Sequence	317	10.2	56.7	25	6	I68100	I68100 Sequence 4
c 246	10.2	56.7	20	6	AR167423	AR167423 Sequence	318	10.2	56.7	25	6	AR012001	AR012001 Sequence
c 247	10.2	56.7	20	6	AR206306	AR206306 Sequence	319	10.2	56.7	25	6	AR049484	AR049484 Sequence
c 248	10.2	56.7	20	6	AX139283	AX139283 Sequence	320	10.2	56.7	25	6	AR049485	AR049485 Sequence
c 249	10.2	56.7	20	6	AX155203	AX155203 Sequence	321	10.2	56.7	25	6	AR049485	AR049485 Sequence
c 250	10.2	56.7	20	6	AX284145	AX284145 Sequence	322	10.2	56.7	25	6	AR049485	AR049485 Sequence
c 251	10.2	56.7	20	6	AX295552	AX295552 Sequence	323	10.2	56.7	25	6	AR051635	AR051635 Sequence
c 252	10.2	56.7	20	6	AX295735	AX295735 Sequence	324	10.2	56.7	25	6	AR051636	AR051636 Sequence
c 253	10.2	56.7	20	6	BD012800	BD012800 A method	325	10.2	56.7	25	6	AR051637	AR051637 Sequence
c 254	10.2	56.7	20	6	BD013025	BD013025 Method of	326	10.2	56.7	25	6	AR111513	AR111513 Sequence
c 255	10.2	56.7	20	6	BD013028	BD013028 Method of	327	10.2	56.7	25	6	AX068237	AX068237 Sequence
c 256	10.2	56.7	20	6	E06986	E06986 5' primer to	328	10.2	56.7	25	6	AX077196	AX077196 Sequence
c 257	10.2	56.7	20	6	E10200	E10200 Synthetic O	329	10.2	56.7	25	6	AR126731	AR126731 Sequence
c 258	10.2	56.7	20	6	E15407	E15407 PCR primer.	330	10.2	56.7	25	6	AR201157	AR201157 Sequence
c 259	10.2	56.7	20	6	E27517	E27517 Modified ma	331	10.2	56.7	25	6	AX034936	AX034936 Sequence
c 260	10.2	56.7	20	6	E33496	E33496 Primer for	332	10.2	56.7	25	6	AX297368	AX297368 Sequence
c 261	10.2	56.7	20	6	E39114	E39114 Microorgan	333	10.2	56.7	25	6	I30071	I30071 Sequence 23
c 262	10.2	56.7	20	6	E39431	E39431 Method for	334	10.2	56.7	25	6	AX095007	AX095007 Sequence
c 263	10.2	56.7	20	6	I41052	I41052 Sequence 3	335	10.2	56.7	25	6	AX095198	AX095198 Sequence
c 264	10.2	56.7	20	6	I62222	I62222 Sequence 3	336	10.2	56.7	25	6	A24876	A24876 oligonucleo
c 265	10.2	56.7	20	23	BD008235	BD008235 A method	337	10.2	56.7	25	6	AX148222	AX148222 Sequence
c 266	10.2	56.7	20	23	BD010058	BD010058 Method of	338	10.2	56.7	25	6	A79363	A79363 Sequence 12
c 267	10.2	56.7	20	23	BD010061	BD010061 Method of	339	10.2	56.7	25	6	A79365	A79365 Sequence 14
c 268	10.2	56.7	21	6	A42348	A42348 Sequence 8	340	10.2	56.7	25	6	A91915	A91915 Sequence 2
c 269	10.2	56.7	21	6	A44379	A44379 Sequence 9	341	10.2	56.7	25	6	AR032175	AR032175 Sequence
c 270	10.2	56.7	21	6	A47166	A47166 Sequence 9	342	10.2	56.7	25	6	AR032177	AR032177 Sequence
c 271	10.2	56.7	21	6	A56642	A56642 Sequence 9	343	10.2	56.7	25	6	AX148222	AX148222 Sequence
c 272	10.2	56.7	21	6	A80363	A80363 Sequence 9	344	10.2	56.7	25	6	AX458675	AX458675 Sequence
c 273	10.2	56.7	21	6	AR111766	AR111766 Sequence	345	10.2	56.7	25	6	BD007603	BD007603 Nematoda-
c 274	10.2	56.7	21	6	AR179806	AR179806 Sequence	346	10.2	56.7	25	6	A87861	A87861 Sequence 9
c 275	10.2	56.7	21	6	AR193505	AR193505 Sequence	347	10.2	56.7	25	6	A89828	A89828 Sequence 9
c 276	10.2	56.7	21	6	AX036326	AX036326 Sequence	348	10.2	56.7	25	6	AR068161	AR068161 Sequence
c 277	10.2	56.7	21	6	AX081341	AX081341 Sequence	349	10.2	56.7	25	6	AR073355	AR073355 Sequence
c 278	10.2	56.7	21	6	AX093783	AX093783 Sequence	350	10.2	56.7	25	6	AX003631	AX003631 Sequence
c 279	10.2	56.7	21	6	AX093732	AX093732 Sequence	351	10.2	56.7	25	6	AX292735	AX292735 Sequence
c 280	10.2	56.7	21	6	AX145917	AX145917 Sequence	352	10.2	56.7	25	6	AX444889	AX444889 Sequence
c 281	10.2	56.7	21	6	AX201239	AX201239 Sequence	353	10.2	56.7	25	6	AX446255	AX446255 Sequence
c 282	10.2	56.7	21	6	AX283171	AX283171 Sequence	354	10.2	56.7	25	6	BD008078	BD008078 Novel pro
c 283	10.2	56.7	21	6	AX283300	AX283300 Sequence	355	10.2	56.7	25	6	A47536	A47536 Sequence 31
c 284	10.2	56.7	21	6	AX384637	AX384637 Sequence	356	10.2	56.7	25	6	AR036752	AR036752 Sequence
							357	10.2	56.7	25	6	AR097947	AR097947 Sequence

C 358	10	55.6	25	6	AX012372	AX012372 Sequence	C 431	9.8	54.4	23	6	E13387	E13387 PCR primer
C 359	9.8	55.6	25	6	E59978	E59978 Highly Acti	C 432	9.8	54.4	24	6	A06972	A06972 Nucleotide
C 360	10	55.6	15	6	A07486	A07486 Nucleotide	C 433	9.8	54.4	24	6	A50031	A50031 Sequence 14
C 361	9.8	54.4	15	6	I35045	I35045 Sequence 13	C 434	9.8	54.4	24	6	AR151703	AR151703 Sequence
C 362	9.8	54.4	15	6	I35046	I35046 Sequence 14	C 435	9.8	54.4	24	6	AR151716	AR151716 Sequence
C 363	9.8	54.4	15	6	I35076	I35076 Sequence 44	C 436	9.8	54.4	24	6	AX080929	AX080929 Sequence
C 364	9.8	54.4	15	6	I35096	I35096 Sequence 64	C 437	9.8	54.4	24	6	AX290518	AX290518 Sequence
C 365	9.8	54.4	15	6	I35200	I35200 Sequence 16	C 438	9.8	54.4	24	6	AX117167	AX117167 Sequence
C 366	9.8	54.4	15	6	I75079	I75079 Sequence 9	C 439	9.8	54.4	24	6	AX132595	AX132595 Sequence
C 367	9.8	54.4	15	6	AR012039	AR012039 Sequence	C 440	9.8	54.4	24	6	AX444527	AX444527 Sequence
C 368	9.8	54.4	16	6	AX431360	AX431360 Sequence	C 441	9.8	54.4	24	6	AX444527	AX444527 Sequence
C 369	9.8	54.4	16	6	E27549	E27549 Probe for d	C 442	9.8	54.4	24	6	AX444527	AX444527 Sequence
C 370	9.8	54.4	17	6	AR191949	AR191949 Sequence	C 443	9.8	54.4	24	6	AX444527	AX444527 Sequence
C 371	9.8	54.4	17	6	AX272861	AX272861 Sequence	C 444	9.8	54.4	24	6	AX444527	AX444527 Sequence
C 372	9.8	54.4	18	6	A26386	A26386 Probe no. 4.	C 445	9.8	54.4	24	6	AX444527	AX444527 Sequence
C 373	9.8	54.4	18	6	A82098	A82098 Sequence 18	C 446	9.8	54.4	24	6	AX444527	AX444527 Sequence
C 374	9.8	54.4	18	6	A82102	A82102 Sequence 22	C 447	9.8	54.4	24	6	AX444527	AX444527 Sequence
C 375	9.8	54.4	18	6	A83186	A83186 Sequence 6	C 448	9.8	54.4	25	6	A85088	A85088 Sequence
C 376	9.8	54.4	18	6	AR034582	AR034582 Sequence	C 449	9.8	54.4	25	6	AX014053	AX014053 Sequence
C 377	9.8	54.4	18	6	AR051727	AR051727 Sequence	C 450	9.8	54.4	25	6	AX042861	AX042861 Sequence
C 378	9.8	54.4	18	6	AR054937	AR054937 Sequence	C 451	9.8	54.4	25	6	AX067200	AX067200 Sequence
C 379	9.8	54.4	18	6	AR069001	AR069001 Sequence	C 452	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 380	9.8	54.4	18	6	AR072241	AR072241 Sequence	C 453	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 381	9.8	54.4	18	6	AR081196	AR081196 Sequence	C 454	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 382	9.8	54.4	18	6	AR095514	AR095514 Sequence	C 455	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 383	9.8	54.4	18	6	AR121144	AR121144 Sequence	C 456	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 384	9.8	54.4	18	6	AR182918	AR182918 Sequence	C 457	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 385	9.8	54.4	18	6	AR196714	AR196714 Sequence	C 458	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 386	9.8	54.4	18	6	AR200050	AR200050 Sequence	C 459	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 387	9.8	54.4	18	6	AX001169	AX001169 Sequence	C 460	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 388	9.8	54.4	18	6	AX001173	AX001173 Sequence	C 461	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 389	9.8	54.4	18	6	BD002000	BD002000 Construct	C 462	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 390	9.8	54.4	18	6	E54927	E54927 Antibodies	C 463	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 391	9.8	54.4	18	6	I08750	I08750 Sequence 12	C 464	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 392	9.8	54.4	18	6	I26352	I26352 Sequence 44	C 465	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 393	9.8	54.4	18	6	I46673	I46673 Sequence 12	C 466	9.8	54.4	25	6	BD006579	BD006579 Secreted
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C 395	9.8	54.4	19	6	A64793	A64793 Sequence 2	C 468	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 396	9.8	54.4	19	6	AR107967	AR107967 Sequence	C 469	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 397	9.8	54.4	19	6	AR199419	AR199419 Sequence	C 470	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 398	9.8	54.4	19	6	AR086224	AR086224 Sequence	C 471	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 399	9.8	54.4	20	6	AR107910	AR107910 Sequence	C 472	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 400	9.8	54.4	20	6	AR136419	AR136419 Sequence	C 473	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 401	9.8	54.4	20	6	AR136420	AR136420 Sequence	C 474	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 402	9.8	54.4	20	6	AR176790	AR176790 Sequence	C 475	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 403	9.8	54.4	20	6	AR195439	AR195439 Sequence	C 476	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 404	9.8	54.4	20	6	AR195439	AR195439 Sequence	C 477	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 405	9.8	54.4	20	6	AX045701	AX045701 Sequence	C 478	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 406	9.8	54.4	20	6	AX076689	AX076689 Sequence	C 479	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 407	9.8	54.4	20	6	AX356073	AX356073 Sequence	C 480	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 408	9.8	54.4	20	6	AX449252	AX449252 Sequence	C 481	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 409	9.8	54.4	20	6	E07460	E07460 Artificial	C 482	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 410	9.8	54.4	20	6	E25019	E25019 Oligonucleo	C 483	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 411	9.8	54.4	21	6	A36142	A36142 Sequence 7	C 484	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 412	9.8	54.4	21	6	AR085665	AR085665 Sequence	C 485	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 413	9.8	54.4	21	6	AR138932	AR138932 Sequence	C 486	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 414	9.8	54.4	21	6	AR208662	AR208662 Sequence	C 487	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 415	9.8	54.4	21	6	AX096936	AX096936 Sequence	C 488	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 416	9.8	54.4	21	6	AX145633	AX145633 Sequence	C 489	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 417	9.8	54.4	21	6	AX145917	AX145917 Sequence	C 490	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 418	9.8	54.4	21	6	I25727	I25727 Sequence 2	C 491	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 419	9.8	54.4	22	6	AR073294	AR073294 Sequence	C 492	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 420	9.8	54.4	22	6	AR130480	AR130480 Sequence	C 493	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 421	9.8	54.4	22	6	AR130480	AR130480 Sequence	C 494	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 422	9.8	54.4	22	6	AR130481	AR130481 Sequence	C 495	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 423	9.8	54.4	22	6	AR130481	AR130481 Sequence	C 496	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 424	9.8	54.4	22	6	AR182249	AR182249 Sequence	C 497	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 425	9.8	54.4	22	6	AR211321	AR211321 Sequence	C 498	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 426	9.8	54.4	22	6	E32640	E32640 Method for	C 499	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 427	9.8	54.4	23	6	A09945	A09945 probe. 1/19	C 500	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 428	9.8	54.4	23	6	A63614	A63614 Sequence 1	C 501	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 429	9.8	54.4	23	6	AR062462	AR062462 Sequence	C 502	9.8	54.4	25	6	BD006579	BD006579 Secreted
C 430	9.8	54.4	23	6	AR112392	AR112392 Sequence	C 503	9.8	54.4	25	6	BD006579	BD006579 Secreted

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505	9.6	53.3	21	6	AX154359	AX154359 Sequence	578	9.4	52.2	17	6	AX423238	AX423238 Sequence
506	9.6	53.3	21	6	AX460047	AX460047 Sequence	579	9.4	52.2	17	6	AX423462	AX423462 Sequence
507	9.6	53.3	21	6	EL3821	EL3821 PCR primer	580	9.4	52.2	17	6	AX423463	AX423463 Sequence
508	9.6	53.3	22	6	A00733	A00733 Nucleotide	581	9.4	52.2	17	6	E08804	E08804 PCR primer
509	9.6	53.3	22	6	A04814	A04814 Oligonucleo	582	9.4	52.2	17	6	I36952	I36952 Sequence 38
510	9.6	53.3	22	6	A65666	A65666 Sequence 10	583	9.4	52.2	17	6	I52677	I52677 Sequence 41
511	9.6	53.3	22	6	AX038531	AX038531 Sequence	584	9.4	52.2	17	6	I56022	I56022 Sequence 3
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514	9.6	53.3	23	6	AJ2831	AJ2831 Synthetic p	587	9.4	52.2	18	6	A15635	A15635 Oligonucleo
515	9.6	53.3	23	6	AX038532	AX038532 Sequence	588	9.4	52.2	18	6	AR038242	AR038242 Sequence
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517	9.6	53.3	23	6	I21879	I21879 Sequence 11	590	9.4	52.2	18	6	AR106850	AR106850 Sequence
518	9.6	53.3	24	6	A07961	A07961 Oligonucleo	591	9.4	52.2	18	6	AR154196	AR154196 Sequence
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521	9.6	53.3	24	6	A35479	A35479 Synthetic 1	594	9.4	52.2	18	6	AR179298	AR179298 Sequence
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529	9.6	53.3	24	6	AX151068	AX151068 Sequence	602	9.4	52.2	19	6	A09039	A09039 Nucleotide
530	9.6	53.3	24	6	AX289140	AX289140 Sequence	603	9.4	52.2	19	6	A98001	A98001 Reverse Com
531	9.6	53.3	24	6	AX290011	AX290011 Sequence	604	9.4	52.2	19	6	AR074441	AR074441 Sequence
532	9.6	53.3	24	6	AX290739	AX290739 Sequence	605	9.4	52.2	19	6	AR081121	AR081121 Sequence
533	9.6	53.3	24	6	AX291009	AX291009 Sequence	606	9.4	52.2	19	6	AR085318	AR085318 Sequence
534	9.6	53.3	24	6	AX292160	AX292160 Sequence	607	9.4	52.2	19	6	AR088066	AR088066 Sequence
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536	9.6	53.3	24	6	AX445063	AX445063 Sequence	609	9.4	52.2	19	6	AR104225	AR104225 Sequence
537	9.6	53.3	24	6	E05645	E05645 Primer. 9/1	610	9.4	52.2	19	6	AR143489	AR143489 Sequence
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539	9.6	53.3	25	6	AR016269	AR016269 Sequence	612	9.4	52.2	19	6	AR171394	AR171394 Sequence
540	9.6	53.3	25	6	AR196785	AR196785 Sequence	613	9.4	52.2	19	6	I34613	I34613 Sequence 34
541	9.6	53.3	25	6	AX006970	AX006970 Sequence	614	9.4	52.2	20	6	A05195	A05195 Oligonucleo
542	9.6	53.3	25	6	AX006971	AX006971 Sequence	615	9.4	52.2	20	6	A07131	A07131 Nucleotide
543	9.6	53.3	25	6	AX038534	AX038534 Sequence	616	9.4	52.2	20	6	A07131	A07131 Nucleotide
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545	9.6	53.3	25	6	I72154	I72154 Sequence 11	618	9.4	52.2	20	6	A90094	A90094 Sequence 27
546	9.6	53.3	25	6	AX471451	AX471451 Sequence	619	9.4	52.2	20	6	AR043513	AR043513 Sequence
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551	9.4	52.2	12	6	A10823	A10823 Oligonucleo	624	9.4	52.2	20	6	AR169924	AR169924 Sequence
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556	9.4	52.2	12	6	I11566	I11566 Oligonucleo	629	9.4	52.2	20	6	AX268882	AX268882 Sequence
557	9.4	52.2	12	6	I14185	I14185 Sequence 17	630	9.4	52.2	20	6	AX355464	AX355464 Sequence
558	9.4	52.2	12	6	I06162	I06162 Sequence 3	631	9.4	52.2	20	6	AX418808	AX418808 Sequence
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560	9.4	52.2	14	6	A17875	A17875 Oligonucleo	633	9.4	52.2	20	6	I32368	I32368 Sequence 37
561	9.4	52.2	15	6	AR166226	AR166226 Sequence	634	9.4	52.2	20	6	A02284	A02284 Synthetic o
562	9.4	52.2	15	6	E16786	E16786 PCR primer	635	9.4	52.2	21	6	A12128	A12128 Oligonucleo
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566	9.4	52.2	16	6	I55637	I55637 Sequence 1	639	9.4	52.2	21	6	AR070809	AR070809 Sequence
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651	9.4	52.2	21	6	I73435	I73435 Sequence 40	724	9.2	51.1	16	6	A65271	A65271 Sequence 2
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C 653	9.4	52.2	22	6	A97972	A97972 Sequence 2	C 726	9.2	51.1	16	6	AR07459	AR07459 Sequence
654	9.4	52.2	22	6	A98011	A98011 Sequence 41	727	9.2	51.1	16	6	AR074601	AR074601 Sequence
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656	9.4	52.2	22	6	AR081198	AR081198 Sequence	729	9.2	51.1	16	6	AX262386	AX262386 Sequence
657	9.4	52.2	22	6	AR095516	AR095516 Sequence	730	9.2	51.1	16	6	I55157	I55157 Sequence 6
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661	9.4	52.2	22	6	AR134751	AR134751 Sequence	C 734	9.2	51.1	17	6	A85063	A85063 Sequence 7
C 662	9.4	52.2	22	6	AX055385	AX055385 Sequence	C 735	9.2	51.1	17	6	AR160338	AR160338 Sequence
C 663	9.4	52.2	22	6	AX098407	AX098407 Sequence	C 736	9.2	51.1	17	6	AR160393	AR160393 Sequence
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C 665	9.4	52.2	22	6	I32323	I32323 Sequence 4	C 738	9.2	51.1	17	6	AR196786	AR196786 Sequence
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C 668	9.4	52.2	23	6	A41619	A41619 Sequence 28	C 741	9.2	51.1	17	6	AX113276	AX113276 Sequence
C 669	9.4	52.2	23	6	A95681	A95681 Sequence 28	C 742	9.2	51.1	17	6	AX263076	AX263076 Sequence
C 670	9.4	52.2	23	6	A95723	A95723 Sequence 28	C 743	9.2	51.1	17	6	AX263077	AX263077 Sequence
C 671	9.4	52.2	23	6	A95765	A95765 Sequence 28	C 744	9.2	51.1	17	6	AX273068	AX273068 Sequence
C 672	9.4	52.2	23	6	A95807	A95807 Sequence 28	C 745	9.2	51.1	17	6	AX398152	AX398152 Sequence
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674	9.4	52.2	23	6	AR082547	AR082547 Sequence	747	9.2	51.1	17	6	AX423555	AX423555 Sequence
C 675	9.4	52.2	23	6	AR086581	AR086581 Sequence	748	9.2	51.1	17	6	AX482616	AX482616 Sequence
C 676	9.4	52.2	23	6	AR086582	AR086582 Sequence	C 749	9.2	51.1	17	6	E35236	E35236 Method for
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679	9.4	52.2	23	6	AR102922	AR102922 Sequence	C 752	9.2	51.1	18	6	A36330	A36330 Sequence 33
C 680	9.4	52.2	23	6	AR103930	AR103930 Sequence	C 753	9.2	51.1	18	6	A42355	A42355 Sequence 15
C 681	9.4	52.2	23	6	AR108101	AR108101 Sequence	C 754	9.2	51.1	18	6	A44388	A44388 Sequence 18
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684	9.4	52.2	23	6	AR156396	AR156396 Sequence	C 757	9.2	51.1	18	6	A56649	A56649 Sequence 16
C 685	9.4	52.2	23	6	AR164798	AR164798 Sequence	C 758	9.2	51.1	18	6	A63182	A63182 Sequence 17
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C 687	9.4	52.2	23	6	AX235696	AX235696 Sequence	C 760	9.2	51.1	18	6	AR009966	AR009966 Sequence
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C 690	9.4	52.2	23	6	I23995	I23995 Sequence 7	C 763	9.2	51.1	18	6	AR032038	AR032038 Sequence
C 691	9.4	52.2	23	6	I58490	I58490 Sequence 18	C 764	9.2	51.1	18	6	AR083367	AR083367 Sequence
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C 693	9.4	52.2	24	6	AX446054	AX446054 Sequence	C 766	9.2	51.1	18	6	AR179813	AR179813 Sequence
C 700	9.4	52.2	24	6	AX350849	AX350849 Sequence	C 767	9.2	51.1	18	6	AR193514	AR193514 Sequence
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C 699	9.4	52.2	24	6	AX045069	AX045069 Sequence	C 773	9.2	51.1	18	6	AX283245	AX283245 Sequence
C 702	9.4	52.2	25	6	A24887	A24887 Oligonucleo	C 774	9.2	51.1	18	6	E21180	E21180 Oligonucleo
C 703	9.4	52.2	25	6	AX38507	AX38507 Sequence 9	C 775	9.2	51.1	18	6	I30784	I30784 Sequence 22
C 704	9.4	52.2	25	6	AR032186	AR032186 Sequence	C 776	9.2	51.1	18	6	I46243	I46243 Sequence 22
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C 706	9.4	52.2	25	6	AR137987	AR137987 Sequence	C 778	9.2	51.1	18	6	I78471	I78471 Sequence 32
707	9.4	52.2	25	6	AR160523	AR160523 Sequence	C 779	9.2	51.1	18	6	I78472	I78472 Sequence 33
708	9.4	52.2	25	6	AX049804	AX049804 Sequence	C 780	9.2	51.1	18	6	I84728	I84728 Sequence 16
709	9.4	52.2	25	6	AX050802	AX050802 Sequence	C 781	9.2	51.1	19	6	A22370	A22370 Oligonucleo
710	9.4	52.2	25	6	AX081601	AX081601 Sequence	C 782	9.2	51.1	19	6	A69625	A69625 Sequence 34
711	9.4	52.2	25	6	AX138771	AX138771 Sequence	C 783	9.2	51.1	19	6	A87312	A87312 Sequence 37
C 712	9.4	52.2	25	6	AX374782	AX374782 Sequence	C 784	9.2	51.1	19	6	AR076118	AR076118 Sequence
713	9.4	52.2	25	6	I42471	I42471 Sequence 1	785	9.2	51.1	19	6	AR119277	AR119277 Sequence
C 714	9.4	52.2	25	6	A08049	A08049 Oligonucleo	786	9.2	51.1	19	6	AR136719	AR136719 Sequence
C 715	9.2	51.1	14	6	A81737	A81737 Sequence 22	787	9.2	51.1	19	6	AX164731	AX164731 Sequence
716	9.2	51.1	15	6	AR034030	AR034030 Sequence	C 788	9.2	51.1	19	6	AX130668	AX130668 Sequence
C 717	9.2	51.1	15	6	AR124039	AR124039 Sequence	C 789	9.2	51.1	19	6	AX131255	AX131255 Sequence
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C 720	9.2	51.1	15	6	AX14411	AX14411 Oligonucleo	792	9.2	51.1	19	6	AX259684	AX259684 Sequence
C 721	9.2	51.1	15	6			C 793	9.2	51.1	19	6	AX268362	AX268362 Sequence
C 722	9.2	51.1	16	6			C 795	9.2	51.1	19	6	AX384645	AX384645 Sequence

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799	9.2	51.1	19	12	AB069218	AB069218 Synthetic	C 872	9.2	51.1	24	6	A46276	A46276 Sequence 2
C 800	9.2	51.1	20	6	A69631	A69631 Sequence 40	C 873	9.2	51.1	24	6	A51319	A51319 Sequence 4
C 801	9.2	51.1	20	6	AR000128	AR000128 Sequence	C 874	9.2	51.1	24	6	A95198	A95198 Sequence 16
C 802	9.2	51.1	20	6	AR060536	AR060536 Sequence	C 875	9.2	51.1	24	6	AR068161	AR068161 Sequence
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C 818	9.2	51.1	20	6	AR211965	AR211965 Sequence	C 890	9.2	51.1	24	6	AX428849	AX428849 Sequence
C 819	9.2	51.1	20	6	AX038529	AX038529 Sequence	C 891	9.2	51.1	24	6	AX443606	AX443606 Sequence
C 820	9.2	51.1	20	6	AX055819	AX055819 Sequence	C 892	9.2	51.1	24	6	AX445111	AX445111 Sequence
C 821	9.2	51.1	20	6	AX193560	AX193560 Sequence	C 893	9.2	51.1	24	6	AX445111	AX445111 Sequence
C 822	9.2	51.1	20	6	AX193562	AX193562 Sequence	C 894	9.2	51.1	24	6	AX445426	AX445426 Sequence
C 823	9.2	51.1	20	6	AX295325	AX295325 Sequence	C 895	9.2	51.1	24	6	AX445965	AX445965 Sequence
C 824	9.2	51.1	20	6	AX297367	AX297367 Sequence	C 896	9.2	51.1	24	6	AX446262	AX446262 Sequence
C 825	9.2	51.1	20	6	AX419736	AX419736 Sequence	C 897	9.2	51.1	24	6	BD003655	BD003655 Sequence
C 826	9.2	51.1	20	6	AX419752	AX419752 Sequence	C 898	9.2	51.1	24	6	106504	106504 Sequence 8
C 827	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 899	9.2	51.1	24	6	116868	116868 Sequence 6
C 828	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 900	9.2	51.1	24	6	124352	124352 Sequence 1
C 829	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 901	9.2	51.1	24	6	133778	133778 Sequence 47
C 830	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 902	9.2	51.1	24	6	HSR270369	HSR270369 Sequence 1
C 831	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 903	9.2	51.1	25	6	A06321	A06321 Artificial
C 832	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 904	9.2	51.1	25	6	A63691	A63691 Sequence 1
C 833	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 905	9.2	51.1	25	6	A86784	A86784 Sequence 11
C 834	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 906	9.2	51.1	25	6	AR019285	AR019285 Sequence
C 835	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 907	9.2	51.1	25	6	AR053530	AR053530 Sequence
C 836	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 908	9.2	51.1	25	6	AR076469	AR076469 Sequence
C 837	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 909	9.2	51.1	25	6	AR089334	AR089334 Sequence
C 838	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 910	9.2	51.1	25	6	AR093534	AR093534 Sequence
C 839	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 911	9.2	51.1	25	6	AR129986	AR129986 Sequence
C 840	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 912	9.2	51.1	25	6	AR137152	AR137152 Sequence
C 841	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 913	9.2	51.1	25	6	AR140156	AR140156 Sequence
C 842	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 914	9.2	51.1	25	6	AR141122	AR141122 Sequence
C 843	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 915	9.2	51.1	25	6	AR145310	AR145310 Sequence
C 844	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 916	9.2	51.1	25	6	AR196785	AR196785 Sequence
C 845	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 917	9.2	51.1	25	6	AR196645	AR196645 Sequence
C 846	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 918	9.2	51.1	25	6	AR196534	AR196534 Sequence
C 847	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 919	9.2	51.1	25	6	AR196482	AR196482 Sequence
C 848	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 920	9.2	51.1	25	6	AR196482	AR196482 Sequence
C 849	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 921	9.2	51.1	25	6	AR196482	AR196482 Sequence
C 850	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 922	9.2	51.1	25	6	AR196482	AR196482 Sequence
C 851	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 923	9.2	51.1	25	6	AR196482	AR196482 Sequence
C 852	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 924	9.2	51.1	25	6	AR196482	AR196482 Sequence
C 853	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 925	9.2	51.1	25	6	AR196482	AR196482 Sequence
C 854	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 926	9.2	51.1	25	6	AR196482	AR196482 Sequence
C 855	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 927	9.2	51.1	25	6	AR196482	AR196482 Sequence
C 856	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 928	9.2	51.1	25	6	AR196482	AR196482 Sequence
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C 859	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 931	9.2	51.1	25	6	AR196482	AR196482 Sequence
C 860	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 932	9.2	51.1	25	6	AR196482	AR196482 Sequence
C 861	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 933	9.2	51.1	25	6	AR196482	AR196482 Sequence
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C 865	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 937	9.2	51.1	25	6	AR196482	AR196482 Sequence
C 866	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 938	9.2	51.1	25	6	AR196482	AR196482 Sequence
C 867	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 939	9.2	51.1	25	6	AR196482	AR196482 Sequence
C 868	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 940	9.2	51.1	25	6	AR196482	AR196482 Sequence
C 869	9.2	51.1	21	6	AX419752	AX419752 Sequence	C 941	9.2	51.1	25	6	AR196482	AR196482 Sequence

942	9	50.0	15	6	AX362596
943	9	50.0	17	6	A10042
944	9	50.0	17	6	AR185975
945	9	50.0	17	6	AR191948
946	9	50.0	17	6	AX139248
947	9	50.0	17	6	AX206986
948	9	50.0	17	6	AX265495
949	9	50.0	17	6	AX265495
950	9	50.0	17	6	AX475043
951	9	50.0	17	6	126676
952	9	50.0	17	6	126677
953	9	50.0	17	6	126664
954	9	50.0	17	6	A76033
955	9	50.0	18	6	A88208
956	9	50.0	18	6	A90175
957	9	50.0	18	6	AR051728
958	9	50.0	18	6	AR117171
959	9	50.0	18	6	AR117181
960	9	50.0	18	6	AR131564
961	9	50.0	18	6	AR150496
962	9	50.0	18	6	AR150506
963	9	50.0	18	6	AR199498
964	9	50.0	18	6	AR200051
965	9	50.0	18	6	AR200969
966	9	50.0	18	6	AR210288
967	9	50.0	18	6	AX203102
968	9	50.0	18	6	AX203104
969	9	50.0	18	6	AX402716
970	9	50.0	18	6	AX419720
971	9	50.0	18	6	BD002001
972	9	50.0	18	6	E05750
973	9	50.0	18	6	126673
974	9	50.0	18	6	149674
975	9	50.0	19	6	A58116
976	9	50.0	19	6	AR169677
977	9	50.0	19	6	AR199419
978	9	50.0	19	6	AX015897
979	9	50.0	19	6	BD012978
980	9	50.0	19	6	E22961
981	9	50.0	19	9	HS010631
982	9	50.0	19	23	BD006629
983	9	50.0	20	6	A16534
984	9	50.0	20	6	AR043512
985	9	50.0	20	6	AR084362
986	9	50.0	20	6	AR086213
987	9	50.0	20	6	AR092920
988	9	50.0	20	6	AR109237
989	9	50.0	20	6	AR124935
990	9	50.0	20	6	AR136418
991	9	50.0	20	6	AR136906
992	9	50.0	20	6	AR144320
993	9	50.0	20	6	AR144333
994	9	50.0	20	6	AR144334
995	9	50.0	20	6	AR144335
996	9	50.0	20	6	AR144336
997	9	50.0	20	6	AR144337
998	9	50.0	20	6	AR163904
999	9	50.0	20	6	AR164003
1000	9	50.0	20	6	AR166697

ALIGNMENTS

RESULT 1
 AR210276
 LOCUS
 DEFINITION Sequence 188 from patent US 6387652.
 ACCESSION AR210276
 VERSION AR210276.1 GI:21512465
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

Unclassified.
 1 (bases 1 to 18)

REFERENCE 1 (bases 1 to 18)
 AUTHORS Haugland, R. and Vesper, S.
 TITLE Method of identifying and quantifying specific fungi and bacteria
 JOURNAL Patent: US 6387652-A 188 14-MAY-2002
 FEATURES
 SOURCE Location/Qualifiers
 1. 18
 /organism="unknown"

BASE COUNT 2 a 8 c 6 g 2 t

Query Match 100.0%; Score 18; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGCCCGGATCCAGGC 18
 DB 1 CTGGCCCGGATCCAGGC 18

RESULT 2
 AX402704
 LOCUS
 DEFINITION Sequence 188 from Patent WO0196612.
 ACCESSION AX402704
 VERSION AX402704.1 GI:21387695

KEYWORDS
 ORGANISM
 SOURCE Stachybotrys chartarum.
 Stachybotrys chartarum.
 Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Stachybotrys.

REFERENCE 1
 AUTHORS Haugland, R. and Vesper, S.
 TITLE Method of identifying and quantifying specific fungi and bacteria
 JOURNAL Patent: WO 0196612-A 188 20-DEC-2001
 UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
 Location/Qualifiers
 1. 18
 /organism="Stachybotrys chartarum"
 /db_xref="taxon:74722"

FEATURES

BASE COUNT 2 a 8 c 6 g 2 t

Query Match 100.0%; Score 18; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGCCCGGATCCAGGC 18
 DB 1 CTGGCCCGGATCCAGGC 18

RESULT 3
 AR169747
 LOCUS
 DEFINITION Sequence 2 from patent US 6291190.
 ACCESSION AR169747
 VERSION AR169747.1 GI:17907655

KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE

1 (bases 1 to 21)
 Behr, M., Small, P., Schoolnik, G. and Wilson, M.A.
 TITLE Molecular differences between species of the M. tuberculosis complex
 JOURNAL Patent: US 6291190-A 2 18-SEP-2001;
 Location/Qualifiers
 1. 21
 /organism="unknown"

BASE COUNT 4 a 11 c 5 g 1 t

Query Match 72.2%; Score 13; DB 6; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGCCCGGATCCAG 16
|||||
Db 9 CGCCCGGATCCAG 21

RESULT 4
AR210194/c AR210194 17 bp DNA linear PAT 20-JUN-2002
LOCUS AR210194/c
DEFINITION Sequence 106 from patent US 6387652.
ACCESSION AR210194
VERSION AR210194.1 GI:21512362
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Haugland R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: US 6387652-A 106 14-MAY-2002;
FEATURES Location/Qualifiers
source
BASE COUNT 0 a 8 c 6 g 3 t
ORIGIN

Query Match 71.1%; Score 12.8; DB 6; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGCCCGGATCCAGGC 18
|||||
Db 17 GCGCCCGGATCCAGGC 2

RESULT 5
AX402622/c AX402622 17 bp DNA linear PAT 07-JUN-2002
LOCUS AX402622/c
DEFINITION Sequence 106 from Patent WO0196612.
ACCESSION AX402622
VERSION AX402622.1 GI:21387613
KEYWORDS
SOURCE Myrothecium verrucaria.
ORGANISM Myrothecium verrucaria
REFERENCE 1
AUTHORS Haugland R. and Vesper, S.
TITLE Method of identifying and quantifying specific fungi and bacteria
JOURNAL Patent: WO 0196612-A 106 20-DEC-2001;
FEATURES Location/Qualifiers
source
BASE COUNT 0 a 8 c 6 g 3 t
ORIGIN

Query Match 71.1%; Score 12.8; DB 6; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGCCCGGATCCAGGC 18
|||||
Db 17 GCGCCCGGATCCAGGC 2

RESULT 6
104828 18 bp DNA linear PAT 02-DEC-1994
LOCUS 104828
DEFINITION Sequence 7 from Patent EP 0212532.
ACCESSION 104828

VERSION 104828.1 GI:591433
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Chan, H.W., Shelton, E.R., Baecker, P.A., Salazar, F.H., Martin, M.A.
TITLE Method for producing fusion proteins
JOURNAL Patent: EP 0212532-A1 7 04-MAR-1987;
FEATURES Location/Qualifiers
source
BASE COUNT 1 a 7 c 7 g 3 t
ORIGIN

Query Match 68.9%; Score 12.4; DB 6; Length 18;
Best Local Similarity 92.9%; Pred. No. 3.1e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCGCCCGGATCC 14
|||||
Db 1 CTGCGCCCGGATCC 14

RESULT 7
I71353/c I71353 22 bp DNA linear PAT 03-APR-1998
LOCUS I71353/c
DEFINITION Sequence 2 from patent US 5681725.
ACCESSION I71353
VERSION I71353.1 GI:3007488
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Jensen, E. Bech.
TITLE Process for producing heme proteins
JOURNAL Patent: US 5681725-A 2 28-OCT-1997;
FEATURES Location/Qualifiers
source
BASE COUNT 4 a 5 c 10 g 3 t
ORIGIN

Query Match 68.9%; Score 12.4; DB 6; Length 22;
Best Local Similarity 92.9%; Pred. No. 3e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCGCCCGGATCC 14
|||||
Db 16 CTGCGCCCGGATCC 3

RESULT 8
AX404363/c AX404363 21 bp DNA linear PAT 14-JUN-2002
LOCUS AX404363/c
DEFINITION Sequence 189 from Patent WO0224747.
ACCESSION AX404363
VERSION AX404363.1 GI:21437644
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Brinkmann, U. and Hoffmeyer, S.
TITLE Polymorphisms in human genes of cardiovascular regulators and their use in diagnostic and therapeutic applications
JOURNAL Patent: WO 0224747-A 189 28-MAR-2002;
FEATURES Location/Qualifiers
source
BASE COUNT 1 a 21
ORGANISM="synthetic construct"

/db_xref="taxon:32630"
/note="artificial sequence-n=a or g"
BASE COUNT 5 a 3 c 9 g 3 t 1 others
ORIGIN

Query Match 67.8%; Score 12.2; DB 6; Length 21;
Best Local Similarity 77.8%; Pred. No. 3.7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGGCCCGGATCCAGC 18
|||
20 CTGGCCGAGATCCAGC 3

RESULT 9
LOCUS AX404364 21 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 190 from Patent WO0224747.
ACCESSION AX404364
VERSION AX404364.1 GI:21437645
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Brinkmann, U. and Hoffmeyer, S.
TITLE Polymorphisms in human genes of cardiovascular regulators and their use in diagnostic and therapeutic applications
JOURNAL Patent: WO 0224747-A 190 28-MAR-2002;
FEATURES
SOURCE location/Qualifiers
1.21.
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="artificial sequence-n=t or c"

BASE COUNT 3 a 9 c 3 g 5 t 1 others
ORIGIN

Query Match 67.8%; Score 12.2; DB 6; Length 21;
Best Local Similarity 77.8%; Pred. No. 3.7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGGCCCGGATCCAGC 18
|||
2 CTGGCCGAGATCCAGC 19

RESULT 10
LOCUS I04832 18 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 11 from Patent EP 0212532.
ACCESSION I04832
VERSION I04832.1 GI:591435
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Chan, H.W., Shelton, E.R., Baecker, P.A., Salazar, F.H., Martin, M.A.
TITLE Method for producing fusion proteins
JOURNAL Patent: EP 0212532-A1 11 04-MAR-1987;
FEATURES
SOURCE location/Qualifiers
1.18
/organism="unknown"

BASE COUNT 1 a 8 c 6 g 3 t
ORIGIN

Query Match 66.7%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGCCGAGATCC 14

|||||
DB 5 GCGCCGAGATCC 16

RESULT 11
LOCUS AX096029 21 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 1207 from Patent WO0118250.
ACCESSION AX096029
VERSION AX096029.1 GI:13512256
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 21)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Lander, E.S., Gargill, M., Ireland, J.S., Bol, S., Daley, G.O. and Mccarthy, J.J.
JOURNAL Single nucleotide polymorphisms in genes
Patent: WO 0118250-A 1207 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium Pharmaceuticals, Inc. (US)
FEATURES
SOURCE location/Qualifiers
1.21
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 2 a 6 c 10 g 2 t 1 others
ORIGIN

Query Match 66.7%; Score 12; DB 6; Length 21;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGCCCGGATCC 14
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18 CTGGCCGAGATCC 5

RESULT 12
LOCUS AR139910 25 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 88 from patent US 6207416.
ACCESSION AR139910
VERSION AR139910.1 GI:14482406
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Tsarev, S.A., Emerson, S.U. and Purcell, R.H.
TITLE Recombinant proteins of a Pakistani strain of hepatitis E and their use in diagnostic methods and vaccines
JOURNAL Patent: US 6207416-A 88 27-MAR-2001;
FEATURES
SOURCE location/Qualifiers
1.25
/organism="unknown"

BASE COUNT 4 a 6 c 10 g 5 t
ORIGIN

Query Match 66.7%; Score 12; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCGGATCCAGC 18
|||
20 CCGGATCCAGC 9

RESULT 13
LOCUS AR167554 25 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 88 from patent US 6287759.
ACCESSION AR167554

VERSION AR167554.1 GI:17903340
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Tearey,S.A., Emerson,S.U. and Purcell,R.H.
TITLE Recombinant proteins of a Pakistani strain of hepatitis E and their use in diagnostic methods and vaccines
JOURNAL Patent: US 6287759-A 88 11-SEP-2001;
FEATURES
source Location/Qualifiers
1..25
/organism="unknown"
BASE COUNT 4 a 6 c 10 g 5 t
ORIGIN
Query Match 66.7%; Score 12; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.5e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 CCGGATCCAGGC 18
Db 20 CCGGATCCAGGC 9

RESULT 14
A38123/c 18 bp DNA linear PAT 05-MAR-1997
LOCUS Sequence 3 from Patent EP0605040.
DEFINITION A38123
ACCESSION A38123.1 GI:2294734
VERSION
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Deweer,P. and Amory,A.
TITLE Pullulanase, micro-organisms producing the same, method for preparation thereof as well as its use
JOURNAL Patent: EP 0605040-A 3 06-JUL-1994;
COMMENT SOLVAY (BE)
Other publication JP 6217770 940809
Other publication CA 2112028 940629
Other publication CN 1090325 940803
Other publication AU 5275893 940707
Other publication FI 935900 940629
Other publication BE 1007723 951010
Other publication BE 1007313 950516
Other publication BE 1006483 940913.
FEATURES
source Location/Qualifiers
1..18
/organism="unclassified"
/db_xref="taxon:32644"
BASE COUNT 2 a 6 c 7 g 3 t
ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.8e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CTGGCCCGGATCCA 15
Db 16 CTGGCCCGGATCCA 2

RESULT 15
A42267/c 18 bp DNA linear PAT 05-MAR-1997
LOCUS Sequence 17 from Patent EP0634490.
DEFINITION A42267
ACCESSION A42267.1 GI:2297757
VERSION
KEYWORDS
SOURCE unidentified.

ORGANISM unidentified.
REFERENCE unclassified.
AUTHORS 1 (bases 1 to 18)
TITLE De,B.E., Lahaya,A., Ledoux,P., Amory,A., Detroz,R., Andre,C. and Vetter,R.
Xylanase derived from a bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use thereof
JOURNAL Patent: EP 0634490-A 17 18-JAN-1995;
COMMENT SOLVAY (BE)
Other publication NZ 260989 950828
Other publication BR 9402834 950613
Other publication JP 7067637 950314
Other publication FI 943389 950116
Other publication CA 2128050 950116
Other publication NO 942652 950116
Other publication AU 6743284 950127
Other publication GB 2279955 950118.
FEATURES
source Location/Qualifiers
1..18
/organism="unclassified"
/db_xref="taxon:32644"
BASE COUNT 2 a 6 c 7 g 3 t
ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.8e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CTGGCCCGGATCCA 15
Db 16 CTGGCCCGGATCCA 2

RESULT 16
AR000469/c 18 bp DNA linear PAT 04-DEC-1998
LOCUS Sequence 3 from patent US 5736375.
DEFINITION AR000469
ACCESSION AR000469.1 GI:3963000
VERSION
KEYWORDS
SOURCE Unknown.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Deweer,P. and Amory,A.
TITLE Expression system for novel pullulanase
JOURNAL Patent: US 5736375-A 3 07-APR-1998;
FEATURES
source Location/Qualifiers
1..18
/organism="unknown"
BASE COUNT 2 a 6 c 7 g 3 t
ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.8e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CTGGCCCGGATCCA 15
Db 16 CTGGCCCGGATCCA 2

RESULT 17
AR044543/c 18 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 3 from patent US 5817498.
DEFINITION AR044543
ACCESSION AR044543.1 GI:5966008
VERSION
KEYWORDS
SOURCE Unknown.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 18)
AUTHORS Deweer, P. and Amory, A.
TITLE Pullulanase producing microorganisms
JOURNAL Patent: US 5817498-A 3 06-OCT-1998;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"

BASE COUNT 2 a 6 c 7 g 3 t
ORIGIN

Query Match 65.6%; Score 11.8; DB 6; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.8e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGGCCCCGATCCA 15
16 CTGGCCCGAGAGCCA 2

RESULT 18
AR098234/c 18 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 3 from patent US 6074854.
DEFINITION AR098234
ACCESSION AR098234
VERSION AR098234.1 GI:12807491
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Deweer, P. and Amory, A.
TITLE Pullulanase, microorganisms which produce it, processes for the
JOURNAL Preparation of this pullulanase and the uses thereof
FEATURES Patent: US 6074854-A 3 13-JUN-2000;
source Location/Qualifiers
1..18
/organism="unknown"

BASE COUNT 2 a 6 c 7 g 3 t
ORIGIN

Query Match 65.6%; Score 11.8; DB 6; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.8e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGGCCCCGATCCA 15
16 CTGGCCCGAGAGCCA 2

RESULT 19
ARI27034/c 18 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 17 from patent US 6180382.
DEFINITION ARI27034
ACCESSION ARI27034
VERSION ARI27034.1 GI:14113627
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS De Buy, E., Lahaye, A., Ledoux, P., Amory, A., Detroz, R., Andre, C. and
TITLE Vetter, R.
Xylanase derived from a bacillus species, expression vectors for
such xylanase and other proteins, host organisms therefor and use
thereof
JOURNAL Patent: US 6180382-A 17 30-JAN-2001;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"

BASE COUNT 2 a 6 c 7 g 3 t
ORIGIN

Query Match 65.6%; Score 11.8; DB 6; Length 13;

Best Local Similarity 86.7%; Pred. No. 5.8e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGGCCCCGATCCA 15
16 CTGGCCCGAGAGCCA 2

RESULT 20
I89306/c 18 bp DNA linear PAT 10-AUG-1998
LOCUS Sequence 3 from patent US 5721127.
DEFINITION I89306
ACCESSION I89306
VERSION I89306.1 GI:3409246
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Deweer, P. and Amory, A.
TITLE Pullulanase
JOURNAL Patent: US 5721127-A 3 24-FEB-1998;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"

BASE COUNT 2 a 6 c 7 g 3 t
ORIGIN

Query Match 65.6%; Score 11.8; DB 6; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.8e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGGCCCCGATCCA 15
16 CTGGCCCGAGAGCCA 2

RESULT 21
I89318/c 18 bp DNA linear PAT 10-AUG-1998
LOCUS Sequence 3 from patent US 5721128.
DEFINITION I89318
ACCESSION I89318
VERSION I89318.1 GI:3409258
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Deweer, P. and Amory, A.
TITLE Process for the production of novel pullulanase
JOURNAL Patent: US 5721128-A 3 24-FEB-1998;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"

BASE COUNT 2 a 6 c 7 g 3 t
ORIGIN

Query Match 65.6%; Score 11.8; DB 6; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.8e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGGCCCCGATCCA 15
16 CTGGCCCGAGAGCCA 2

RESULT 22
I93614/c 18 bp DNA linear PAT 01-DEC-1998
LOCUS Sequence 3 from patent US 5731174.
DEFINITION I93614
ACCESSION I93614
VERSION I93614.1 GI:3938084
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Demeer, P. and Amory, A.
TITLE Process for the saccharification of starch
JOURNAL Patent: US 5731174-A 3 24-MAR-1998;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
BASE COUNT 2 a 6 c 7 g 3 t
ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.6e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CTGCGCCCGATCCGA 15
Db 16 CTGCGCCAGAGCCA 2
RESULT 23
A32651/c 24 bp DNA linear PAT 30-JUL-1996
LOCUS A32651
DEFINITION Synthetic HBBag gene adapter sequence.
ACCESSION A32651
VERSION A32651.1 GI:1567500
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 24)
AUTHORS Thoma, H.A.D.
TITLE Peptide comprising hepatitis B surface antigen
JOURNAL Patent: EP 0304578-A 34 01-MAR-1989;
FEATURES location/Qualifiers
source 1..24
/organism="synthetic construct"
/db_xref="taxon:32630"
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ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 24;
Best Local Similarity 86.7%; Pred. No. 5.6e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGCGCCCGATCCAG 16
Db 24 TGAGCTCGATCCAG 10
RESULT 24
A32652 24 bp DNA linear PAT 30-JUL-1996
LOCUS A32652
DEFINITION Synthetic HBBag gene adapter sequence.
ACCESSION A32652
VERSION A32652.1 GI:1567501
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 24)
AUTHORS Thoma, H.A.D.
TITLE Peptide comprising hepatitis B surface antigen
JOURNAL Patent: EP 0304578-A 35 01-MAR-1989;
FEATURES location/Qualifiers
source 1..24
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 5 a 6 c 7 g 6 t

ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 24;
Best Local Similarity 86.7%; Pred. No. 5.6e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGCGCCCGATCCAG 16
Db 5 TGAGCTCGATCCAG 19
RESULT 25
AR097798/c 24 bp DNA linear PAT 14-FEB-2001
LOCUS AR097798
DEFINITION Sequence 25 from patent US 6072049.
ACCESSION AR097798
VERSION AR097798.1 GI:12806528
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Thoma, H.A.
TITLE Hepatitis B surface antigen vaccine
JOURNAL Patent: US 6072049-A 25 06-JUN-2000;
FEATURES location/Qualifiers
source 1..24
/organism="unknown"
BASE COUNT 7 a 6 c 5 g 6 t
ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 24;
Best Local Similarity 86.7%; Pred. No. 5.6e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGCGCCCGATCCAG 16
Db 24 TGAGCTCGATCCAG 10
RESULT 26
AR097799 24 bp DNA linear PAT 14-FEB-2001
LOCUS AR097799
DEFINITION Sequence 26 from patent US 6072049.
ACCESSION AR097799
VERSION AR097799.1 GI:12806529
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Thoma, H.A.
TITLE Hepatitis B surface antigen vaccine
JOURNAL Patent: US 6072049-A 26 06-JUN-2000;
FEATURES location/Qualifiers
source 1..24
/organism="unknown"
BASE COUNT 5 a 6 c 7 g 6 t
ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 24;
Best Local Similarity 86.7%; Pred. No. 5.6e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGCGCCCGATCCAG 16
Db 5 TGAGCTCGATCCAG 19
RESULT 27
191779 24 bp DNA linear PAT 01-DEC-1998
LOCUS 191779
DEFINITION Sequence 13 from patent US 5726025.

ACCESSION 191779
 VERSION 191779.1 GI:3936249
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 24)
 AUTHORS Kirschner, M.W., King, R.W. and Peters, J.-M.
 TITLE Assay and reagents for detecting inhibitors of ubiquitin-dependent degradation of cell cycle regulatory proteins
 JOURNAL Patent: US 5726025-A 13 10-MAR-1998;
 FEATURES Location/Qualifiers
 source 1..24
 /organism="unknown"
 BASE COUNT 3 a 7 c 10 g 4 t
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 Query Match 65.6%; Score 11.8; DB 6; Length 24;
 Best Local Similarity 86.7%; Pred. No. 5.6e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 GCGCCGGATCCAGG 17
 Db 1 GCGCCGGATCCATG 15
 RESULT 28
 A75774/c 25 bp DNA linear PAT 15-OCT-1999
 LOCUS A75774 Sequence 43 from Patent WO9322437.
 ACCESSION A75774
 VERSION A75774.1 GI:6065722
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Fransen, L. and Devos, K.
 TITLE NEW POLYPEPTIDES AND PEPTIDES, NUCLEIC ACIDS CODING FOR THEM, AND THEIR USE IN THE FIELD OF TUMOR THERAPY, INFLAMMATION OR IMMUNOLOGY
 JOURNAL Patent: WO 9322437-A 43 11-NOV-1993;
 INNOGENETICS NV (BE); FRANSSEN LUCIA (BE)
 FEATURES Location/Qualifiers
 source 1..25
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 /db_xref="taxon:9606"
 /cell_line="THP-1"
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 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 CGCCCGATCCAGG 18
 Db 17 CGCCCTGCTCCAGGC 3
 RESULT 29
 AR085110/c 25 bp DNA linear PAT 01-SEP-2000
 LOCUS AR085110 Sequence 43 from patent US 5981277.
 ACCESSION AR085110
 VERSION AR085110.1 GI:10011881
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Fransen, L., Devos, K., Van De Voorde, A. and Van Heuverswyn, H.
 TITLE Polypeptides and peptides, nucleic acids coding for them, and their

use in the field of tumor therapy, inflammation or immunology
 JOURNAL Patent: US 5981277-A 43 09-NOV-1999;
 FEATURES Location/Qualifiers
 source 1..25
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 BASE COUNT 2 a 7 c 11 g 5 t
 ORIGIN
 Query Match 65.6%; Score 11.8; DB 6; Length 25;
 Best Local Similarity 86.7%; Pred. No. 5.5e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 CGCCCGATCCAGG 18
 Db 17 CGCCCTGCTCCAGGC 3
 RESULT 30
 AX322593/c 19 bp DNA linear PAT 07-JUN-2002
 LOCUS AX322593 Sequence 54 from Patent WO0192539.
 DEFINITION AX322593
 ACCESSION AX322593
 VERSION AX322593.1 GI:18093613
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1
 AUTHORS Ben-Bassat, A., Cattermole, M., Gatenby, A.A., Gibson, K.J., Ramos-Gonzales, M.I., Ramos, D.L. and Sarislahti, S.
 TITLE Method for the production of p-hydroxybenzoate in species of Pseudomonas and Agrobacterium
 JOURNAL Patent: WO 0192539-A 54 06-DEC-2001;
 E.I. DUPONT DE NEMOURS AND COMPANY, Legal Patent Records Center (US)
 FEATURES Location/Qualifiers
 source 1..19
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="primer-primer used for sequencing pcu"
 BASE COUNT 2 a 5 c 7 g 5 t
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 Best Local Similarity 77.8%; Pred. No. 7.1e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CTGGCGCCGATCCAGG 18
 Db 18 CAGCACCCGATCCAGGC 1
 RESULT 31
 AR021129/c 21 bp DNA linear PAT 05-DEC-1998
 LOCUS AR021129 Sequence 23 from patent US 5789248.
 ACCESSION AR021129
 VERSION AR021129.1 GI:3975744
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Federad, O., Hovig, E., Engedraaten, O., Maelandsmo, G. and Agrawal, S.
 TITLE CAPT-specific oligonucleotides and method of inhibiting metastatic cancer
 JOURNAL Patent: US 5789248-A 23 04-AUG-1998;
 FEATURES Location/Qualifiers
 source 1..21
 /organism="unknown"
 BASE COUNT 5 a 3 c 10 g 3 t
 ORIGIN

Query Match 64.4%; Score 11.6; DB 6; Length 21;
Best Local Similarity 77.8%; Pred. No. 7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGGCGCCGATCCAGGC 18
DB 18 CTGCTCCGAGATCTGAC 1

RESULT 32
LOCUS AX404361 21 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 187 from Patent WO0224747.
ACCESSION AX404361
VERSION AX404361.1 GI:21437642
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Brinkmann, U. and Hoffmeyer, S.
TITLE Polymorphisms in human genes of cardiovascular regulators and their use in diagnostic and therapeutic applications
JOURNAL Patent: WO 0224747-A 187 28-MAR-2002;
Epidaurus Biotechnology AG (DE)
FEATURES
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/note="artificial sequence"

BASE COUNT 6 a 3 c 9 g 3 t
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Best Local Similarity 77.8%; Pred. No. 7e+05;
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QY 1 CTGGCGCCGATCCAGGC 18
DB 20 CTTCGCCAGTATCCAGC 3

RESULT 33
LOCUS AX404362 21 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 188 from Patent WO0224747.
ACCESSION AX404362
VERSION AX404362.1 GI:21437643
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Brinkmann, U. and Hoffmeyer, S.
TITLE Polymorphisms in human genes of cardiovascular regulators and their use in diagnostic and therapeutic applications
JOURNAL Patent: WO 0224747-A 188 28-MAR-2002;
Epidaurus Biotechnology AG (DE)
FEATURES
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/db_xref="taxon:32630"
/note="artificial sequence"

BASE COUNT 3 a 9 c 3 g 6 t
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Query Match 64.4%; Score 11.6; DB 6; Length 21;
Best Local Similarity 77.8%; Pred. No. 7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGGCGCCGATCCAGGC 18
DB 2 CTTCGCCAGTATCCAGC 19

RESULT 34
LOCUS AX404365 21 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 191 from Patent WO0224747.
ACCESSION AX404365
VERSION AX404365.1 GI:21437646
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Brinkmann, U. and Hoffmeyer, S.
TITLE Polymorphisms in human genes of cardiovascular regulators and their use in diagnostic and therapeutic applications
JOURNAL Patent: WO 0224747-A 191 28-MAR-2002;
Epidaurus Biotechnology AG (DE)
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/db_xref="taxon:32630"
/note="artificial sequence"

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Query Match 64.4%; Score 11.6; DB 6; Length 21;
Best Local Similarity 77.8%; Pred. No. 7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGGCGCCGATCCAGGC 18
DB 20 CTTCGCCAGTATCCAGC 3

RESULT 35
LOCUS AX404366 21 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 192 from Patent WO0224747.
ACCESSION AX404366
VERSION AX404366.1 GI:21437647
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Brinkmann, U. and Hoffmeyer, S.
TITLE Polymorphisms in human genes of cardiovascular regulators and their use in diagnostic and therapeutic applications
JOURNAL Patent: WO 0224747-A 192 28-MAR-2002;
Epidaurus Biotechnology AG (DE)
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/db_xref="taxon:32630"
/note="artificial sequence"

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Query Match 64.4%; Score 11.6; DB 6; Length 21;
Best Local Similarity 77.8%; Pred. No. 7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGGCGCCGATCCAGGC 18
DB 2 CTTCGCCAGTATCCAGC 19

RESULT 36
LOCUS AR021109 22 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 3 from patent US 5769248.
ACCESSION AR021109

VERSION AR021109.1 GI:3975724
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 22)
 AUTHORS Foderstad, O., Hovig, E., Engebraaten, O., Maelandsmo, G. and Agrawal, S.
 TITLE CAPL-specific oligonucleotides and method of inhibiting metastatic cancer
 JOURNAL Patent: US 5789248-A 3 04-AUG-1998;
 FEATURES Location/Qualifiers
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 /organism="unknown"
 BASE COUNT 5 a 3 c 11 g 3 t
 ORIGIN
 Query Match 64.4%; Score 11.6; DB 6; Length 22;
 Best Local Similarity 77.8%; Pred. No. 6.9e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 CTGGCCCGGATCCAGGC 18
 18 CTGCTCCAGATCCTGAC 1
 Db
 RESULT 37
 LOCUS AR021110 22 bp DNA linear PAT 05-DEC-1998
 DEFINITION Sequence 4 from patent US 5789248.
 ACCESSION AR021110
 VERSION AR021110.1 GI:3975725
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 22)
 AUTHORS Foderstad, O., Hovig, E., Engebraaten, O., Maelandsmo, G. and Agrawal, S.
 TITLE CAPL-specific oligonucleotides and method of inhibiting metastatic cancer
 JOURNAL Patent: US 5789248-A 4 04-AUG-1998;
 FEATURES Location/Qualifiers
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 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 CTGGCCCGGATCCAGGC 18
 18 CTGCTCCAGATCCTGAC 1
 Db
 RESULT 38
 LOCUS AR036253 22 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 3 from patent US 5872007.
 ACCESSION AR036253
 VERSION AR036253.1 GI:5952921
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 22)
 AUTHORS Foderstad, O., Hovig, E., Engebraaten, O., Maelandsmo, G. and Agrawal, S.
 TITLE CAPL-specific oligonucleotides and methods of inhibiting metastatic cancer
 JOURNAL Patent: US 5872007-A 3 16-FEB-1999;
 FEATURES Location/Qualifiers
 source 1..22
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 Best Local Similarity 77.8%; Pred. No. 6.9e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 CTGGCCCGGATCCAGGC 18
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 RESULT 39
 LOCUS AR036254 22 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 4 from patent US 5872007.
 ACCESSION AR036254
 VERSION AR036254.1 GI:5952922
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 22)
 AUTHORS Foderstad, O., Hovig, E., Engebraaten, O., Maelandsmo, G. and Agrawal, S.
 TITLE CAPL-specific oligonucleotides and methods of inhibiting metastatic cancer
 JOURNAL Patent: US 5872007-A 4 16-FEB-1999;
 FEATURES Location/Qualifiers
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 /organism="unknown"
 BASE COUNT 5 a 3 c 11 g 3 t
 ORIGIN
 Query Match 64.4%; Score 11.6; DB 6; Length 22;
 Best Local Similarity 77.8%; Pred. No. 6.9e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 CTGGCCCGGATCCAGGC 18
 18 CTGCTCCAGATCCTGAC 1
 Db
 RESULT 40
 LOCUS AX031299 24 bp DNA linear PAT 20-SEP-2000
 DEFINITION Sequence 21 from Patent WO9914321.
 ACCESSION AX031299
 VERSION AX031299.1 GI:10278627
 KEYWORDS Unidentified.
 SOURCE Unidentified.
 ORGANISM Unidentified.
 REFERENCE 1 (bases 1 to 24)
 AUTHORS O'Reilly, L., Puthalakath, H., Adams, J., O'Connor, L., Cory, S., Huang, D. C. and Strasser, A.
 TITLE Novel therapeutic molecules
 JOURNAL Patent: WO 9914321-A 21 25-MAR-1999;
 INST MEDICAL W & B HALL (AU); PUTHALAKATH HANSA (AU); REILLY LORRAINE O (AU); ADAMS JERRY (AU); CONNOR LIAM O (AU); CORY SUZANNE (AU); HUANG DAVID C S (AU); STRASSER ANDREAS (AU)
 FEATURES Location/Qualifiers
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 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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 18 CTGCTCCAGATCCTGAC 1
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BASE COUNT 5 a 3 c 11 g 3 t
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 Query Match 64.4%; Score 11.6; DB 6; Length 22;
 Best Local Similarity 77.8%; Pred. No. 6.9e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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 18 CTGCTCCAGATCCTGAC 1
 Db
 RESULT 39
 LOCUS AR036254 22 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 4 from patent US 5872007.
 ACCESSION AR036254
 VERSION AR036254.1 GI:5952922
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 22)
 AUTHORS Foderstad, O., Hovig, E., Engebraaten, O., Maelandsmo, G. and Agrawal, S.
 TITLE CAPL-specific oligonucleotides and methods of inhibiting metastatic cancer
 JOURNAL Patent: US 5872007-A 4 16-FEB-1999;
 FEATURES Location/Qualifiers
 source 1..22
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 BASE COUNT 5 a 3 c 11 g 3 t
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 Query Match 64.4%; Score 11.6; DB 6; Length 22;
 Best Local Similarity 77.8%; Pred. No. 6.9e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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 18 CTGCTCCAGATCCTGAC 1
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 RESULT 40
 LOCUS AX031299 24 bp DNA linear PAT 20-SEP-2000
 DEFINITION Sequence 21 from Patent WO9914321.
 ACCESSION AX031299
 VERSION AX031299.1 GI:10278627
 KEYWORDS Unidentified.
 SOURCE Unidentified.
 ORGANISM Unidentified.
 REFERENCE 1 (bases 1 to 24)
 AUTHORS O'Reilly, L., Puthalakath, H., Adams, J., O'Connor, L., Cory, S., Huang, D. C. and Strasser, A.
 TITLE Novel therapeutic molecules
 JOURNAL Patent: WO 9914321-A 21 25-MAR-1999;
 INST MEDICAL W & B HALL (AU); PUTHALAKATH HANSA (AU); REILLY LORRAINE O (AU); ADAMS JERRY (AU); CONNOR LIAM O (AU); CORY SUZANNE (AU); HUANG DAVID C S (AU); STRASSER ANDREAS (AU)
 FEATURES Location/Qualifiers
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 /db_xref="taxon:32644"
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 Query Match 64.4%; Score 11.6; DB 6; Length 24;
 Best Local Similarity 77.8%; Pred. No. 6.9e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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 18 CTGCTCCAGATCCTGAC 1
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Db 18 CTGCGCCGAGACTTGC 1

Search completed: June 7, 2003, 08:51:19
Job time : 406.418 secs

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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 08:05:49 / Search time 1030.58 Seconds
(without alignments)
282.866 Million cell updates/sec

Title: US-10-080-959a-5

Sequence: 1 ctgcgcgccgacccagc 18

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Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 18144

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: em_estba:*
2: em_esthm:*
3: em_estin:*
4: em_estmu:*
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6: em_estpl:*
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8: em_hic:*
9: gb_est1:*
10: gb_est2:*
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12: gb_est3:*
13: gb_est4:*
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23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rnd:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	11.2	62.2	23 13 BM394673	BM394673 50072-2-5
2	10.6	58.9	23 13 BM394673	BM394673 50072-2-5
3	10.6	58.9	24 17 A2634834	A2634834 1M0490C19
4	10.4	57.8	23 17 A2848503	A2848503 2M0149H02
5	10	55.6	19 17 A2855545	A2855545 2M0159F09
6	10	55.6	21 17 A2791884	A2791884 2M043A02

C 7	9.6	53.3	20 17 A2591658	A2591658 1M0401F19
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C 22	8.6	47.8	23 17 A2410218	A2410218 1M0182F23
C 23	8.6	47.8	23 17 A2979817	A2979817 2M0256F09
C 24	8.6	47.8	24 13 BM397860	BM397860 5009-0-38
C 25	8.6	47.8	24 17 TA368A07P	TA368A07P 5009-0-38
C 26	8.6	47.8	25 14 L32061	L32061 HMXPB8D18.H
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C 37	8.4	46.7	25 9 A1913416	A1913416 t277A09.x
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C 230	7.2	40.0	24	17	AZ834292	AZ834292	1M0216M23	C 303	7	38.9	24	17	AZ455814	AZ455814	1M0258B21
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C 233	7.2	40.0	25	9	AA923337	AA923337	T. brucei	C 306	7	38.9	24	17	AZ762096	AZ762096	1M0556J18
C 234	7.2	40.0	25	9	AA970868	AA970868	OP13E12.8	C 307	7	38.9	24	17	TA110D11P	TA110D11P	
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C 240	7.2	40.0	25	9	AA1720628	AA1720628	as70G12.x	C 313	7	38.9	25	9	AA1443365	AA1443365	BA31A10.x
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C 242	7.2	40.0	25	13	BM396165	BM396165	5009-0-18	C 315	7	38.9	25	9	AA1471126	AA1471126	tf90E05.x
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C 257	7.2	40.0	20	14	BO901239	BO901239	hasp002xa	C 330	7	38.9	25	17	AA2790171	AA2790171	SAUK_0546
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C 259	7.2	40.0	20	17	AA2484500	AA2484500	1M0311C01	C 332	7	38.9	25	17	AA2840574	AA2840574	KG05441-5
C 260	7.2	40.0	20	17	AA2600447	AA2600447	1M0418H15	C 333	7	38.9	25	17	AA2840574	AA2840574	KG05441-5
C 261	7.2	40.0	20	17	AA2637794	AA2637794	1M0497D20	C 334	7	38.9	25	17	AA2840574	AA2840574	KG05441-5
C 262	7.2	40.0	20	17	AA2662848	AA2662848	1M0542K07	C 335	7	38.9	25	17	AA2840574	AA2840574	KG05441-5
C 263	7.2	40.0	20	17	AA2764505	AA2764505	1M0560M06	C 336	7	38.9	25	17	AA2840574	AA2840574	KG05441-5
C 264	7.2	40.0	20	17	AA2764505	AA2764505	1M0560M06	C 337	7	38.9	25	17	AA2840574	AA2840574	KG05441-5
C 265	7.2	40.0	20	17	AA2782314	AA2782314	2M0022D03	C 338	7	38.9	25	17	AA2840574	AA2840574	KG05441-5
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C 267	7.2	40.0	20	17	AA2816586	AA2816586	2M0085H2	C 340	7	38.9	25	17	AA2840574	AA2840574	KG05441-5
C 268	7.2	40.0	20	17	AA2858804	AA2858804	2M0164F10	C 341	7	38.9	25	17	AA2840574	AA2840574	KG05441-5
C 269	7.2	40.0	21	17	AA2307451	AA2307451	1M0009B09	C 342	7	38.9	25	17	AA2840574	AA2840574	KG05441-5
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C 278	7.2	40.0	21	17	AA2956040	AA2956040	2M0222D03	C 351	7	38.9	25	17	AA2840574	AA2840574	KG05441-5
C 279	7.2	40.0	21	17	AA2981459	AA2981459	2M0258G21	C 352	7	38.9	25	17	AA2840574	AA2840574	KG05441-5
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C 282	7.2	40.0	22	17	AA2425344	AA2425344	1M0205G19	C 355	7	38.9	25	17	AA2840574	AA2840574	KG05441-5
C 283	7.2	40.0	22	17	AA2660257	AA2660257	1M0538F13	C 356	7	38.9	25	17	AA2840574	AA2840574	KG05441-5
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C 285	7.2	40.0	22	17	AA455010	AA455010	T. brucei	C 358	7	38.9	25	17	AA2840574	AA2840574	KG05441-5
C 286	7.2	40.0	23	17	AA2307822	AA2307822	1M0010J11	C 359	7	38.9	25	17	AA2840574	AA2840574	KG05441-5
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C 289	7.2	40.0	23	17	AA2448352	AA2448352	2M0246A06	C 362	7	38.9	25	17	AA2840574	AA2840574	KG05441-5
C 290	7.2	40.0	23	17	AA2781489	AA2781489	2M0019N20	C 363	7	38.9	25	17	AA2840574	AA2840574	KG05441-5
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C 292	7.2	40.0	23	17	AA2822965	AA2822965	2M0096L11	C 365	7	38.9	25	17	AA2840574	AA2840574	KG05441-5
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C 294	7.2	40.0	23	17	AA2954677	AA2954677	2M0220C24	C 367	7	38.9	25	17	AA2840574	AA2840574	KG05441-5
C 295	7.2	40.0	23	17	AA2954677	AA2954677	2M0220C24	C 368	7	38.9	25	17	AA2840574	AA2840574	KG05441-5
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C 297	7.2	40.0	23	17	AA2954677	AA2954677	2M0220C24	C 370	7	38.9	25	17	AA2840574	AA2840574	KG05441-5
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373	6.8	37.8	22	17	AZ584779	AZ584779	1M0389112	C 446	6.6	36.7	20	17	AZ773092	AZ773092	1M0584K20
374	6.8	37.8	22	17	AZ788996	AZ788996	2M0035C02	C 447	6.6	36.7	20	17	AZ789755	AZ789755	2M0037O13
375	6.8	37.8	22	17	AZ984502	AZ984502	2M0265U05	C 448	6.6	36.7	20	17	AZ810573	AZ810573	2M0076K11
376	6.8	37.8	23	10	AM247451	AM247451	2819438.5	C 449	6.6	36.7	20	17	AZ832127	AZ832127	2M0112M17
377	6.8	37.8	23	17	AZ309657	AZ309657	1M0016C24	C 450	6.6	36.7	21	9	AL585450	AL585450	AL585450
378	6.8	37.8	23	17	AZ342826	AZ342826	1M0076C04	C 451	6.6	36.7	21	13	BM395436	BM395436	50072-2-9
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380	6.8	37.8	23	17	AZ470337	AZ470337	1M0284D21	C 453	6.6	36.7	21	17	AZ443871	AZ443871	1M0238I07
381	6.8	37.8	23	17	AZ480676	AZ480676	1M0302F23	C 454	6.6	36.7	21	17	AZ466689	AZ466689	1M0277L03
382	6.8	37.8	23	17	AZ769548	AZ769548	1M0570I20	C 455	6.6	36.7	21	17	AZ466689	AZ466689	1M0277L03
383	6.8	37.8	23	17	AZ771520	AZ771520	1M0573H21	C 456	6.6	36.7	21	17	AZ511843	AZ511843	1M0357K05
384	6.8	37.8	23	17	AZ781778	AZ781778	2M0021E24	C 457	6.6	36.7	21	17	AZ785825	AZ785825	2M0030G05
385	6.8	37.8	23	17	AZ806883	AZ806883	2M0069B15	C 458	6.6	36.7	21	17	AZ794048	AZ794048	2M0047H07
C 386	6.8	37.8	23	17	HSMC03F05	HSMC03F05		C 459	6.6	36.7	21	17	AZ794048	AZ794048	2M0047H07
C 387	6.8	37.8	23	17	TA215B01P	TA215B01P		C 460	6.6	36.7	21	17	AZ801929	AZ801929	2M0060A09
C 388	6.8	37.8	24	17	AZ307299	AZ307299	1M0008D23	C 461	6.6	36.7	21	17	AZ819369	AZ819369	2M0089O21
C 389	6.8	37.8	24	17	AZ313141	AZ313141	1M0029D19	C 462	6.6	36.7	21	17	AZ830003	AZ830003	2M0109A04
C 390	6.8	37.8	24	17	AZ313141	AZ313141	1M0029D19	C 463	6.6	36.7	21	17	AZ841128	AZ841128	2M0138P22
C 391	6.8	37.8	24	17	AZ336588	AZ336588	1M0224H20	C 464	6.6	36.7	21	17	AZ841128	AZ841128	2M0138P22
C 392	6.8	37.8	24	17	AZ437306	AZ437306	1M0225D03	C 465	6.6	36.7	21	17	AZ873829	AZ873829	2M0187C15
C 393	6.8	37.8	24	17	AZ486765	AZ486765	1M0319P08	C 466	6.6	36.7	22	9	AA904202	AA904202	0920E11.s
C 394	6.8	37.8	24	17	AZ608837	AZ608837	1M0433L14	C 467	6.6	36.7	22	9	AI035419	AI035419	ub46d05.r
C 395	6.8	37.8	24	17	AZ770304	AZ770304	1M0571K14	C 468	6.6	36.7	22	9	AI118718	AI118718	uc11h07.r
C 396	6.8	37.8	24	17	AZ77167	AZ77167	2M0011H19	C 469	6.6	36.7	22	9	AI267916	AI267916	qoz3h07.x
C 397	6.8	37.8	24	17	AZ805942	AZ805942	2M0067B10	C 470	6.6	36.7	22	9	AI739042	AI739042	w134f01.x
C 398	6.8	37.8	24	17	AZ807296	AZ807296	2M0070K03	C 471	6.6	36.7	22	13	BM399021	BM399021	5009-0-52
C 399	6.8	37.8	25	9	AA930851	AA930851	vz71b06.s	C 472	6.6	36.7	22	14	D21051	D21051	HUMGS02036
C 400	6.8	37.8	25	9	AI181643	AI181643	ub79h08.r	C 473	6.6	36.7	22	17	AZ402846	AZ402846	1M0170A20
C 401	6.8	37.8	25	9	AI299118	AI299118	qm14g07.x	C 474	6.6	36.7	22	17	AZ482065	AZ482065	1M0306M20
C 402	6.8	37.8	25	9	AI344221	AI344221	lc02h03.x	C 475	6.6	36.7	22	17	AZ623338	AZ623338	1M0460O19
C 403	6.8	37.8	25	9	AI594892	AI594892	vel2c06.x	C 476	6.6	36.7	22	17	AZ801946	AZ801946	2M0050E07
C 404	6.8	37.8	25	9	AI654281	AI654281	cg89f08.x	C 477	6.6	36.7	22	17	AZ822589	AZ822589	2M0095P21
C 405	6.8	37.8	25	9	AI914687	AI914687	ct26f09.x	C 478	6.6	36.7	22	17	AZ831937	AZ831937	2M011P22
C 406	6.8	37.8	25	10	AM004243	AM004243	701552628	C 479	6.6	36.7	22	17	AZ863707	AZ863707	2M0171N19
C 407	6.8	37.8	25	12	BF732128	BF732128	EST-NGR-1	C 480	6.6	36.7	22	17	AZ963488	AZ963488	2M0232J12
C 408	6.8	37.8	25	13	BI094828	BI094828	EST-CD34N	C 481	6.6	36.7	22	17	AZ984948	AZ984948	2M0266F12
C 409	6.8	37.8	25	13	BM399506	BM399506	5009-0-58	C 482	6.6	36.7	22	17	TA205F050	TA205F050	
C 410	6.8	37.8	25	13	BM400580	BM400580	5009-0-76	C 483	6.6	36.7	22	17	TA259H01Q	TA259H01Q	
C 411	6.8	37.8	25	17	AZ510410	AZ510410	1M0354H21	C 484	6.6	36.7	23	13	BG927951	BG927951	HNC45-1-F
C 412	6.8	37.8	25	17	AZ584819	AZ584819	1M0389A13	C 485	6.6	36.7	23	13	BG927951	BG927951	HNC45-1-F
C 413	6.8	37.8	25	17	AZ760021	AZ760021	1M0535F20	C 486	6.6	36.7	23	13	BM397594	BM397594	5009-0-35
C 414	6.8	37.8	25	17	AZ781069	AZ781069	2M0018P19	C 487	6.6	36.7	23	17	AZ316049	AZ316049	1M0066G07
C 415	6.8	37.8	25	17	AZ799779	AZ799779	2M0057K19	C 488	6.6	36.7	23	17	AZ392483	AZ392483	1M0155D08
C 416	6.8	37.8	25	17	AZ809724	AZ809724	2M0073B21	C 489	6.6	36.7	23	17	AZ605022	AZ605022	1M0426G12
C 417	6.8	37.8	25	17	AZ861588	AZ861588	2M0168J04	C 490	6.6	36.7	23	17	AZ808080	AZ808080	1M0426G12
C 418	6.8	37.8	25	17	BH759431	BH759431	KG04006-5	C 491	6.6	36.7	23	17	AZ844206	AZ844206	2M0143I11
C 419	6.8	37.8	25	17	TA274G11Q	TA274G11Q		C 492	6.6	36.7	23	17	TA134E100	TA134E100	
C 420	6.6	36.7	14	10	BE516032	BE516032	WHE0629.B	C 493	6.6	36.7	23	17	TA157C09Q	TA157C09Q	
C 421	6.6	36.7	15	12	BF219911	BF219911	601296879	C 494	6.6	36.7	23	17	TA67E07P	TA67E07P	
C 422	6.6	36.7	16	10	BE586084	BE586084	BEt#8PT7	C 495	6.6	36.7	24	13	BM393818	BM393818	
C 423	6.6	36.7	17	13	BM395525	BM395525	50072-2-5	C 496	6.6	36.7	24	13	BM396332	BM396332	5009-0-2
C 424	6.6	36.7	18	13	BM395302	BM395302	50072-2-8	C 497	6.6	36.7	24	13	BM396445	BM396445	5009-0-20
C 425	6.6	36.7	19	2	HSM007596	HSM007596		C 498	6.6	36.7	24	13	BM397719	BM397719	5009-0-36
C 426	6.6	36.7	19	9	AI811474	AI811474	FW3G04.x	C 499	6.6	36.7	24	17	AZ314206	AZ314206	1M0030H19
C 427	6.6	36.7	19	17	AZ307864	AZ307864	1M0010F16	C 500	6.6	36.7	24	17	AZ341038	AZ341038	1M0073B16
C 428	6.6	36.7	19	17	AZ400662	AZ400662	1M0167K06	C 501	6.6	36.7	24	17	AZ379773	AZ379773	1M0135H09
C 429	6.6	36.7	19	17	AZ488204	AZ488204	1M0318B21	C 502	6.6	36.7	24	17	AZ428114	AZ428114	1M0210A01
C 430	6.6	36.7	19	17	AZ493833	AZ493833	1M0328P11	C 503	6.6	36.7	24	17	AZ474773	AZ474773	1M0292F21
C 431	6.6	36.7	19	17	AZ661787	AZ661787	1M0540T06	C 504	6.6	36.7	24	17	AZ492799	AZ492799	1M0327B10
C 432	6.6	36.7	19	17	AZ864822	AZ864822	2M0174C08	C 505	6.6	36.7	24	17	AZ500040	AZ500040	1M0338K07
C 433	6.6	36.7	19	17	AZ948421	AZ948421	2M0211A01	C 506	6.6	36.7	24	17	AZ827494	AZ827494	1M0403M24
C 434	6.6	36.7	20	2	HSM008181	HSM008181		C 507	6.6	36.7	24	17	TA245F07P	TA245F07P	
C 435	6.6	36.7	20	2	HSM008199	HSM008199		C 508	6.6	36.7	24	17	TA379A12Q	TA379A12Q	
C 436	6.6	36.7	20	13	BM393608	BM393608	50072-2-1	C 509	6.6	36.7	25	9	AA034350	AA034350	
C 437	6.6	36.7	20	13	BM393440	BM393440	50072-2-3	C 510	6.6	36.7	25	9	AA880151	AA880151	
C 438	6.6	36.7	20	13	BM395025	BM395025	50072-2-7	C 511	6.6	36.7	25	9	AA908578	AA908578	
C 439	6.6	36.7	20	13	BM395527	BM395527	50072-2-9	C 512	6.6	36.7	25	9	AA908578	AA908578	
C 440	6.6	36.7	20	14	CO1261	CO1261	HUMGS000799	C 513	6.6	36.7	25	9	AI023012	AI023012	0w57f01.s
C 441	6.6	36.7	20	17	AZ336487	AZ336487	1M0066J19	C 514	6.6	36.7	25	9	AI025765	AI025765	0v94f03.s
C 442	6.6	36.7	20	17	AZ424667	AZ424667	1M0237C01	C 515	6.6	36.7	25	9	AI081705	AI081705	
C 443	6.6	36.7	20	17	AZ497752	AZ497752	1M0334B14	C 516	6.6	36.7	25	9	AI123486	AI123486	qno1e11.x
C 444	6.6	36.7	20	17	AZ648363	AZ648363	1M0517A24	C 517	6.6	36.7	25	12	BG896256	BG896256	HOA28-1-F

C 518	6.6	36.7	25	13	BM395408	BM395408 50072-2-8	C 591	6.4	35.6	21	9	AL585450
C 519	6.6	36.7	25	13	BM395454	BM395454 50072-2-9	C 592	6.4	35.6	21	13	BM395685
C 520	6.6	36.7	25	13	BM400880	BM400880 5009-0-8-	C 593	6.4	35.6	21	13	BM397213
C 521	6.6	36.7	25	14	D21049	D21049 HUMS02034	C 594	6.4	35.6	21	13	BM397525
C 522	6.6	36.7	25	14	AZ579573	AZ579573 1M0367M05	C 595	6.4	35.6	21	13	BM399000
C 523	6.6	36.7	25	17	AZ595024	AZ595024 1M0407D23	C 596	6.4	35.6	21	13	BM401202
C 524	6.6	36.7	25	17	AZ767918	AZ767918 1M0567B09	C 597	6.4	35.6	21	14	D42275
C 525	6.6	36.7	25	17	AZ785586	AZ785586 2M0029N04	C 598	6.4	35.6	21	17	AZ307929
C 526	6.6	36.7	25	17	AZ804762	AZ804762 2M0065N12	C 599	6.4	35.6	21	17	AZ309732
C 527	6.6	36.7	25	17	AZ807605	AZ807605 2M0070L05	C 600	6.4	35.6	21	17	AZ220581
C 528	6.6	36.7	25	17	AZ828517	AZ828517 2M0105J02	C 601	6.4	35.6	21	17	AZ220773
C 529	6.6	36.7	25	17	TA352B06	TA352B06 50072-2-8	C 602	6.4	35.6	21	17	AZ242046
C 530	6.4	35.6	11	13	BM395328	BM395328 50072-2-1	C 603	6.4	35.6	21	17	AZ400597
C 531	6.4	35.6	13	13	BM394028	BM394028 50072-2-1	C 604	6.4	35.6	21	17	AZ455471
C 532	6.4	35.6	14	13	BM392794	BM392794 50071-2-1	C 605	6.4	35.6	21	17	AZ455821
C 533	6.4	35.6	14	13	BM394089	BM394089 50072-2-1	C 606	6.4	35.6	21	17	AZ580960
C 534	6.4	35.6	14	13	BM395363	BM395363 50072-2-8	C 607	6.4	35.6	21	17	AZ581103
C 535	6.4	35.6	15	13	BM395188	BM395188 50072-2-7	C 608	6.4	35.6	21	17	AZ584607
C 536	6.4	35.6	16	9	AA939272	AA939272 CQ31B0C.S	C 609	6.4	35.6	21	17	AZ598709
C 537	6.4	35.6	16	9	AI357296	AI357296 CQ15H01.X	C 610	6.4	35.6	21	17	AZ645766
C 538	6.4	35.6	16	9	AI648507	AI648507 LZ54C09.X	C 611	6.4	35.6	21	17	AZ775019
C 539	6.4	35.6	17	13	BM394186	BM394186 50072-2-2	C 612	6.4	35.6	21	17	AZ808124
C 540	6.4	35.6	18	13	BM395123	BM395123 50072-2-7	C 613	6.4	35.6	21	17	AZ813392
C 541	6.4	35.6	18	13	BM399697	BM399697 5009-0-60	C 614	6.4	35.6	21	17	AZ817328
C 542	6.4	35.6	19	9	AA878744	AA878744 CFB5A08.S	C 615	6.4	35.6	22	9	AZ967472
C 543	6.4	35.6	19	9	AA885697	AA885697 C134F01.S	C 616	6.4	35.6	22	9	AA894572
C 544	6.4	35.6	19	9	AA953971	AA953971 C088H01.S	C 617	6.4	35.6	22	9	AA908583
C 545	6.4	35.6	19	9	AI056541	AI056541 CQ98C11.X	C 618	6.4	35.6	22	9	AA933996
C 546	6.4	35.6	19	9	AI252235	AI252235 CQ78H03.X	C 619	6.4	35.6	22	9	AI039313
C 547	6.4	35.6	19	9	AI471695	AI471695 C199F04.X	C 620	6.4	35.6	22	9	AI1160625
C 548	6.4	35.6	19	13	BM399684	BM399684 5009-0-60	C 621	6.4	35.6	22	9	AI1219368
C 549	6.4	35.6	19	14	C00981	C00981 HUMS000337	C 622	6.4	35.6	22	9	AI566835
C 550	6.4	35.6	19	14	C01186	C01186 HUMS000788	C 623	6.4	35.6	22	9	AU256517
C 551	6.4	35.6	19	17	AZ403537	AZ403537 1M0171M05	C 624	6.4	35.6	22	9	AU259732
C 552	6.4	35.6	19	17	AZ424532	AZ424532 1M0204L07	C 625	6.4	35.6	22	17	AZ304010
C 553	6.4	35.6	19	17	AZ480415	AZ480415 1M0301K24	C 626	6.4	35.6	22	17	AZ309912
C 554	6.4	35.6	19	17	AZ514467	AZ514467 1M0361B19	C 627	6.4	35.6	22	17	AZ312636
C 555	6.4	35.6	19	17	AZ662546	AZ662546 1M0541P08	C 628	6.4	35.6	22	17	AZ313399
C 556	6.4	35.6	19	17	AZ761834	AZ761834 1M0556E19	C 629	6.4	35.6	22	17	AZ430045
C 557	6.4	35.6	19	17	AZ776235	AZ776235 1M0566I09	C 630	6.4	35.6	22	17	AZ623402
C 558	6.4	35.6	19	17	AZ771560	AZ771560 1M0574A03	C 631	6.4	35.6	22	17	AZ655408
C 559	6.4	35.6	19	17	AZ794950	AZ794950 2M0004M16	C 632	6.4	35.6	22	17	AZ655548
C 560	6.4	35.6	19	17	AZ791433	AZ791433 2M0004A24	C 633	6.4	35.6	22	17	AZ658507
C 561	6.4	35.6	19	17	AZ806669	AZ806669 2M0068G19	C 634	6.4	35.6	22	17	AZ786587
C 562	6.4	35.6	19	17	AZ807749	AZ807749 2M0070L17	C 635	6.4	35.6	22	17	AZ810548
C 563	6.4	35.6	19	17	AZ817291	AZ817291 2M0086P05	C 636	6.4	35.6	22	17	AZ829837
C 564	6.4	35.6	19	17	AZ825396	AZ825396 2M0100N04	C 637	6.4	35.6	22	17	AZ873093
C 565	6.4	35.6	19	17	AZ837373	AZ837373 2M0132C07	C 638	6.4	35.6	22	17	AZ950407
C 566	6.4	35.6	19	17	AZ861634	AZ861634 2M0168B18	C 639	6.4	35.6	22	17	AZ974353
C 567	6.4	35.6	19	17	AZ954781	AZ954781 2M0220C07	C 640	6.4	35.6	22	17	TA120D06P
C 568	6.4	35.6	19	17	AZ969805	AZ969805 2M0242O12	C 641	6.4	35.6	22	17	TA177A09Q
C 569	6.4	35.6	19	17	AZ994163	AZ994163 2M0279F05	C 642	6.4	35.6	23	10	AM698813
C 570	6.4	35.6	20	12	BF966452	BF966452 602287066	C 643	6.4	35.6	23	13	BM396189
C 571	6.4	35.6	20	13	BM396970	BM396970 5009-0-27	C 644	6.4	35.6	23	13	BM397770
C 572	6.4	35.6	20	13	BM400174	BM400174 5009-0-68	C 645	6.4	35.6	23	13	BM398278
C 573	6.4	35.6	20	17	AZ307471	AZ307471 1M0009K12	C 646	6.4	35.6	23	14	D25865
C 574	6.4	35.6	20	17	AZ308410	AZ308410 1M0011A24	C 647	6.4	35.6	23	17	AZ336049
C 575	6.4	35.6	20	17	AZ309960	AZ309960 1M0017P23	C 648	6.4	35.6	23	17	AZ350054
C 576	6.4	35.6	20	17	AZ339816	AZ339816 1M0071M24	C 649	6.4	35.6	23	17	AZ380370
C 577	6.4	35.6	20	17	AZ368205	AZ368205 1M0118L07	C 650	6.4	35.6	23	17	AZ430197
C 578	6.4	35.6	20	17	AZ368092	AZ368092 1M0119B01	C 651	6.4	35.6	23	17	AZ471912
C 579	6.4	35.6	20	17	AZ499543	AZ499543 1M0337F19	C 652	6.4	35.6	23	17	AZ472899
C 580	6.4	35.6	20	17	AZ581146	AZ581146 1M0369G14	C 653	6.4	35.6	23	17	AZ475845
C 581	6.4	35.6	20	17	AZ583699	AZ583699 1M0378G15	C 654	6.4	35.6	23	17	AZ619403
C 582	6.4	35.6	20	17	AZ585902	AZ585902 1M0391M24	C 655	6.4	35.6	23	17	AZ657934
C 583	6.4	35.6	20	17	AZ624644	AZ624644 1M0459N12	C 656	6.4	35.6	23	17	AZ660176
C 584	6.4	35.6	20	17	AZ623068	AZ623068 1M0460C21	C 657	6.4	35.6	23	17	AZ666452
C 585	6.4	35.6	20	17	AZ775974	AZ775974 2M0009H14	C 658	6.4	35.6	23	17	AZ773601
C 586	6.4	35.6	20	17	AZ819520	AZ819520 2M0009I07	C 659	6.4	35.6	23	17	AZ785578
C 587	6.4	35.6	20	17	AZ828287	AZ828287 2M00096E02	C 660	6.4	35.6	23	17	AZ785661
C 588	6.4	35.6	20	17	AZ823598	AZ823598 2M00097B08	C 661	6.4	35.6	23	17	AZ808123
C 589	6.4	35.6	20	17	AZ823524	AZ823524 2M00167A13	C 662	6.4	35.6	23	17	AZ834608
C 590	6.4	35.6	21	2	HSM008113	AL1043263 Homo sapi	C 663	6.4	35.6	23	17	AZ991587

C 664	6.4	35.6	23	17	AZ991587	AZ991587 2M0275H20	737	6.4	35.6	25	17	AZ967791	AZ967791 2M0238G20
C 665	6.4	35.6	23	17	BH846769	BH846769 SALK 0103	738	6.4	35.6	25	17	BH840574	BH840574 KC05441-5
C 666	6.4	35.6	23	17	TA121H00	AL463056 T. brucei	739	6.4	35.6	25	17	TA124F1P	AL465301 T. brucei
C 667	6.4	35.6	23	17	TA122H08P	AL462672 T. brucei	740	6.4	35.6	25	17	TA125H10P	AL463225 T. brucei
C 668	6.4	35.6	23	17	TA36D05P	AL465046 T. brucei	741	6.4	35.6	25	17	TA125H10P	AL463225 T. brucei
C 669	6.4	35.6	23	17	TA97H11P	AL461062 T. brucei	742	6.4	35.6	15	10	AM059513	AM059513 HUTb_bvsc
C 670	6.4	35.6	24	10	AM247823	AM247823 2820397.3	743	6.2	34.4	15	10	AM059513	AM059513 5009-0-6
C 671	6.4	35.6	24	13	BM396049	BM396049 5009-0-16	744	6.2	34.4	16	9	A1248882	A1248882 qv73e07.x
C 672	6.4	35.6	24	13	BM397803	BM397803 5009-0-37	745	6.2	34.4	16	9	A1248882	BM395110 50072-2-7
C 673	6.4	35.6	24	13	BM398293	BM398293 5009-0-43	746	6.2	34.4	16	13	HSN007775	A1042925 Homo sapi
C 674	6.4	35.6	24	14	BM399781	BM399781 5009-0-61	747	6.2	34.4	17	13	BM398854	BM398854 5009-0-5
C 675	6.4	35.6	24	14	D18741	D18741 MUGSG01803	748	6.2	34.4	17	13	BM400706	BM400706 5009-0-77
C 676	6.4	35.6	24	17	AZ307138	AZ307138 1M0008G01	749	6.2	34.4	18	13	BM394214	BM394214 50072-2-2
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C 678	6.4	35.6	24	17	AZ354113	AZ354113 1M0093F15	751	6.2	34.4	18	13	BM400305	BM400305 5009-0-70
C 679	6.4	35.6	24	17	AZ374677	AZ374677 1M0127C12	752	6.2	34.4	18	13	BM400816	BM400816 5009-0-79
C 680	6.4	35.6	24	17	AZ437877	AZ437877 1M0226K02	753	6.2	34.4	19	9	AA953971	AA953971 o088h01.8
C 681	6.4	35.6	24	17	AZ451051	AZ451051 1M0250D12	754	6.2	34.4	19	9	A1758301	A1758301 ty06a07.x
C 682	6.4	35.6	24	17	AZ455814	AZ455814 1M0256B21	755	6.2	34.4	19	13	BM400016	BM400016 5009-0-64
C 683	6.4	35.6	24	17	AZ457781	AZ457781 1M0261J14	756	6.2	34.4	19	13	BM401275	BM401275 5009-0-85
C 684	6.4	35.6	24	17	AZ474773	AZ474773 1M0292F21	757	6.2	34.4	19	17	AZ307864	AZ307864 1M0010P16
C 685	6.4	35.6	24	17	AZ476600	AZ476600 1M0295K02	758	6.2	34.4	19	17	AZ422762	AZ422762 1M0201P12
C 686	6.4	35.6	24	17	AZ481339	AZ481339 1M0303B10	759	6.2	34.4	19	17	AZ481449	AZ481449 1M0303N07
C 687	6.4	35.6	24	17	AZ481339	AZ481339 1M0303B10	760	6.2	34.4	19	17	AZ612157	AZ612157 1M0438L21
C 688	6.4	35.6	24	17	AZ491197	AZ491197 1M0324C10	761	6.2	34.4	19	17	AZ651803	AZ651803 1M0522N11
C 689	6.4	35.6	24	17	AZ583540	AZ583540 1M0378G01	762	6.2	34.4	19	17	AZ763411	AZ763411 1M0558B24
C 690	6.4	35.6	24	17	AZ585771	AZ585771 1M0391L12	763	6.2	34.4	19	17	AZ817291	AZ817291 2M0086P05
C 691	6.4	35.6	24	17	AZ587584	AZ587584 1M0395C23	764	6.2	34.4	19	17	AZ830469	AZ830469 2M0109C14
C 692	6.4	35.6	24	17	AZ607692	AZ607692 1M0430I13	765	6.2	34.4	19	17	AZ833844	AZ833844 2M0116O07
C 693	6.4	35.6	24	17	AZ626098	AZ626098 1M0466I09	766	6.2	34.4	19	17	AZ849133	AZ849133 2M0150L21
C 694	6.4	35.6	24	17	AZ629107	AZ629107 1M0481C22	767	6.2	34.4	19	17	AZ861876	AZ861876 2M0168F22
C 695	6.4	35.6	24	17	AZ663558	AZ663558 1M0543E13	768	6.2	34.4	20	9	AU013891	AU013891 AU013891
C 696	6.4	35.6	24	17	AZ663647	AZ663647 1M0543G20	769	6.2	34.4	20	9	AU257181	AU257181 AU257181
C 697	6.4	35.6	24	17	AZ771365	AZ771365 1M0573A02	770	6.2	34.4	20	13	BM401005	BM401005 5009-0-81
C 698	6.4	35.6	24	17	AZ794953	AZ794953 2M0048N21	771	6.2	34.4	20	13	BM401265	BM401265 5009-0-85
C 699	6.4	35.6	24	17	AZ807296	AZ807296 2M0070K03	772	6.2	34.4	20	14	BQ789787	BQ789787 hsg6002AB
C 700	6.4	35.6	24	17	AZ815479	AZ815479 2M0083D15	773	6.2	34.4	20	17	AZ303903	AZ303903 1M0003B18
C 701	6.4	35.6	24	17	AZ821550	AZ821550 2M0094C23	774	6.2	34.4	20	17	AZ436745	AZ436745 1M0082D09
C 702	6.4	35.6	24	17	AZ831825	AZ831825 2M0094E16	775	6.2	34.4	20	17	AZ434383	AZ434383 1M0220C17
C 703	6.4	35.6	24	17	AZ833475	AZ833475 2M0115O05	776	6.2	34.4	20	17	AZ478557	AZ478557 1M0298N08
C 704	6.4	35.6	24	17	BH861287	BH861287 SALK 0679	777	6.2	34.4	20	17	AZ478557	AZ478557 1M0298N08
C 705	6.4	35.6	24	17	TA178F08P	AL474698 T. brucei	778	6.2	34.4	20	17	AZ626475	AZ626475 1M0466E16
C 706	6.4	35.6	24	17	TA306B12P	AL451238 T. brucei	779	6.2	34.4	20	17	AZ638950	AZ638950 1M0499E08
C 707	6.4	35.6	24	17	TA386D10Q	AL458275 T. brucei	780	6.2	34.4	20	17	AZ654127	AZ654127 2M0219K09
C 708	6.4	35.6	25	9	AA917443	AA917443 o151D05.8	781	6.2	34.4	21	9	AU258828	AU258828 AU258828
C 709	6.4	35.6	25	9	AA174382	AA174382 an18F09.8	782	6.2	34.4	21	13	BM396885	BM396885 5009-0-26
C 710	6.4	35.6	25	9	AA181406	AA181406 uc59D04.x	783	6.2	34.4	21	13	BM398097	BM398097 5009-0-40
C 711	6.4	35.6	25	9	AA1206423	AA1206423 q922h05.x	784	6.2	34.4	21	13	BM400027	BM400027 5009-0-65
C 712	6.4	35.6	25	9	AA1261405	AA1261405 qK08C04.x	785	6.2	34.4	21	17	AZ307817	AZ307817 1M0010I09
C 713	6.4	35.6	25	9	AA1624477	AA1624477 t668e04.x	786	6.2	34.4	21	17	AZ2420773	AZ2420773 1M0198E18
C 714	6.4	35.6	25	9	AA1757084	AA1757084 E15STe04	787	6.2	34.4	21	17	AZ421118	AZ421118 1M0199D16
C 715	6.4	35.6	25	13	BG929095	BG929095 HNC11-1-C	788	6.2	34.4	21	17	AZ445481	AZ445481 1M0241P15
C 716	6.4	35.6	25	13	BM397641	BM397641 5009-0-35	789	6.2	34.4	21	17	AZ472579	AZ472579 1M0287F21
C 717	6.4	35.6	25	13	BM398307	BM398307 5009-0-43	790	6.2	34.4	21	17	AZ472691	AZ472691 1M0288L04
C 718	6.4	35.6	25	13	BM398324	BM398324 5009-0-44	791	6.2	34.4	21	17	AZ636817	AZ636817 1M0495C20
C 719	6.4	35.6	25	13	BM398453	BM398453 5009-0-45	792	6.2	34.4	21	17	AZ765539	AZ765539 1M0562K19
C 720	6.4	35.6	25	14	H93534	H93534 yv08912.r1	793	6.2	34.4	21	17	AZ871389	AZ871389 2M0184A14
C 721	6.4	35.6	25	14	L32051	L32051 HUMKPK46A.H	794	6.2	34.4	21	17	AZ943767	AZ943767 2M0204L03
C 722	6.4	35.6	25	17	AQ025250	AQ025250 EP(3)3067	795	6.2	34.4	21	17	AA908697	AA908697 o101a07.8
C 723	6.4	35.6	25	17	AZ307438	AZ307438 1M0009B03	796	6.2	34.4	21	17	AA910535	AA910535 OK56F03.8
C 724	6.4	35.6	25	17	AZ307545	AZ307545 1M0009H22	797	6.2	34.4	22	9	AA910535	AA910535 OK56F03.8
C 725	6.4	35.6	25	17	AZ308692	AZ308692 1M0011M20	798	6.2	34.4	22	9	AA910535	AA910535 OK56F03.8
C 726	6.4	35.6	25	17	AZ377112	AZ377112 1M0131J16	799	6.2	34.4	22	9	AA911591	AA911591 cd930b07.8
C 727	6.4	35.6	25	17	AZ447958	AZ447958 1M0204L17	800	6.2	34.4	22	9	AA981296	AA981296 ua23903.x
C 728	6.4	35.6	25	17	AZ456321	AZ456321 1M0258O03	801	6.2	34.4	22	9	AA981296	AA981296 ua23903.x
C 729	6.4	35.6	25	17	AZ514858	AZ514858 1M0361O16	802	6.2	34.4	22	9	AA989077	AA989077 or88e03.8
C 730	6.4	35.6	25	17	AZ592331	AZ592331 1M0403J09	803	6.2	34.4	22	9	AA989077	AA989077 or88e03.8
C 731	6.4	35.6	25	17	AZ621173	AZ621173 1M0458B17	804	6.2	34.4	22	9	AA128425	AA128425 qc57f09.x
C 732	6.4	35.6	25	17	AZ763622	AZ763622 1M0551I11	805	6.2	34.4	22	9	AA129547	AA129547 mp22f03.x
C 733	6.4	35.6	25	17	AZ795988	AZ795988 2M0051H07	806	6.2	34.4	22	9	AA1439277	AA1439277 t154f02.x
C 734	6.4	35.6	25	17	AZ806897	AZ806897 2M0068F13	807	6.2	34.4	22	9	AA1440140	AA1440140 t162d04.x
C 735	6.4	35.6	25	17	AZ816218	AZ816218 2M0084C19	808	6.2	34.4	22	9	AA1560825	AA1560825 t940d09.x
C 736	6.4	35.6	25	17	AZ867891	AZ867891 2M0178I21	809	6.2	34.4	22	9	AA1581087	AA1581087 t327b11.x

C 810	6.2	34.4	22	9	A1687266	A1687266 tp94dl0.x	C 883	6.2	34.4	25	9	A1262558	A1262558 qk42e08.x
C 811	6.2	34.4	22	9	A1738559	A1738559 w339g02.x	C 884	6.2	34.4	25	9	A1276868	A1276868 gv65a10.x
C 812	6.2	34.4	22	13	BM401155	BM401155 5009-0-83	C 885	6.2	34.4	25	9	A1277421	A1277421 qm64e02.x
C 813	6.2	34.4	22	17	AZ331565	AZ331565 IM0059M06	C 886	6.2	34.4	25	9	A1298122	A1298122 qm64e06.x
C 814	6.2	34.4	22	17	AZ339902	AZ339902 IM0071003	C 887	6.2	34.4	25	9	A1343358	A1443358 t414d09.x
C 815	6.2	34.4	22	17	AZ429020	AZ429020 IM0212F17	C 888	6.2	34.4	25	9	A1521520	A151520 t064d05.x
C 816	6.2	34.4	22	17	AZ468023	AZ468023 IM0279L15	C 889	6.2	34.4	25	9	A1584521	A1584521 t995a407.x
C 817	6.2	34.4	22	17	AZ481923	AZ481923 IM0306L06	C 890	6.2	34.4	25	9	A1628239	A1628239 t932e04.x
C 818	6.2	34.4	22	17	AZ486633	AZ486633 IM0314L14	C 891	6.2	34.4	25	9	A1638719	A1638719 t124e01.x
C 819	6.2	34.4	22	17	AZ501345	AZ501345 IM0340L11	C 892	6.2	34.4	25	9	A1660931	A1660931 wF20a11.x
C 820	6.2	34.4	22	17	AZ501345	AZ501345 IM0340L11	C 893	6.2	34.4	25	9	AA592778	AA592778 v029e12.x
C 821	6.2	34.4	22	17	AZ592201	AZ592201 IM0402K24	C 894	6.2	34.4	25	13	BM396646	BM396646 5009-0-20
C 822	6.2	34.4	22	17	AZ785866	AZ785866 IM0030002	C 895	6.2	34.4	25	13	BM400594	BM400594 5009-0-76
C 823	6.2	34.4	22	17	AZ828017	AZ828017 IM0104H18	C 896	6.2	34.4	25	13	BM400628	BM400628 5009-0-76
C 824	6.2	34.4	22	17	AZ958390	AZ958390 IM0225L07	C 897	6.2	34.4	25	13	BM400628	BM400628 5009-0-76
C 825	6.2	34.4	22	17	AZ976229	AZ976229 IM0251N06	C 898	6.2	34.4	25	17	AZ206874	AZ206874 IM0008E07
C 826	6.2	34.4	22	17	TA140A04P	TA140A04P T. brucei	C 899	6.2	34.4	25	17	AZ317298	AZ317298 IM0035N21
C 827	6.2	34.4	22	17	TA223B07P	TA223B07P T. brucei	C 900	6.2	34.4	25	17	AZ459969	AZ459969 IM0285D10
C 828	6.2	34.4	22	17	TA70B110	TA70B110 T. brucei	C 901	6.2	34.4	25	17	AZ491057	AZ491057 IM0324I24
C 829	6.2	34.4	23	2	HSN004394	HSN004394 Homo sapi	C 902	6.2	34.4	25	17	AZ776661	AZ776661 IM0010C05
C 830	6.2	34.4	23	2	HSN004394	HSN004394 Homo sapi	C 903	6.2	34.4	25	17	AZ793814	AZ793814 IM0047J13
C 831	6.2	34.4	23	10	AW246048	AW246048 2821455.5	C 904	6.2	34.4	25	17	AZ794198	AZ794198 IM0047J20
C 832	6.2	34.4	23	17	AZ330740	AZ330740 IM0056G07	C 905	6.2	34.4	25	17	AZ807031	AZ807031 IM0069B02
C 833	6.2	34.4	23	17	AZ343048	AZ343048 IM0076K17	C 906	6.2	34.4	25	17	AZ810739	AZ810739 IM0076C02
C 834	6.2	34.4	23	17	AZ388663	AZ388663 IM0148J15	C 907	6.2	34.4	25	17	AZ966313	AZ966313 IM0236C18
C 835	6.2	34.4	23	17	AZ463102	AZ463102 IM0271A15	C 908	6.2	34.4	25	17	BH852925	BH852925 SALK 0757
C 836	6.2	34.4	23	17	AZ480676	AZ480676 IM0302P23	C 909	6.2	34.4	25	17	TA114E04P	TA114E04P T. brucei
C 837	6.2	34.4	23	17	AZ593454	AZ593454 IM0405C03	C 910	6.2	34.4	25	17	TA17B020	TA17B020 T. brucei
C 838	6.2	34.4	23	17	AZ608730	AZ608730 IM0433E07	C 911	6.2	34.4	25	17	TA182C05P	TA182C05P T. brucei
C 839	6.2	34.4	23	17	AZ639181	AZ639181 IM0499D03	C 912	6.2	34.4	25	17	HSN008038	HSN008038 Homo sapi
C 840	6.2	34.4	23	17	AZ784767	AZ784767 IM0027P17	C 913	6.2	34.4	25	17	BH127401	BH127401 G-1c19.x
C 841	6.2	34.4	23	17	AZ808080	AZ808080 IM0071I22	C 914	6.2	34.4	25	17	BH169716	BH169716 SALK 0017
C 842	6.2	34.4	23	17	AZ821572	AZ821572 IM0094G21	C 915	6.2	34.4	25	17	BH169716	BH169716 SALK 0017
C 843	6.2	34.4	23	17	AZ822831	AZ822831 IM0096J21	C 916	6.2	34.4	25	12	BM395715	BM395715 H0A2-H-4
C 844	6.2	34.4	23	17	AZ844206	AZ844206 IM0131I11	C 917	6.2	34.4	25	16	BM393920	BM393920 5007-2-1
C 845	6.2	34.4	23	17	AZ869816	AZ869816 IM0182N06	C 918	6.2	34.4	25	13	BM395336	BM395336 50072-2-8
C 846	6.2	34.4	23	17	AZ971749	AZ971749 IM0245C21	C 919	6.2	34.4	25	19	AA954509	AA954509 o8b1d05.x
C 847	6.2	34.4	23	17	TA215B01P	TA215B01P T. brucei	C 920	6.2	34.4	25	19	A1027333	A1027333 o46a807.x
C 848	6.2	34.4	23	17	TA260H01P	TA260H01P T. brucei	C 921	6.2	34.4	25	19	A1476315	A1476315 t415c09.x
C 849	6.2	34.4	24	9	AL047412	AL047412 DKEZP586E	C 922	6.2	34.4	25	19	A1476315	A1476315 t415c09.x
C 850	6.2	34.4	24	9	AL047412	AL047412 DKEZP586E	C 923	6.2	34.4	25	19	A1476315	A1476315 t415c09.x
C 851	6.2	34.4	24	9	AU258060	AU258060 AU258060	C 924	6.2	34.4	25	14	CO1216	CO1216 HUNG000792
C 852	6.2	34.4	24	10	AM059812	AM059812 LEF01.YS	C 925	6.2	34.4	25	14	CO1991	CO1991 HUNG000792
C 853	6.2	34.4	24	13	BM395654	BM395654 50072-2-9	C 926	6.2	34.4	25	17	AZ303466	AZ303466 IM0003C05
C 854	6.2	34.4	24	13	BM396627	BM396627 5009-0-23	C 927	6.2	34.4	25	17	AZ303767	AZ303767 IM0003C03
C 855	6.2	34.4	24	13	BM398868	BM398868 5009-0-5-	C 928	6.2	34.4	25	17	AZ323590	AZ323590 IM0045A07
C 856	6.2	34.4	24	13	BM400107	BM400107 5009-0-66	C 929	6.2	34.4	25	17	AZ444046	AZ444046 IM0239N04
C 857	6.2	34.4	24	14	Z20614	Z20614 HSAACNVA.T	C 930	6.2	34.4	25	17	AZ475705	AZ475705 IM0294B02
C 858	6.2	34.4	24	17	AO050534	AO050534 nbxb0004b	C 931	6.2	34.4	25	17	AZ485264	AZ485264 IM0312N02
C 859	6.2	34.4	24	17	AZ317731	AZ317731 IM0035P22	C 932	6.2	34.4	25	17	AZ495849	AZ495849 IM0435C18
C 860	6.2	34.4	24	17	AZ318208	AZ318208 IM0037H08	C 933	6.2	34.4	25	17	AZ610451	AZ610451 IM0459I15
C 861	6.2	34.4	24	17	AZ392919	AZ392919 IM0155E16	C 934	6.2	34.4	25	17	AZ622447	AZ622447 IM0459I15
C 862	6.2	34.4	24	17	AZ405843	AZ405843 IM0174A20	C 935	6.2	34.4	25	17	AZ765310	AZ765310 IM0562M12
C 863	6.2	34.4	24	17	AZ428700	AZ428700 IM0212L16	C 936	6.2	34.4	25	17	AZ803756	AZ803756 IM0064M15
C 864	6.2	34.4	24	17	AZ443047	AZ443047 IM0237I06	C 937	6.2	34.4	25	17	AZ861832	AZ861832 IM0168H21
C 865	6.2	34.4	24	17	AZ617463	AZ617463 IM0448P15	C 938	6.2	34.4	25	17	AZ862758	AZ862758 IM0170005
C 866	6.2	34.4	24	17	AZ655864	AZ655864 IM0547I04	C 939	6.2	34.4	25	17	AZ938271	AZ938271 IM0196J13
C 867	6.2	34.4	24	17	AZ780307	AZ780307 IM0017J04	C 940	6.2	34.4	25	17	AZ938271	AZ938271 IM0196J13
C 868	6.2	34.4	24	17	AZ812679	AZ812679 IM0079H03	C 941	6.2	34.4	25	9	AU007069	AU007069 AU007069
C 869	6.2	34.4	24	17	AZ956336	AZ956336 IM0222F13	C 942	6.2	34.4	25	9	AU011386	AU011386 AU011386
C 870	6.2	34.4	24	17	TA186D08P	TA186D08P T. brucei	C 943	6.2	34.4	25	9	AU011387	AU011387 AU011387
C 871	6.2	34.4	24	17	TA207E12Q	TA207E12Q T. brucei	C 944	6.2	34.4	25	9	AU011388	AU011388 AU011388
C 872	6.2	34.4	24	17	TA238D04Q	TA238D04Q T. brucei	C 945	6.2	34.4	25	9	AU255029	AU255029 AU255029
C 873	6.2	34.4	24	17	TA305G10P	TA305G10P T. brucei	C 946	6.2	34.4	25	9	AU256590	AU256590 AU256590
C 874	6.2	34.4	24	17	TA306C09Q	TA306C09Q T. brucei	C 947	6.2	34.4	25	9	AU257221	AU257221 AU257221
C 875	6.2	34.4	25	9	AA926871	AA926871 o155c11.s	C 948	6.2	34.4	25	14	D20001	D20001 HUNG000971
C 876	6.2	34.4	25	9	A1002379	A1002379 oq87f02.s	C 949	6.2	34.4	25	17	AZ2308291	AZ2308291 IM0011E10
C 877	6.2	34.4	25	9	A1024239	A1024239 oq71902.s	C 950	6.2	34.4	25	17	AZ2329318	AZ2329318 IM0053P05
C 878	6.2	34.4	25	9	A1040331	A1040331 oq33b07.x	C 951	6.2	34.4	25	17	AZ375604	AZ375604 IM0129L06
C 879	6.2	34.4	25	9	A1127762	A1127762 qc31d01.x	C 952	6.2	34.4	25	17	AZ377958	AZ377958 IM0132G02
C 880	6.2	34.4	25	9	A1147073	A1147073 oq33c05.s	C 953	6.2	34.4	25	17	AZ402821	AZ402821 IM0170L13
C 881	6.2	34.4	25	9	A1147073	A1147073 oq33c05.s	C 954	6.2	34.4	25	17	AZ442786	AZ442786 IM0237J08
C 882	6.2	34.4	25	9	A1262558	A1262558 qk42e08.x	C 955	6.2	34.4	25	17	AZ468517	AZ468517 IM0281N01

956	6	33.3	20	17	AZ473332	AZ473322	1M0289H08
C 957	6	33.3	20	17	AZ473332	AZ473322	1M0289H08
C 958	6	33.3	20	17	AZ475852	AZ475852	1M0294A18
959	6	33.3	20	17	AZ484500	AZ484500	1M0311C01
C 960	6	33.3	20	17	AZ486007	AZ486007	1M0313E17
C 961	6	33.3	20	17	AZ491509	AZ491509	1M0325B09
C 962	6	33.3	20	17	AZ500772	AZ500772	1M0339N15
C 963	6	33.3	20	17	AZ512414	AZ512414	1M0357J21
C 964	6	33.3	20	17	AZ526355	AZ526355	1M0403M11
C 965	6	33.3	20	17	AZ600911	AZ600911	1M0418M21
C 966	6	33.3	20	17	AZ619289	AZ619289	1M0436E13
C 967	6	33.3	20	17	AZ619289	AZ619289	1M0436E13
968	6	33.3	20	17	AZ621188	AZ621188	1M0454G13
C 969	6	33.3	20	17	AZ628809	AZ628809	1M0481C17
970	6	33.3	20	17	AZ659612	AZ659612	1M0537A07
C 971	6	33.3	20	17	AZ780308	AZ780308	2M0017U05
C 972	6	33.3	20	17	AZ789090	AZ789090	2M0036C12
C 973	6	33.3	20	17	AZ808057	AZ808057	2M0071C22
C 974	6	33.3	20	17	AZ813013	AZ813013	2M0080P02
975	6	33.3	20	17	AZ828387	AZ828387	2M0105P13
C 976	6	33.3	20	17	AZ830457	AZ830457	2M0109P11
977	6	33.3	20	17	AZ833695	AZ833695	2M0115N20
C 978	6	33.3	20	17	AZ833695	AZ833695	2M0115N20
C 979	6	33.3	20	17	AZ835025	AZ835025	2M0129I02
C 980	6	33.3	20	17	AZ836069	AZ836069	2M0130J11
C 981	6	33.3	20	17	AZ839901	AZ839901	2M0136P11
C 982	6	33.3	20	17	AZ845320	AZ845320	2M0145M02
C 983	6	33.3	20	17	AZ859065	AZ859065	2M0164F06
984	6	33.3	20	17	AZ938837	AZ938837	2M0197L06
C 985	6	33.3	20	17	AZ949076	AZ949076	2M0212D23
C 986	6	33.3	20	17	AZ952391	AZ952391	2M0217P07
C 987	6	33.3	20	17	AZ953211	AZ953211	2M0218P15
C 988	6	33.3	20	17	AZ985308	AZ985308	2M0267D11
C 989	6	33.3	20	17	AZ995436	AZ995436	2M0281F18
C 990	6	33.3	20	17	AZ995535	AZ995535	2M0281F18
991	6	33.3	21	14	D20707	D20707	HUMG501683
992	6	33.3	21	17	AZ306118	AZ306118	1M0007003
993	6	33.3	21	17	AZ313630	AZ313630	1M0030I06
C 994	6	33.3	21	17	AZ313630	AZ313630	1M0030I06
995	6	33.3	21	17	AZ348213	AZ348213	1M0084N15
C 996	6	33.3	21	17	AZ442098	AZ442098	1M0234F12
C 997	6	33.3	21	17	AZ495585	AZ495585	1M0331H02
998	6	33.3	21	17	AZ526636	AZ526636	257PBH06
999	6	33.3	21	17	AZ581771	AZ581771	1M0370P10
1000	6	33.3	21	17	AZ594960	AZ594960	1M0407E16

ALIGNMENTS

RESULT 1
BM394673/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BM394673
50072-2-5-D08.r.1 Chilcoat/Turkewitz cDNA (large fraction)
Turkewitz, A.P., Katter, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel
J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu
Seq primer: T3
Location/Qualifiers
1. 23
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_id="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT
1 a 11 c 8 g 3 t

Query Match 62.2%; Score 11.2; DB 13; Length 23;
Best Local Similarity 81.2%; Pred. No. 3.4e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCGCCGATCCAGGC 18
19 GGGCCCGACCATGC 4

Db

RESULT 2
BM394673
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BM394673
50072-2-5-D08.r.1 Chilcoat/Turkewitz cDNA (large fraction)
Turkewitz, A.P., Katter, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel
J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
source
Location/Qualifiers
1. 23
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_id="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT
1 a 11 c 8 g 3 t

Query Match 58.9%; Score 10.6; DB 13; Length 23;
Best Local Similarity 76.5%; Pred. No. 6.2e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TGGCGCCGATCCAGGC 18
1 TGGCGCATGGTCCGGGC 17

Db

RESULT 3
AZ634834
LOCUS
DEFINITION

AZ634834
24 bp DNA linear GSS 13-DEC-2000
1M0490C19R Mouse 10kb plasmid U9GCM library Mus musculus genomic

ACCESSION AZ634834
VERSION AZ634834.1 GI:11757024
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0490 row: C column: 19
Seq primer: CACACAGGAACAGCATGACCC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1..24
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0490C19"
/clone_1lb="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 7 c 6 g 4 t
ORIGIN
Query Match 58.9%; Score 10.6; DB 17; Length 24;
Best Local Similarity 76.5%; Pred. No. 6.2e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TCGCCCGGATCCAGGC 18
DB 22 TGTGCTCGATCCAGTC 6

RESULT 4
AZ648503 23 bp DNA linear GSS 21-FEB-2001
LOCUS
DEFINITION 2M0149H02R Mouse 10kb plasmid UUCG1M library Mus musculus genomic

ACCESSION AZ648503
VERSION AZ648503.1 GI:13031656
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0149 row: H column: 02
Seq primer: CACACAGGAACAGCATGACCC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1..23
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0149H02"
/clone_1lb="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 10 c 6 g 5 t
ORIGIN
Query Match 57.8%; Score 10.4; DB 17; Length 23;
Best Local Similarity 71.7%; Pred. No. 7.6e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGCCCGGATCCA 15
DB 9 CTCCCGGATCCA 20

RESULT 5
AZ655545 19 bp DNA linear GSS 21-FEB-2001
LOCUS
DEFINITION 2M0159F09R Mouse 10kb plasmid UUCG1M library Mus musculus genomic

accession A2855545 clone UUGC2M0159F09 R, DNA sequence.
 version A2855545.1 GI:13045816
 keywords GSS.
 source house mouse.
 organism Mus musculus.
 reference Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
 authors Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
 title Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 journal Unpublished (2000)
 comment Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 insert length: 10000 Std Error: 0.00
 plate: 0159 row: F column: 09
 seq primer: CACACAGAAACACCTATGACC
 class: plasmid ends
 high quality sequence stop: 19.
 location/qualifiers
 1. 19
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0159F09"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptor and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

base count 2 a 5 c 7 t
 origin
 query match 55.6%; Score 10; DB 17; Length 19;
 best local similarity 100.0%; Pred. No. 1.1e+06;
 matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

cy 5 GCCCGATCC 14
 |||||
 db 3 GCCCGATCC 12

result 6
 AZ791884/c 21 bp DNA linear GSS 16-FEB-2001
 locus 2M0043A02P Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 definition

accession A2791884 clone UUGC2M0043A02 F, DNA sequence.
 version A2791884.1 GI:12935238
 keywords GSS.
 source house mouse.
 organism Mus musculus.
 reference Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)
 authors Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
 title Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 journal Unpublished (2000)
 comment Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 insert length: 10000 Std Error: 0.00
 plate: 0043 row: A column: 02
 seq primer: CGTTGTAACGACGCCAGT
 class: plasmid ends
 high quality sequence stop: 21.
 location/qualifiers
 1. 21
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0043A02"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptor and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

base count 3 a 4 c 6 t
 origin
 query match 55.6%; Score 10; DB 17; Length 21;
 best local similarity 72.2%; Pred. No. 1.1e+06;
 matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

cy 1 CTGCGCCCGATCCAGGC 18
 |||||
 db 20 CAGCTTACGATCCAGAC 3

result 7
 AZ591658/c 20 bp DNA linear GSS 13-DEC-2000
 locus 1M0401F19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 definition

clone UUGC1M0401P19 R, DNA sequence.

ACCESSION AZ591658
 VERSION AZ591658.1 GI:11713848
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weis
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0401 row: F column: 19
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
 1..20
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0401P19"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g114732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 8 c 6 g 3 t
 ORIGIN

Query Match 53.3%; Score 9.6; DB 17; Length 20;
 Best Local Similarity 75.0%; Pred. No. 1.7e+06;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 1 CTGGCCCGGATCCAG 16
 |||||
 Db 19 CAGCGCTGGCTCCAG 4

RESULT 8
 AZ305158 21 bp DNA linear GSS 29-SEP-2000
 LOCUS
 DEFINITION 1M0005K11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0005K11 R, DNA sequence.

ACCESSION AZ305158
 VERSION AZ305158.1 GI:10341896
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weis
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0005 row: K column: 11
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers
 1..21
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0005K11"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g114732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 11 c 4 g 6 t
 ORIGIN

Query Match 53.3%; Score 9.6; DB 17; Length 21;
 Best Local Similarity 75.0%; Pred. No. 1.7e+06;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 1 CTGGCCCGGATCCAG 16
 |||||
 Db 6 CTGGCTCCGCTCCCG 21

RESULT 9
 AZ834643 21 bp DNA linear GSS 20-FEB-2001
 LOCUS
 DEFINITION 2M0117N24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

```

ACCESSION      AZ2834643
VERSION        AZ2834643.1
KEYWORDS       GI:13004551
SOURCE         house mouse.
ORGANISM       Mus musculus.
REFERENCE      Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Islam,H., Loyagci,A., Barber,M., Baccorn,T., Duval,B., Hamil,C.,
                M., Rose,M., Rose,R., Meenen,E., Pedersen,T., Reilly
                and Wright,D., Weiser,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
                University of Utah
                Genome Center
                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
                84112, USA
                Tel.: 801 585 5606
                Fax: 801 585 7177
                Email: ddunn@genetics.utah.edu
                Insert Length: 10000 Std Error: 0.00
                Plate: 0117 row: N column: 24
                Seq primer: CGTCTAAGACGCGCCAGT
                Class: plasmid ends
                High quality sequence stop: 21.
FEATURES
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    1..21
    /organism="Mus musculus"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC2M011N24"
    /clone_11b="Mouse 10kb plasmid UUGC1M library"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /note="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adapted DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of PWD42 (g1|4732114|gbl|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adapted mouse DNA was annealed to
    adapted vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."
BASE COUNT
ORIGIN         1 a
                5 c
                10 g
                5 t
Query Match    53.3%; Score 9.6; DB 17; Length 21;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches        12; Conservative 0; Mismatches 4; Indels 0; Gaps 0,
QY             1 CTGGCGCCCGGATCCAG 16
                ||| ||| ||| ||| |||
DB             17 CTGAGCCCCCACCAG 2
                ||| ||| ||| ||| |||
RESULT 10
LOCUS         AZ487506
DEFINITION    AZ487506 Mouse 10kb plasmid UUGC1M library Mus musculus genomic

```

```

ACCESSION   clonc UGCGIM0317P10 F, DNA sequence.
VERSION     A2487506
KEYWORDS    A2487506.1 GI:10655316
SOURCE      GSS.
ORGANISM    Mus musculus
            house mouse.
            Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE    1 (bases 1 to 24)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamtl,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiser,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel.: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert length: 10000 Std Error: 0.00
            Plate: 0317 row: P column: 10
            Seg primer: CGTGTAAACGACGGCCACT
            Class: plasmid ends
            High quality sequence stop: 24.
FEATURES             location/Qualifiers
     source           1..24
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UGCGIM0317P10"
                     /clone_lib="Mouse 10kb plasmid library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                     /note="Vector: PMD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptor DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid RL. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptor mouse DNA was annealed to
                     adaptor vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT   4 a          5 c          9 g          6 t
ORIGIN
Query Match      53.3%; Score 9.6; DB 17; Length 24;
Best Local Similarity 75.0%; Pred.No. 1.7e+06;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY              2 TGCGCCCCGCATCCAGG 17
                |||||
Db              5 TGTGCCCGCGTACAAG 20
                |||||
RESULT 11
LOCUS      TA118G04F/c               25 bp        DNA                  linear      GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 118g04, forward sequence.

```

genomic survey sequence.

ACCESSION AL463737 GI:11832909
 VERSION AL463737.1 GI:11832909
 KEYWORDS Trypanosoma brucei.
 SOURCE Trypanosoma brucei
 ORGANISM Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

REFERENCE 1 (bases 1 to 25)
 AUTHORS Hall, N., Bowman, S., Lennard, N. J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S. E., Rajandream, M. A. and Barrell, B. G.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
 COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J. C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers
 1..25
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="118904"

BASE COUNT 10 a 6 c 4 g 5 t
 ORIGIN

Query Match 53.3%; Score 9.6; DB 17; Length 25;
 Best Local Similarity 75.0%; Pred. No. 1.7e+06;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TGCGCCGATCCAGG 17
 Db 25 TGTGACCGATCAAGG 10

RESULT 12
 LOCUS AZ314246 24 bp DNA linear GSS 29-SEP-2000
 DEFINITION IM0031A01F Mouse 10kb plasmid UGCCIM library Mus musculus genomic clone UGCCIM0031A01 F, DNA sequence.
 ACCESSION AZ314246
 VERSION AZ314246.1 GI:10359945
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 24)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
 Tel: 801 585 5606

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0031 row: A column: 01
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1..24
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UCCIM0031A01"
 /clone_lib="Mouse 10kb plasmid UGCCIM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD22ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 6 c 9 g 6 t
 ORIGIN

Query Match 51.1%; Score 9.2; DB 17; Length 24;
 Best Local Similarity 78.6%; Pred. No. 2.5e+06;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 GCCCGATCCAGG 18
 Db 6 GCCCGATCCAGG 19

RESULT 13
 LOCUS AZ634834 24 bp DNA linear GSS 13-DEC-2000
 DEFINITION IM0490C19R Mouse 10kb plasmid UGCCIM library Mus musculus genomic clone UGCCIM0490C19 R, DNA sequence.
 ACCESSION AZ634834
 VERSION AZ634834.1 GI:11757024
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 24)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
 Tel: 801 585 5606

Email: cdunn@genetics.utah.edu
Fax: 801 585 7177
Insert length: 10000 Std Error: 0.00
Plate: 0490 row: C column: 19
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid end
High quality sequence stop: 24.

FEATURES
SOURCE

BASE COUNT
ORIGIN

Query Match	51.1%;	Score 9.2;	DB 17;	Length 24;
Best Local Similarity	78.6%;	Pred. No. 2.5e+06;		
Matches 11;	Conservative	0;	Mismatches 3;	Indels 0;
			Gaps	0

QY	5	GCCCCGATCCAGGC	18
Db	6	GACTGGATCGAGGC	19

RESULT 14	AA909237/c			
LOCUS	AA909237	25 bp	mRNA	linear
DEFINITION	O108C04.81 Soares_NFL_T GBC S1 Homo sapiens cDNA clone			

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANIS

REFERENCE	1 (bases 1 to 25)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D.

FEATURES

SOURCE

```

FEATURES
source
Location/Qualifiers
1..25
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1522854"
/clone_id="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL99, testis NH9, and B-cell
NCL CGAP GCBI) were mixed, and 88 circles were made in
vivo. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
1.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Donaldo."
BASE COUNT
0 a 5 c 16 g 4 t
ORIGIN

```

BASE COUNT
ORIGIN

Query Match	51.1%;	Score 9.2;	DB 9;	Length 25;
Best Local Similarity	78.6%;	Pred. No. 2.5e+06;		
Matches 11; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY 4 CGCCCGATCCAGG 17
|||
Db 14 CGCCCGACCCAGG 1

RESULT	15
AZ785457	
LOCUS	
DEFINITION	23 bp DNA linear GSS 16-FEB-2001
DESCRIPTION	AZ785457
FEATURES	200023A2AF Mouse 1kb plasmid UOUC1M library Mus musculus genomic clone UOUC2M0025A2A F, DNA sequence.

ACCESSION	A2785457
VERSION	A2785457.1
KEYWORDS	GSS.
SOURCE	house mouse.
ORGANISM	Mus musculus

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

FEATURES
SOURCE

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
8 a 7 c 5 g 3 t

Query Match 50.0%; Score 9; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 GATCCAGGC 18
|||||
Db 15 GATCCAGGC 23

RESULT 16
LOCUS AZ342826/c 23 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0076C04F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG1M0076C04 F, DNA sequence.

ACCESSION AZ342826
VERSION AZ342826.1 GI:10420451
KEYWORDS GSS.

SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiser,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiser
University of Utah Genome Center
Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: C column: 04
Seq primer: CGTGTAAACGACGCGCAGCT
Class: plasmid ends
High quality sequence stop: 23.

FEATURES
SOURCE location/Qualifiers
1..23
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0076C04"
/clone_1lb="Mouse 10kb plasmid UGCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
5 a 7 c 6 g 5 t

Query Match 48.9%; Score 8.8; DB 17; Length 23;
Best Local Similarity 83.3%; Pred. No. 3.8e+06;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GCGCCCGATCC 14
|||||
Db 12 GTGCCCGATCC 1

RESULT 17
LOCUS AZ827973 23 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0104P1R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG2M0104P1 R, DNA sequence.

ACCESSION AZ827973
VERSION AZ827973.1 GI:12997881
KEYWORDS GSS.

SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiser,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiser
University of Utah Genome Center
Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0104 row: P column: 11
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.

FEATURES
SOURCE location/Qualifiers
1..23
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0104P1"
/clone_1lb="Mouse 10kb plasmid UGCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

Query Match 48.9%; Score 8.8; DB 17; Length 25;
 Best Local Similarity 83.3%; Pred. No. 3.8e+06;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGCCCGCATCC 14
 |||||
 19 GCGCCGCTATCC 8

RESULT 20
 AA954509/c 19 bp mRNA linear EST 23-JUN-1998
 LOCUS
 DEFINITION
 AA954509
 ON81005.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
 IMAGE:1563081 3' similar to TR:Q24035 Q24035 ENA POLYPEPTIDE.
 /contains element MSRI repetitive element /, mRNA sequence.
 AA954509
 AA954509.1 GI:3118204
 EST.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 19)
 NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapsb-remail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Trace considered overall poor quality
 Insert Length: 754 Std Error: 0.00
 Seq primer: -40m13 fwd. ST from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..19
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1563081"
 /clone_1lb="Soares_NFL_T_GBC_S1"
 /lab_host="DH10B"
 /note="Organ: pooled; Vector: pT7FD-Pac (pharmacia) with
 a modified polylinker; Site 1: Not I; Site 2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NBHL19W, testis NRT, and B-cell
 NCI-CCAP CGB1) were mixed and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 I.M.A.G.E. clones 297480-302087 682632-687239,
 726408-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo."

BASE COUNT
 ORIGIN
 1 a 11 c 7 g 0 t

Query Match 47.8%; Score 8.6; DB 9; Length 19;
 Best Local Similarity 73.3%; Pred. No. 4.6e+06;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GCGCCCGCATCCAGG 17
 |||||
 16 GCGCCCGGCGCTGG 2

RESULT 21
 BM395601/c 23 bp mRNA linear EST 17-JAN-2002
 LOCUS
 DEFINITION
 5009-0-1-C04.t.1 Chilcoat/Turkewitz cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.
 BM395601
 ACCESSION

VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

BM395601.1 GI:18195654
 EST.
 Tetrahymena thermophila.
 Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymena.
 1 (bases 1 to 23)
 Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel
 J., and Klobutcher,L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: 73.
 Location/Qualifiers
 1..23
 /organism="Tetrahymena thermophila"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_1lb="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript SK+; Details on library
 preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT
 ORIGIN
 9 a 6 c 6 g 2 t

Query Match 47.8%; Score 8.6; DB 13; Length 23;
 Best Local Similarity 73.3%; Pred. No. 4.6e+06;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 CGCCCGCATCCAGG 18
 |||||
 23 CGCGTGGCTCCAGC 9

RESULT 22
 AZ410218/c 23 bp DNA linear GSS 03-OCT-2000
 LOCUS
 DEFINITION
 AZ410218
 IM0182F23F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 clone UGCGIM0182F23 F, DNA sequence.
 AZ410218
 AZ410218.1 GI:10534231
 GSS.
 house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 23)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmood,M., Meenen,B., Pedersen,T., Kelly
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts.
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0182 row: F column: 23
 Seq primer: CGTTGTAACAGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 23.

JOURNAL
 COMMENT

FEATURES
SOURCE

Location/Qualifiers
1..23

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGCM0182F23"
/clone_1lb="Mouse 10kb plasmid UUCGCM library"
/sex="Male"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

2 a 0 c 14 g 7 t

Query Match 47.8%; Score 8.6; DB 17; Length 23;
Best Local Similarity 73.3%; Pred. No. 4.6e+06;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 1 CTGCGCCCGGATCCA 15
Db 19 CTCACCCCGCATCCA 5

RESULT 23 23 bp DNA linear GSS 27-APR-2001
LOCUS A2979817
DEFINITION 2M0256F09R Mouse 10kb plasmid UUCGCM library Mus musculus genomic
ACCESSION c1one UUCGCM0256F09 R, DNA sequence.
VERSION A2979817
KEYWORDS A2979817.1 GI:13851044
GSS.

SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0256 row: F column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.

FEATURES
SOURCE

Location/Qualifiers
1..23

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGCM0256F09"
/clone_1lb="Mouse 10kb plasmid UUCGCM library"
/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

5 a 8 c 3 g 7 t

Query Match 47.8%; Score 8.6; DB 17; Length 23;
Best Local Similarity 73.3%; Pred. No. 4.6e+06;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 4 CGCCCGATCCAGGC 18
Db 3 CTCCTTATCCAGGC 17

RESULT 24 24 bp mRNA linear EST 17-JAN-2002
LOCUS BM397860
DEFINITION 5009-0-38-B08.t.1 Chilcoat/Turkewitz cDNA (large fraction)
ACCESSION Tetrahymena thermophila cDNA, mRNA sequence.
VERSION BM397860
KEYWORDS BM397860.1 GI:18197913
EST.

SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila

REFERENCE Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena. 1 (bases 1 to 24)

AUTHORS Turkewitz,A.P., Karier,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
SOURCE

Location/Qualifiers
1..24

/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_1lb="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+, Details on library preparation can be found in Chilcoat and Turkewitz (2001)


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/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

BASE COUNT 2 a 5 c 5 g 7 t
ORIGIN

Query Match 46.7%; Score 8.4; DB 17; Length 19;
Best Local Similarity 90.0%; Pred. No. 5.7e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 GGATCCAGGC 18
|||||
12 GGATCCGGGC 3

Db 12 GGATCCGGGC 3

RESULT 28
LOCUS A2858446 19 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0163D08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0163D08 R, DNA sequence.
ACCESSION A2858446
VERSION A2858446.1 GI:13051622
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0163 row: D column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. 19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0163D08"
/clone_1kb="Mouse 10kb plasmid UUGC1M library"

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/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

BASE COUNT 3 a 5 c 5 g 6 t
ORIGIN

Query Match 46.7%; Score 8.4; DB 17; Length 19;
Best Local Similarity 90.0%; Pred. No. 5.7e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 GGATCCAGGC 18
|||||
10 GGATCCGGGC 19

Db 10 GGATCCGGGC 19

RESULT 29
LOCUS A2858446/C 19 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0163D08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0163D08 R, DNA sequence.
ACCESSION A2858446
VERSION A2858446.1 GI:13051622
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0163 row: D column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. 19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0163D08"
/clone_1kb="Mouse 10kb plasmid UUGC1M library"

/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN
3 a 5 c 5 g 6 t

Query Match 46.7%; Score 8.4; DB 17; Length 19;
Best Local Similarity 90.0%; Pred. No. 5,7e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGGATCC 14
|||
Db 19 GCCAGATCC 10

RESULT 30
AZ628022/c 20 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0476A13P Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM0476A13 F, DNA sequence.
ACCESSION AZ628022
VERSION AZ628022.1 GI:11750212
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A.
and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0476 row: A column: 13
Seq primer: CGTGTGAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM0476A13"
/clone_1lb="Mouse 10kb plasmid UGCM library"

/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN
8 a 6 c 4 g 2 t

Query Match 46.7%; Score 8.4; DB 17; Length 20;
Best Local Similarity 90.0%; Pred. No. 5,7e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GGATCCAGGC 18
|||
Db 17 GGTTCCAGGC 8

RESULT 31
AZ657644 20 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0534B02F Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM0534B02 F, DNA sequence.
ACCESSION AZ657644
VERSION AZ657644.1 GI:11794790
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A.
and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0534 row: B column: 02
Seq primer: CGTGTGAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM0534B02"
/clone_1lb="Mouse 10kb plasmid UGCM library"

/sex="Male"
/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
2 a 11 c 4 g 3 t

Query Match 46.7%; Score 8.4; DB 17; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.7e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 3; Gaps 0;

QY 5 GCCCGGATCC 14
|||||
Db 3 GCCCGGATCC 12

RESULT 32
AZ961140 20 bp DNA linear GSS 27-APR-2001
LOCUS
DEFINITION 2M0229P20F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0229P20 F, DNA sequence.
ACCESSION
AZ961140
VERSION
A2961140.1 GI:13832367
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Telam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
'M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0229 row: P column: 20
Seq primer: CGTTGTAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. 20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0229P20"
/clone_lib="Mouse 10kb plasmid UUGC2M library"

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

/sex="Female"
/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
1 a 8 c 7 g 4 t

Query Match 46.7%; Score 8.4; DB 17; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.7e+06;
Matches 9; Conservative 0; Mismatches 1; Indels 3; Gaps 0;

QY 1 CTGCGCCCGG 10
|||||
Db 9 CTGCGCTCGG 18

RESULT 33
AA989077/c 22 bp mRNA linear EST 27-JUN-1998
LOCUS
DEFINITION cr88a03.s1 NCI CGAP Lu5 Homo sapiens CDNA clone IMAGE:1602940.3
similar to TR:015816 Q15816 TRANSMEMBRANE PROTEIN JNGSD 1. [2]
TR:014902 ; contains TR1.b2 MSRI repetitive element ;, mRNA
sequence.
ACCESSION
AA989077
VERSION
AA989077.1 GI:3174648
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 22)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Christopher Morkaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLN at:
www.bio.lnl.gov/bdrp/image/image.html

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1602940"
/clone_lib="NCI-CGAP_Lu5"

BASE COUNT	1 a	10 c	9 g	2 t	
ORIGIN	/lab host="FDH10B" /note="Organ: Lung; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoId, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT733 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima BonaIdo. "				
Query Match	46.7%;	Score 8.4;	DB 9;	Length 22;	
Best Local Similarity	90.0%;	Pred. No. 5.7e+06;			
Matches	9;	Conservative	0;	Mismatches	1;
				Indels	0;
				Gaps	0;
Oy	4	CGCCCGGATC	13		
Db	15	CGCCCGGACC	6		
RESULT 34					
LOCUS	A1086217	22 bp	mRNA	linear	EST 28-AUG-1998
DEFINITION	A1086217.81 Soares_fetal_liver_spleen_INFUS_S1 Homo sapiens cDNA clone IMAGE:1654103 3' similar to TR:Q15041 Q15041 mRNA ; mRNA sequence.				
ACCESSION	A1086217				
VERSION	A1086217.1	GI:3424640			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	1 (bases 1 to 22)				
AUTHORS	NCI-CCAG http://www.ncbi.nlm.nih.gov/ncicgap.				
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
JOURNAL	Unpublished (1997)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgsapb-romall.nih.gov This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Insert Length: 812 Std Error: 0.00 Seq primer: -40m13 fwd. RT from Amersham High quality sequence stop: 1.				
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Source	1..22				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/clone="IMAGE:1654103"				
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	/sex="male"				
	/dev_stage="20 week-post conception fetus"				
	/lab_host="FDH10B (ampicillin resistant)"				
	/note="Organ: Liver and spleen; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Pac I; Site 2: Eco RI This is a subcloned version of The original Soares fetal liver spleen INFUS library. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5', AATCGAGAGATTATTAAGACTCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT733 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima BonaIdo."				
BASE COUNT	5 a	5 c	6 g	5 t	1 others
ORIGIN					
Query Match	46.7%;	Score 8.4;	DB 9;	Length 22;	
Best Local Similarity	90.0%;	Pred No. 5.7e+06;			

Matches	9;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	9	GGATCCAGGC	18						
Db	7	GGAACGAGGC	16						
RESULT 35									
DEFINITION	AA878803		25 bp	mRNA		linear	EST 14-APR-1998		
LOCUS	068604.81	NCI CGAP L45	Homo sapiens	cDNA clone IMAGE:1437246 3'					
VERSION	similar to SW:PPPM HUMAN P10161	SALIVARY PROLINE-RICH PROTEIN PO							
KEYWORDS	/containing TARI.ct3	TARI repetitive element							
ACCESSION	AA878803								
VERSION	AA878803.1	GI:2987768							
KEYWORDS	EST.								
SOURCE	human.								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
TITLE	1 (bases 1 to 25)								
COMMENT	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.								
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),								
COMMENT	Tumor Gene Index								
FEATURES	Unpublished (1997)								
SOURCE	Contact: Robert Strauberg, Ph.D.								
	Email: cgaps-remail.nih.gov								
	unknown library type								
	Trace considered overall poor quality								
	Insert length: 185 Std Error: 0.00								
	Seq primer: -40ml3 fwd. ER from Amersham								
	High quality sequence, stop: 1.								
	Location/Qualifiers								
	1. .25								
	/organism="Homo sapiens"								
	/db_xref="taxon:9606"								
	/clone="IMAGE:1437246"								
	/clone_id="NCI_CGAP_L45"								
	/tissue_type="hepatic adenoma"								
	/lab_host="DH10B"								
	/note="Organ: liver; Vector: PCMV-SPORT4; Site_1: SalI;								
	Site_2: NciI; Cloned unidirectionally. Primer: oligo dt.								
	Average insert size 0.8 kb."								
	4 a 12 c 8 g 1 t								
BASE COUNT	4								
ORIGIN									
Query Match									
Best Local Similarity	90.0%;	Score 8.4;	DB 9;	Length 25;					
Matches	9;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	2	TGCGCCCGGA	11						
Db	3	TGCCCCCGGA	12						
RESULT 36									
DEFINITION	A1119986		25 bp	mRNA		linear	EST 02-SEP-1998		
LOCUS	u25b01.r1	Soares mammary_gland NBMMg	Mus musculus	cDNA clone					
VERSION	IMAGE:1386985 5'	similar to TR:000399	000399	WS-3. ''					
KEYWORDS	sequence.								
ACCESSION	A1119986								
VERSION	A1119986.1	GI:3520310							
KEYWORDS	EST.								
SOURCE	house mouse.								
ORGANISM	Mus musculus								
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
	1 (bases 1 to 25)								
	Maria,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,								
	Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,								
	Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,								
	Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and								

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 3 a 8 c 5 g 9 t

ORIGIN

Query Match 46.7%; Score 8.4; DB 17; Length 25;
 Best Local Similarity 90.0%; Pred. No. 5.7e+06;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGGCCCGGAT 12
 Db 13 GGGCCCGGAT 4

RESULT 39
 LOCUS BM393804 15 bp mRNA linear EST 17-JAN-2002
 DEFINITION 50072-2-11-B12.r.1 Chilcoat/Turkewitz cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM393804
 VERSION BM393804.1 GI:18193857
 KEYWORDS EST.

SOURCE Tetrahymena thermophila.
 ORGANISM Tetrahymena thermophila

REFERENCE 1 (bases 1 to 15)
 Hymenostomatida; Tetrahymena; Tetrahymena.

AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel
 J. and Klobutcher, L.
 TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
 JOURNAL Unpublished (2002)
 COMMENT Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.

FEATURES
 source Location/Qualifiers

1..15
 /organism="Tetrahymena thermophila"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library
 preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."
 BASE COUNT 2 a 4 c 7 g 2 t

Query Match 45.6%; Score 8.2; DB 13; Length 15;
 Best Local Similarity 76.9%; Pred. No. 6.9e+06;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGGCCCGGATCCA 15
 Db 15 GGGCCCGGATCCA 3

RESULT 40
 LOCUS BM394186 17 bp mRNA linear EST 17-JAN-2002
 DEFINITION 50072-2-2-D09.r.1 Chilcoat/Turkewitz cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM394186
 VERSION BM394186.1 GI:18194239
 KEYWORDS EST.

SOURCE Tetrahymena thermophila.
 ORGANISM Tetrahymena thermophila

REFERENCE 1 (bases 1 to 17)
 Hymenostomatida; Tetrahymena; Tetrahymena.

AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel
 J. and Klobutcher, L.
 TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
 JOURNAL Unpublished (2002)
 COMMENT Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.

FEATURES
 source Location/Qualifiers

1..17
 /organism="Tetrahymena thermophila"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library
 preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."
 BASE COUNT 1 a 4 c 8 g 4 t

Query Match 45.6%; Score 8.2; DB 13; Length 17;
 Best Local Similarity 76.9%; Pred. No. 6.9e+06;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGGCCCGGATCCA 15
 Db 17 GGGCCCGGATCCA 5

Search completed: June 7, 2003, 09:44:33
 Job time: 1050.58 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 08:51:24 ; Search time 68.7273 Seconds

(without alignments)
366.546 Million cell updates/sec

Title: US-10-080-959a-5

Perfect score: 18
Sequence: 1 ctcgcccgatccagc 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 359952

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	9	US-10-080-959a-5
2	12.2	67.8	24	9	US-09-911-176b-28
3	12.2	67.8	24	9	US-10-180-762-28
4	12.2	67.8	24	9	US-10-241-258-28
5	11.6	64.4	19	10	US-09-997-664-54
6	11.4	63.3	19	9	US-09-423-800-34
7	11.4	63.3	19	9	US-10-182-018-34
8	11.4	63.3	21	9	US-10-085-906-496
9	11.4	63.3	22	9	US-09-990-385-20
10	11.2	62.2	16	9	US-09-961-077-531
11	11.2	62.2	17	9	US-09-864-785-315
12	11.2	62.2	17	9	US-09-864-785-2821
13	11.2	62.2	17	9	US-10-020-141-15
14	11.2	62.2	17	9	US-09-866-108-651
15	11.2	62.2	17	10	US-09-866-108-652
16	11.2	62.2	18	9	US-09-961-077-621
17	11.2	62.2	21	10	US-09-734-188-37
18	11.2	62.2	22	9	US-10-118-100-2

20	11.2	62.2	23	10	US-09-813-289-3	Sequence 3, Appl1
21	11.2	62.2	23	9	US-10-118-100-36	Sequence 16, Appl1
22	11.2	62.2	24	9	US-10-199-550-17	Sequence 17, Appl1
23	11.2	62.2	25	10	US-09-866-108-3580	Sequence 3580, Ap
24	11.2	62.2	25	10	US-09-866-108-3581	Sequence 3581, Ap
25	11.2	62.2	25	10	US-09-866-108-3582	Sequence 3582, Ap
26	11.2	62.2	25	10	US-09-866-108-3583	Sequence 3583, Ap
27	11.2	62.2	25	10	US-09-866-108-3584	Sequence 3584, Ap
28	11.2	62.2	25	10	US-09-866-108-3585	Sequence 3585, Ap
29	11.2	62.2	25	10	US-09-866-108-3586	Sequence 3586, Ap
30	11.2	62.2	25	10	US-09-866-108-3587	Sequence 3587, Ap
31	11.2	62.2	25	10	US-09-866-108-3588	Sequence 3588, Ap
32	11.2	62.2	25	10	US-09-866-108-3589	Sequence 3589, Ap
33	10.8	60.0	18	9	US-10-080-959a-5	Sequence 5, Appl1
34	10.8	60.0	19	9	US-10-251-482-17	Sequence 17, Appl1
35	10.8	60.0	20	9	US-10-057-550-82	Sequence 82, Appl1
36	10.8	60.0	20	9	US-10-122-434-7	Sequence 7, Appl1
37	10.8	60.0	21	10	US-09-733-151-8	Sequence 8, Appl1
38	10.8	60.0	24	9	US-09-940-185-964	Sequence 94, Appl1
39	10.8	60.0	25	9	US-10-076-157-21	Sequence 21, Appl1
40	10.6	58.9	17	9	US-09-864-785-1566	Sequence 1566, Ap
41	10.6	58.9	17	9	US-09-930-423-385	Sequence 385, Ap
42	10.6	58.9	17	10	US-09-866-108-2580	Sequence 2580, Ap
43	10.6	58.9	24	9	US-10-095-672a-26	Sequence 26, Appl1
44	10.6	58.9	24	9	US-10-095-672a-75	Sequence 75, Appl1
45	10.6	58.9	24	9	US-09-940-185-2057	Sequence 2057, Ap
46	10.6	58.9	24	10	US-09-853-830-138	Sequence 138, Ap
47	10.6	58.9	24	10	US-09-729-043a-4	Sequence 4, Appl1
48	10.6	58.9	24	10	US-09-997-664-56	Sequence 56, Appl1
49	10.6	58.9	25	9	US-09-879-461-34	Sequence 34, Appl1
50	10.6	58.9	25	10	US-09-866-108-5509	Sequence 5509, Ap
51	10.6	58.9	25	10	US-09-866-108-5510	Sequence 5510, Ap
52	10.6	58.9	25	10	US-09-866-108-5511	Sequence 5511, Ap
53	10.6	58.9	25	10	US-09-866-108-5512	Sequence 5512, Ap
54	10.6	58.9	25	10	US-09-866-108-5513	Sequence 5513, Ap
55	10.6	58.9	25	10	US-09-866-108-5514	Sequence 5514, Ap
56	10.6	58.9	25	10	US-09-866-108-5515	Sequence 5515, Ap
57	10.6	58.9	25	10	US-09-866-108-5516	Sequence 5516, Ap
58	10.6	58.9	25	10	US-09-866-108-5517	Sequence 5517, Ap
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60	10.4	57.8	20	9	US-09-949-427-144	Sequence 144, Appl1
61	10.4	57.8	21	9	US-09-754-949-14	Sequence 14, Appl1
62	10.4	57.8	21	9	US-10-113-852a-12	Sequence 12, Appl1
63	10.4	57.8	21	10	US-09-814-777a-59	Sequence 59, Appl1
64	10.4	57.8	24	9	US-09-860-474-3	Sequence 3, Appl1
65	10.4	57.8	24	9	US-09-860-474-3	Sequence 3, Appl1
66	10.4	57.8	24	9	US-10-067-956-39	Sequence 39, Appl1
67	10.4	57.8	24	10	US-09-449-204-17	Sequence 17, Appl1
68	10.4	57.8	24	10	US-09-449-204-17	Sequence 17, Appl1
69	10.4	57.8	25	9	US-10-068-674-31	Sequence 31, Appl1
70	10.4	57.8	25	10	US-09-790-399-24	Sequence 24, Appl1
71	10.2	56.7	16	9	US-09-760-294-1	Sequence 1, Appl1
72	10.2	56.7	17	9	US-09-864-785-334	Sequence 334, Appl1
73	10.2	56.7	17	9	US-09-961-077-173	Sequence 173, Appl1
74	10.2	56.7	17	9	US-09-930-423-1353	Sequence 1353, Ap
75	10.2	56.7	17	10	US-09-866-108-650	Sequence 650, Appl1
76	10.2	56.7	17	10	US-09-866-108-653	Sequence 653, Appl1
77	10.2	56.7	17	10	US-09-866-108-6336	Sequence 6336, Ap
78	10.2	56.7	17	10	US-09-866-108-6397	Sequence 6397, Ap
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80	10.2	56.7	18	8	US-08-981-824-44	Sequence 44, Appl1
81	10.2	56.7	19	9	US-09-968-561a-334	Sequence 334, Appl1
82	10.2	56.7	19	9	US-09-941-447a-45	Sequence 45, Appl1
83	10.2	56.7	19	9	US-10-007-127a-9	Sequence 9, Appl1
84	10.2	56.7	19	9	US-10-272-419-28	Sequence 28, Appl1
85	10.2	56.7	19	9	US-10-209-372-23	Sequence 23, Appl1
86	10.2	56.7	19	9	US-09-192-854-196	Sequence 196, Appl1
87	10.2	56.7	19	10	US-09-753-143-10	Sequence 10, Appl1
88	10.2	56.7	19	10	US-09-954-314-128	Sequence 128, Appl1
89	10.2	56.7	20	8	US-08-424-550b-142	Sequence 142, Appl1
90	10.2	56.7	20	8	US-09-324-097-16	Sequence 16, Appl1
91	10.2	56.7	20	9	US-09-135-238b-25	Sequence 25, Appl1
92	10.2	56.7	20	9	US-09-135-238b-25	Sequence 25, Appl1

C 93	10.2	56.7	20	9	US-09-863-049A-15	Sequence 15, Appl	C 166	9.8	54.4	15	9	US-09-880-113A-271	Sequence 211, App
C 94	10.2	56.7	20	9	US-09-940-244-291	Sequence 291, App	C 167	9.8	54.4	16	9	US-09-853-126-139	Sequence 139, App
C 95	10.2	56.7	20	9	US-09-975-036-1	Sequence 1, Appl	C 168	9.8	54.4	16	9	US-09-880-113A-267	Sequence 267, App
C 96	10.2	56.7	20	9	US-09-940-925A-151	Sequence 151, App	C 169	9.8	54.4	16	10	US-09-801-484A-139	Sequence 139, App
C 97	10.2	56.7	20	9	US-10-145-280-2	Sequence 2, Appl	C 170	9.8	54.4	17	9	US-09-864-785-667	Sequence 667, App
C 98	10.2	56.7	20	9	US-10-145-280-2	Sequence 2, Appl	C 171	9.8	54.4	17	9	US-09-864-785-2141	Sequence 2141, App
C 99	10.2	56.7	20	9	US-10-181-177-36	Sequence 96, Appl	C 172	9.8	54.4	17	9	US-09-864-785-2963	Sequence 2963, App
C 100	10.2	56.7	20	9	US-09-516-043-9	Sequence 9, Appl	C 173	9.8	54.4	17	9	US-09-864-785-2964	Sequence 2964, App
C 101	10.2	56.7	20	9	US-09-953-047-62	Sequence 62, Appl	C 174	9.8	54.4	17	9	US-10-234-266-13	Sequence 13, Appl
C 102	10.2	56.7	20	9	US-10-145-314-2	Sequence 2, Appl	C 175	9.8	54.4	17	9	US-10-234-266-14	Sequence 14, Appl
C 103	10.2	56.7	20	10	US-09-891-517-76	Sequence 76, Appl	C 176	9.8	54.4	17	9	US-09-848-754A-1015	Sequence 1015, App
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C 105	10.2	56.7	20	10	US-09-848-185-1	Sequence 1, Appl	C 178	9.8	54.4	17	9	US-09-848-754A-3191	Sequence 3191, App
C 106	10.2	56.7	20	10	US-09-749-7288-48	Sequence 48, Appl	C 179	9.8	54.4	17	9	US-09-848-754A-3192	Sequence 3192, App
C 107	10.2	56.7	21	9	US-09-835-371-9	Sequence 9, Appl	C 180	9.8	54.4	17	9	US-09-930-423-384	Sequence 384, App
C 108	10.2	56.7	21	9	US-09-835-370-9	Sequence 9, Appl	C 181	9.8	54.4	17	9	US-09-930-423-1353	Sequence 1353, App
C 109	10.2	56.7	21	9	US-09-802-1108-29	Sequence 29, Appl	C 182	9.8	54.4	17	9	US-09-930-423-1481	Sequence 1481, App
C 110	10.2	56.7	21	9	US-09-802-1108-31	Sequence 31, Appl	C 183	9.8	54.4	17	9	US-09-930-423-1482	Sequence 1482, App
C 111	10.2	56.7	21	9	US-10-151-542A-25	Sequence 25, Appl	C 184	9.8	54.4	17	9	US-09-930-423-1482	Sequence 1482, App
C 112	10.2	56.7	21	10	US-09-726-774-64	Sequence 64, Appl	C 185	9.8	54.4	17	9	US-09-866-108-2581	Sequence 2581, App
C 113	10.2	56.7	21	10	US-09-660-774-9	Sequence 9, Appl	C 186	9.8	54.4	17	10	US-09-866-108-2582	Sequence 2582, App
C 114	10.2	56.7	22	10	US-09-750-373-47	Sequence 47, Appl	C 187	9.8	54.4	17	10	US-09-866-108-2583	Sequence 2583, App
C 115	10.2	56.7	22	10	US-09-750-373-55	Sequence 55, Appl	C 188	9.8	54.4	17	10	US-09-866-108-2584	Sequence 2584, App
C 116	10.2	56.7	22	10	US-10-124-038-11	Sequence 11, Appl	C 189	9.8	54.4	17	10	US-09-961-077-1179	Sequence 1179, App
C 117	10.2	56.7	23	9	US-09-860-784-57	Sequence 57, Appl	C 190	9.8	54.4	18	9	US-10-181-603-40	Sequence 40, Appl
C 118	10.2	56.7	23	10	US-10-090-455-16	Sequence 16, Appl	C 191	9.8	54.4	18	9	US-10-096-986-46	Sequence 46, Appl
C 119	10.2	56.7	24	9	US-10-090-455-16	Sequence 16, Appl	C 192	9.8	54.4	18	9	US-09-216-393-350	Sequence 350, App
C 120	10.2	56.7	24	9	US-09-952-267-97	Sequence 97, Appl	C 193	9.8	54.4	19	10	US-09-880-313A-205	Sequence 205, App
C 121	10.2	56.7	24	9	US-09-940-185-2276	Sequence 2276, App	C 194	9.8	54.4	19	9	US-09-880-313A-235	Sequence 235, App
C 122	10.2	56.7	24	9	US-09-940-185-3623	Sequence 3623, App	C 195	9.8	54.4	19	9	US-09-880-313A-229	Sequence 229, App
C 123	10.2	56.7	25	9	US-09-969-844-10	Sequence 10, Appl	C 196	9.8	54.4	19	9	US-10-053-243-1	Sequence 1, Appl
C 124	10.2	56.7	25	10	US-09-784-423-125	Sequence 125, App	C 197	9.8	54.4	20	9	US-10-053-243-1	Sequence 1, Appl
C 125	10.2	56.7	25	10	US-09-866-108-3579	Sequence 3579, App	C 198	9.8	54.4	20	9	US-10-053-243-1	Sequence 1, Appl
C 126	10.2	56.7	25	10	US-09-866-108-3579	Sequence 3579, App	C 199	9.8	54.4	20	9	US-10-053-243-1	Sequence 1, Appl
C 127	10.2	56.7	25	10	US-09-866-108-11288	Sequence 11288, App	C 200	9.8	54.4	20	9	US-09-906-939A-30	Sequence 30, App
C 128	10.2	56.7	25	10	US-09-866-108-11289	Sequence 11289, App	C 201	9.8	54.4	20	9	US-09-865-866-134	Sequence 134, App
C 129	10.2	56.7	25	10	US-09-866-108-11290	Sequence 11290, App	C 202	9.8	54.4	20	9	US-09-920-677-11	Sequence 11, App
C 130	10.2	56.7	25	10	US-09-866-108-11291	Sequence 11291, App	C 203	9.8	54.4	20	9	US-09-920-677-12	Sequence 12, App
C 131	10.2	56.7	25	10	US-09-866-108-11292	Sequence 11292, App	C 204	9.8	54.4	20	9	US-09-920-677-13	Sequence 13, App
C 132	10.2	56.7	25	10	US-09-866-108-11293	Sequence 11293, App	C 205	9.8	54.4	20	9	US-09-920-677-14	Sequence 14, App
C 133	10.2	56.7	25	10	US-09-866-108-11294	Sequence 11294, App	C 206	9.8	54.4	21	9	US-10-006-593-72	Sequence 72, App
C 134	10.2	56.7	25	10	US-09-866-108-11295	Sequence 11295, App	C 207	9.8	54.4	21	10	US-09-765-081-386	Sequence 386, App
C 135	10.2	56.7	25	10	US-09-866-108-11296	Sequence 11296, App	C 208	9.8	54.4	22	9	US-09-990-385-20	Sequence 20, App
C 136	10.2	56.7	25	10	US-09-866-108-11297	Sequence 11297, App	C 209	9.8	54.4	22	9	US-10-131-591A-76	Sequence 76, App
C 137	10.2	56.7	25	10	US-09-866-108-11298	Sequence 11298, App	C 210	9.8	54.4	22	9	US-09-750-410-29	Sequence 29, App
C 138	10.2	56.7	25	10	US-09-972-467-5	Sequence 5, Appl	C 211	9.8	54.4	22	9	US-10-161-025-6	Sequence 6, Appl
C 139	10.2	56.7	25	10	US-09-963-285-22	Sequence 22, Appl	C 212	9.8	54.4	23	9	US-09-520-538-15	Sequence 15, App
C 140	10.2	56.7	15	9	US-09-877-705A-107	Sequence 107, App	C 213	9.8	54.4	23	9	US-09-507-338-75	Sequence 75, App
C 141	10.2	56.7	15	9	US-09-877-705A-108	Sequence 108, App	C 214	9.8	54.4	23	10	US-09-016-159-1	Sequence 1, Appl
C 142	10.2	56.7	15	9	US-09-877-738A-107	Sequence 107, App	C 215	9.8	54.4	23	12	US-10-101-747-3	Sequence 3, Appl
C 143	10.2	56.7	15	9	US-09-877-738A-108	Sequence 108, App	C 216	9.8	54.4	24	9	US-10-211-673-14	Sequence 14, App
C 144	10.2	56.7	20	9	US-10-181-846-160	Sequence 160, App	C 217	9.8	54.4	24	9	US-09-940-188-982	Sequence 982, App
C 145	10.2	56.7	20	10	US-09-848-696-9	Sequence 9, Appl	C 218	9.8	54.4	24	9	US-09-940-188-1424	Sequence 1424, App
C 146	10.2	56.7	20	12	US-10-090-624-18	Sequence 18, Appl	C 219	9.8	54.4	24	9	US-09-940-188-2734	Sequence 2734, App
C 147	10.2	56.7	21	9	US-10-012-898-22	Sequence 22, Appl	C 220	9.8	54.4	24	10	US-09-777-430A-79	Sequence 79, Appl
C 148	10.2	56.7	22	10	US-09-899-980A-32	Sequence 32, Appl	C 221	9.8	54.4	24	10	US-09-285-355C-18	Sequence 18, Appl
C 149	10.2	56.7	22	10	US-09-940-185-1344	Sequence 1344, App	C 222	9.8	54.4	24	10	US-09-997-664-56	Sequence 56, Appl
C 150	10.2	56.7	24	9	US-09-940-185-2710	Sequence 2710, App	C 223	9.8	54.4	25	9	US-09-847-101B-26	Sequence 26, Appl
C 151	10.2	56.7	25	10	US-10-061-943A-24	Sequence 24, Appl	C 224	9.8	54.4	25	9	US-10-215-112-8440	Sequence 8440, App
C 152	10.2	56.7	25	10	US-09-866-108-3582	Sequence 3582, App	C 225	9.8	54.4	25	9	US-09-507-367-78	Sequence 78, Appl
C 153	10.2	56.7	25	10	US-09-866-108-3583	Sequence 3583, App	C 226	9.8	54.4	25	10	US-09-866-108-5518	Sequence 5518, App
C 154	10.2	56.7	25	10	US-09-866-108-3584	Sequence 3584, App	C 227	9.8	54.4	25	10	US-09-866-108-5519	Sequence 5519, App
C 155	10.2	56.7	25	10	US-09-866-108-3585	Sequence 3585, App	C 228	9.8	54.4	25	10	US-09-866-108-5520	Sequence 5520, App
C 156	10.2	56.7	25	10	US-09-866-108-3586	Sequence 3586, App	C 229	9.8	54.4	25	10	US-09-866-108-5521	Sequence 5521, App
C 157	10.2	56.7	25	10	US-09-866-108-3587	Sequence 3587, App	C 230	9.8	54.4	17	9	US-09-961-077-80	Sequence 80, Appl
C 158	10.2	56.7	25	10	US-09-866-108-3588	Sequence 3588, App	C 231	9.8	54.4	17	9	US-09-961-077-82	Sequence 82, Appl
C 159	10.2	56.7	25	10	US-09-866-108-3589	Sequence 3589, App	C 232	9.8	54.4	17	9	US-09-780-533A-647	Sequence 647, App
C 160	9.8	54.4	15	9	US-09-880-313A-211	Sequence 211, App	C 233	9.6	53.3	17	9	US-09-848-754A-104	Sequence 104, App
C 161	9.8	54.4	15	9	US-09-880-313A-217	Sequence 217, App	C 234	9.6	53.3	17	9	US-09-848-754A-104	Sequence 104, App
C 162	9.8	54.4	15	9	US-09-880-313A-223	Sequence 223, App	C 235	9.6	53.3	17	9	US-09-848-754A-1068	Sequence 1068, App
C 163	9.8	54.4	15	9	US-09-880-313A-225	Sequence 225, App	C 236	9.6	53.3	17	9	US-09-848-754A-1069	Sequence 1069, App
C 164	9.8	54.4	15	9	US-09-880-313A-235	Sequence 235, App	C 237	9.6	53.3	17	9	US-09-930-423-1483	Sequence 1483, App
C 165	9.8	54.4	15	9	US-09-880-313A-247	Sequence 247, App	C 238	9.6	53.3	17	9		

229	9.6	53.3	17	10	US-09-866-108-651	Sequence 651, App	C 312	9.4	52.2	22	9	US-09-907-824-92	Sequence 92, Appl
240	9.6	53.3	17	10	US-09-866-108-652	Sequence 652, App	C 313	9.4	52.2	22	9	US-09-907-841-92	Sequence 92, Appl
241	9.6	53.3	17	10	US-09-866-108-2579	Sequence 2579, Ap	C 314	9.4	52.2	22	9	US-09-904-011-92	Sequence 92, Appl
C 242	9.6	53.3	18	9	US-10-252-408-21	Sequence 21, Appl	C 315	9.4	52.2	22	9	US-09-906-742-92	Sequence 92, Appl
C 243	9.6	53.3	19	9	US-10-251-482-17	Sequence 17, Appl	C 316	9.4	52.2	22	9	US-09-906-838-92	Sequence 92, Appl
C 244	9.6	53.3	20	9	US-09-964-261-286	Sequence 286, App	C 317	9.4	52.2	22	9	US-09-907-613-92	Sequence 92, Appl
C 245	9.6	53.3	20	9	US-09-949-427-144	Sequence 144, App	C 318	9.4	52.2	22	9	US-09-907-942-92	Sequence 92, Appl
C 246	9.6	53.3	20	9	US-09-906-158-42	Sequence 42, Appl	C 319	9.4	52.2	22	9	US-09-904-820-92	Sequence 92, Appl
C 248	9.6	53.3	20	9	US-10-122-434-9	Sequence 9, Appl	C 320	9.4	52.2	22	9	US-09-904-859-92	Sequence 92, Appl
C 249	9.6	53.3	20	9	US-09-953-047-62	Sequence 62, Appl	C 321	9.4	52.2	22	9	US-09-909-204-92	Sequence 92, Appl
C 250	9.6	53.3	20	10	US-09-899-440-10	Sequence 10, Appl	C 322	9.4	52.2	22	9	US-09-904-786-92	Sequence 92, Appl
C 251	9.6	53.3	20	10	US-09-734-847A-63	Sequence 63, Appl	C 323	9.4	52.2	22	9	US-09-906-646-92	Sequence 92, Appl
C 252	9.6	53.3	20	10	US-09-734-847A-64	Sequence 64, Appl	C 324	9.4	52.2	22	9	US-09-906-700-92	Sequence 92, Appl
C 253	9.6	53.3	20	10	US-09-800-629A-172	Sequence 172, App	C 325	9.4	52.2	22	9	US-09-902-903-92	Sequence 92, Appl
C 254	9.6	53.3	21	9	US-09-964-261-287	Sequence 287, App	C 326	9.4	52.2	22	9	US-09-903-748A-92	Sequence 92, Appl
C 255	9.6	53.3	21	9	US-09-093-972C-985	Sequence 985, App	C 327	9.4	52.2	22	9	US-09-903-786-92	Sequence 92, Appl
C 256	9.6	53.3	21	10	US-09-728-466-39	Sequence 39, Appl	C 328	9.4	52.2	22	9	US-09-902-736-92	Sequence 92, Appl
C 257	9.6	53.3	22	10	US-09-765-081-259	Sequence 259, App	C 329	9.4	52.2	22	9	US-09-904-119-92	Sequence 92, Appl
C 258	9.6	53.3	22	9	US-09-964-261-288	Sequence 288, App	C 330	9.4	52.2	22	9	US-09-904-956-92	Sequence 92, Appl
C 259	9.6	53.3	23	9	US-09-144-886-7	Sequence 7, Appl	C 331	9.4	52.2	22	9	US-09-907-794-92	Sequence 92, Appl
C 260	9.6	53.3	23	9	US-09-964-261-389	Sequence 289, App	C 332	9.4	52.2	22	9	US-09-902-692-92	Sequence 92, Appl
C 261	9.6	53.3	24	8	US-08-887-505-48	Sequence 48, Appl	C 333	9.4	52.2	22	9	US-09-903-820-92	Sequence 92, Appl
C 262	9.6	53.3	24	9	US-09-964-261-290	Sequence 290, App	C 334	9.4	52.2	22	9	US-09-903-843-92	Sequence 92, Appl
C 263	9.6	53.3	24	9	US-09-940-185-1518	Sequence 1518, App	C 335	9.4	52.2	22	9	US-09-904-462-92	Sequence 92, Appl
C 264	9.6	53.3	25	9	US-09-773-539-9	Sequence 9, Appl	C 336	9.4	52.2	22	9	US-09-905-056-92	Sequence 92, Appl
C 265	9.6	53.3	25	9	US-09-964-261-291	Sequence 291, App	C 337	9.4	52.2	22	9	US-09-907-925-92	Sequence 92, Appl
C 266	9.6	53.3	25	9	US-09-961-077-1250	Sequence 1250, Ap	C 338	9.4	52.2	22	9	US-09-904-553-92	Sequence 92, Appl
C 267	9.6	53.3	25	9	US-10-215-112-1196	Sequence 1196, A	C 339	9.4	52.2	22	9	US-09-905-381-92	Sequence 92, Appl
C 268	9.6	53.3	25	10	US-09-866-108-3580	Sequence 3580, Ap	C 340	9.4	52.2	22	9	US-09-909-064-92	Sequence 92, Appl
C 269	9.6	53.3	25	10	US-09-866-108-3581	Sequence 3581, Ap	C 341	9.4	52.2	22	9	US-09-905-088-92	Sequence 92, Appl
C 270	9.4	52.2	15	10	US-09-866-108-5508	Sequence 5508, Ap	C 342	9.4	52.2	22	9	US-09-907-575-92	Sequence 92, Appl
C 271	9.4	52.2	15	10	US-09-919-758-7	Sequence 7, Appl	C 343	9.4	52.2	22	9	US-09-902-759-92	Sequence 92, Appl
C 272	9.4	52.2	15	10	US-09-873-075A-4	Sequence 4, Appl	C 344	9.4	52.2	22	9	US-09-905-075-92	Sequence 92, Appl
C 273	9.4	52.2	17	9	US-09-864-785-668	Sequence 668, App	C 345	9.4	52.2	22	9	US-09-902-534-92	Sequence 92, Appl
C 274	9.4	52.2	17	9	US-09-982-658A-3	Sequence 3, Appl	C 346	9.4	52.2	22	9	US-09-907-713-92	Sequence 92, Appl
C 275	9.4	52.2	17	9	US-09-971-631-3	Sequence 3, Appl	C 347	9.4	52.2	22	9	US-09-907-979-92	Sequence 92, Appl
C 276	9.4	52.2	17	9	US-09-848-754A-2230	Sequence 2230, Ap	C 348	9.4	52.2	22	9	US-09-902-615-92	Sequence 92, Appl
C 277	9.4	52.2	17	10	US-09-866-108-6772	Sequence 6772, Ap	C 349	9.4	52.2	22	9	US-09-903-925-92	Sequence 92, Appl
C 278	9.4	52.2	17	10	US-09-866-108-6773	Sequence 6773, Ap	C 350	9.4	52.2	22	9	US-09-909-320-92	Sequence 92, Appl
C 279	9.4	52.2	17	10	US-09-866-108-6774	Sequence 6774, Ap	C 351	9.4	52.2	22	10	US-09-909-320-92	Sequence 92, Appl
C 280	9.4	52.2	17	10	US-09-866-108-6775	Sequence 6775, Ap	C 352	9.4	52.2	22	10	US-09-909-088B-92	Sequence 92, Appl
C 281	9.4	52.2	17	10	US-09-866-108-6776	Sequence 6776, Ap	C 353	9.4	52.2	23	9	US-10-084-686-1	Sequence 1, Appl
C 282	9.4	52.2	17	10	US-09-866-108-6777	Sequence 6777, Ap	C 354	9.4	52.2	23	9	US-09-507-362-76	Sequence 76, Appl
C 283	9.4	52.2	17	10	US-09-866-108-6778	Sequence 6778, Ap	C 355	9.4	52.2	23	10	US-09-725-752-28	Sequence 28, Appl
C 284	9.4	52.2	18	9	US-09-954-534A-36	Sequence 36, Appl	C 356	9.4	52.2	24	9	US-09-852-416-10	Sequence 10, Appl
C 285	9.4	52.2	18	9	US-09-974-685-36	Sequence 36, Appl	C 357	9.4	52.2	24	9	US-09-839-446-49	Sequence 49, Appl
C 286	9.4	52.2	18	9	US-09-093-972C-4	Sequence 4, Appl	C 358	9.4	52.2	24	9	US-09-940-185-1524	Sequence 1524, Ap
C 287	9.4	52.2	18	10	US-09-865-807-36	Sequence 36, Appl	C 359	9.4	52.2	24	9	US-09-940-185-2509	Sequence 2509, Ap
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C 289	9.4	52.2	18	10	US-09-969-373-2911	Sequence 2911, Ap	C 361	9.4	52.2	24	10	US-09-898-570-49	Sequence 49, Appl
C 290	9.4	52.2	19	9	US-09-967-237-4	Sequence 4, Appl	C 362	9.4	52.2	25	9	US-09-867-145-48	Sequence 48, Appl
C 291	9.4	52.2	19	10	US-09-772-719-4	Sequence 4, Appl	C 363	9.4	52.2	25	9	US-10-215-112-2486	Sequence 2486, Ap
C 292	9.4	52.2	19	10	US-09-918-951-12	Sequence 12, Appl	C 364	9.4	52.2	25	9	US-10-215-112-2850	Sequence 2850, Ap
C 293	9.4	52.2	20	9	US-09-888-326-492	Sequence 492, App	C 365	9.4	52.2	25	9	US-10-215-112-4114	Sequence 4114, Ap
C 294	9.4	52.2	20	9	US-10-057-550-78	Sequence 78, Appl	C 366	9.4	52.2	25	9	US-10-215-112-8314	Sequence 8314, Ap
C 295	9.4	52.2	20	9	US-10-112-653-511	Sequence 511, App	C 367	9.4	52.2	25	10	US-09-866-108-11664	Sequence 11664, A
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C 297	9.4	52.2	20	9	US-10-067-125-51	Sequence 51, Appl	C 369	9.4	52.2	25	10	US-09-866-108-11666	Sequence 11666, A
C 298	9.4	52.2	20	9	US-09-776-479-534	Sequence 534, App	C 370	9.4	52.2	25	10	US-09-866-108-11667	Sequence 11667, A
C 299	9.4	52.2	20	9	US-10-001-076-38	Sequence 38, Appl	C 371	9.4	52.2	25	10	US-09-866-108-11668	Sequence 11668, A
C 300	9.4	52.2	20	10	US-09-758-881-56	Sequence 56, Appl	C 372	9.4	52.2	25	10	US-09-866-108-11669	Sequence 11669, A
C 301	9.4	52.2	20	10	US-09-007-093-10	Sequence 10, Appl	C 373	9.4	52.2	25	10	US-09-866-108-11670	Sequence 11670, A
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C 304	9.4	52.2	20	10	US-09-984-198-79	Sequence 79, Appl	C 376	9.4	52.2	25	10	US-09-866-108-11673	Sequence 11673, A
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C 306	9.4	52.2	21	9	US-09-808-602-40	Sequence 40, Appl	C 378	9.4	52.2	25	10	US-09-866-108-11675	Sequence 11675, A
C 307	9.4	52.2	21	9	US-09-808-602-41	Sequence 41, Appl	C 379	9.4	52.2	25	10	US-09-866-108-11676	Sequence 11676, A
C 308	9.4	52.2	21	9	US-10-158-160A-66	Sequence 26, Appl	C 380	9.4	52.2	25	10	US-09-866-108-11677	Sequence 11677, A
C 309	9.4	52.2	21	9	US-09-952-213D-8	Sequence 8, Appl	C 381	9.4	52.2	25	10	US-09-866-108-11678	Sequence 11678, A
C 310	9.4	52.2	22	9	US-09-905-291A-92	Sequence 92, Appl	C 382	9.4	52.2	25	10	US-09-911-346-12	Sequence 12, Appl
C 311	9.4	52.2	22	9	US-09-902-853-92	Sequence 92, Appl	C 383	9.4	52.2	25	10	US-09-751-100B-101	Sequence 101, App
							C 384	9.2	51.1	14	9	US-10-076-106-1	Sequence 1, Appl

C 385	9.2	51.1	14	9	US-10-076-106-1	Sequence 1, Appl1	458	9.2	51.1	20	9	US-10-181-107-120	Sequence 120, App
386	9.2	51.1	15	9	US-09-864-785-3720	Sequence 3720, Ap	C 459	9.2	51.1	20	9	US-10-238-443-87	Sequence 87, Appl
387	9.2	51.1	15	9	US-10-118-100-38	Sequence 38, Appl	C 460	9.2	51.1	20	9	US-10-076-170	Sequence 170, Appl
388	9.2	51.1	15	10	US-09-953-242-14	Sequence 14, Appl	C 461	9.2	51.1	20	9	US-10-016-159-19	Sequence 19, Appl
389	9.2	51.1	16	8	US-08-591-486B-39	Sequence 39, Appl	C 462	9.2	51.1	20	9	US-10-166-841-3	Sequence 3, Appl1
390	9.2	51.1	16	9	US-09-821-278-5	Sequence 2, Appl1	C 463	9.2	51.1	20	10	US-09-758-881-21	Sequence 21, Appl
391	9.2	51.1	16	9	US-09-760-294-2	Sequence 5, Appl1	C 464	9.2	51.1	20	10	US-09-735-995-55	Sequence 50, Appl
392	9.2	51.1	17	9	US-09-978-295A-544	Sequence 544, App	C 465	9.2	51.1	20	10	US-09-602-669-70	Sequence 70, Appl
393	9.2	51.1	17	9	US-09-978-697-544	Sequence 544, App	C 466	9.2	51.1	20	10	US-09-734-847A-62	Sequence 62, Appl
394	9.2	51.1	17	9	US-09-864-785-333	Sequence 333, App	C 467	9.2	51.1	20	10	US-09-952-053-21	Sequence 21, Appl
395	9.2	51.1	17	9	US-09-864-785-467	Sequence 467, App	C 468	9.2	51.1	20	10	US-09-832-448-23	Sequence 23, Appl
396	9.2	51.1	17	9	US-09-864-785-468	Sequence 468, App	C 469	9.2	51.1	20	10	US-09-734-847A-62	Sequence 62, Appl
397	9.2	51.1	17	9	US-09-864-785-2101	Sequence 2101, Ap	C 470	9.2	51.1	20	10	US-09-952-053-21	Sequence 21, Appl
398	9.2	51.1	17	9	US-09-864-785-2864	Sequence 2864, App	C 471	9.2	51.1	20	10	US-09-791-406-21	Sequence 21, Appl
399	9.2	51.1	17	9	US-09-999-832A-544	Sequence 544, App	C 472	9.2	51.1	20	10	US-09-964-261-287	Sequence 261, Appl
400	9.2	51.1	17	9	US-09-825-805-387	Sequence 387, App	C 473	9.2	51.1	21	9	US-10-101-461-9	Sequence 9, Appl1
401	9.2	51.1	17	9	US-09-825-805-857	Sequence 857, App	C 474	9.2	51.1	21	9	US-09-964-261-287	Sequence 261, Appl
402	9.2	51.1	17	9	US-09-978-189-544	Sequence 544, App	C 475	9.2	51.1	21	9	US-09-860-788C-116	Sequence 116, Appl
403	9.2	51.1	17	9	US-09-961-077-1251	Sequence 1251, Ap	C 476	9.2	51.1	21	9	US-09-984-842-18	Sequence 18, Appl
404	9.2	51.1	17	9	US-09-961-077-1251	Sequence 1251, Ap	C 477	9.2	51.1	21	9	US-09-984-842-18	Sequence 18, Appl
405	9.2	51.1	17	9	US-09-978-608A-544	Sequence 544, App	C 478	9.2	51.1	21	9	US-10-206-839-105	Sequence 105, App
406	9.2	51.1	17	9	US-09-818-875-467	Sequence 467, App	C 479	9.2	51.1	21	10	US-09-765-081-434	Sequence 434, App
407	9.2	51.1	17	9	US-09-818-875-467	Sequence 467, App	C 480	9.2	51.1	21	10	US-09-776-874A-18	Sequence 18, Appl
408	9.2	51.1	17	9	US-09-818-875-468	Sequence 468, App	C 481	9.2	51.1	21	12	US-10-066-151-43	Sequence 43, Appl
409	9.2	51.1	17	9	US-09-978-191A-544	Sequence 544, App	C 482	9.2	51.1	22	9	US-09-964-261-288	Sequence 268, App
410	9.2	51.1	17	9	US-09-978-403A-544	Sequence 544, App	C 483	9.2	51.1	22	10	US-10-124-038-36	Sequence 36, Appl1
411	9.2	51.1	17	9	US-09-978-564A-544	Sequence 544, App	C 484	9.2	51.1	22	10	US-09-739-843-6	Sequence 6, Appl1
412	9.2	51.1	17	9	US-09-978-565A-544	Sequence 544, App	C 485	9.2	51.1	22	10	US-09-899-980A-32	Sequence 32, Appl
413	9.2	51.1	17	9	US-09-978-585A-544	Sequence 544, App	C 486	9.2	51.1	22	10	US-09-417-791-9	Sequence 9, Appl1
414	9.2	51.1	17	9	US-10-017-081A-544	Sequence 544, App	C 487	9.2	51.1	22	10	US-09-417-791-11	Sequence 11, Appl
415	9.2	51.1	17	9	US-09-978-82A-544	Sequence 544, App	C 488	9.2	51.1	22	10	US-09-934-332-14	Sequence 14, Appl
416	9.2	51.1	17	9	US-09-981-915A-544	Sequence 544, App	C 489	9.2	51.1	22	10	US-09-997-664-10	Sequence 10, Appl
417	9.2	51.1	17	9	US-09-999-833A-544	Sequence 544, App	C 490	9.2	51.1	23	8	US-08-812-933A-37	Sequence 37, Appl
418	9.2	51.1	17	9	US-10-167-749-544	Sequence 544, App	C 491	9.2	51.1	23	8	US-08-812-933A-38	Sequence 38, Appl
419	9.2	51.1	17	9	US-09-918-585A-544	Sequence 544, App	C 492	9.2	51.1	23	9	US-09-964-261-289	Sequence 289, App
420	9.2	51.1	17	9	US-09-877-478-455	Sequence 455, App	C 493	9.2	51.1	23	9	US-10-124-038-12	Sequence 12, Appl
421	9.2	51.1	17	9	US-09-877-478-2391	Sequence 2391, Ap	C 494	9.2	51.1	23	9	US-10-124-038-13	Sequence 13, Appl
422	9.2	51.1	17	9	US-09-877-478-2392	Sequence 2392, Ap	C 495	9.2	51.1	23	10	US-09-871-615-3	Sequence 3, Appl1
423	9.2	51.1	17	9	US-09-978-423A-544	Sequence 544, App	C 496	9.2	51.1	24	9	US-09-860-784-74	Sequence 74, Appl
424	9.2	51.1	17	9	US-10-013-921A-544	Sequence 544, App	C 497	9.2	51.1	24	9	US-09-964-261-290	Sequence 290, App
425	9.2	51.1	17	9	US-09-848-754A-824	Sequence 824, App	C 498	9.2	51.1	24	9	US-10-027-661A-1	Sequence 1, Appl1
426	9.2	51.1	17	9	US-09-978-193A-544	Sequence 544, App	C 499	9.2	51.1	24	9	US-10-175-268-1	Sequence 1, Appl1
427	9.2	51.1	17	9	US-10-013-929A-544	Sequence 544, App	C 500	9.2	51.1	24	9	US-10-121-058-42	Sequence 42, Appl
428	9.2	51.1	17	9	US-09-999-830A-544	Sequence 544, App	C 501	9.2	51.1	24	9	US-10-124-038-17	Sequence 17, Appl
429	9.2	51.1	17	9	US-09-978-757A-544	Sequence 544, App	C 502	9.2	51.1	24	9	US-09-992-665-308	Sequence 308, App
430	9.2	51.1	17	9	US-10-055-719-10	Sequence 10, Appl	C 503	9.2	51.1	24	9	US-09-992-665-347	Sequence 347, App
431	9.2	51.1	17	9	US-09-930-423-1484	Sequence 1484, Ap	C 504	9.2	51.1	24	9	US-09-940-185-61	Sequence 61, Appl
432	9.2	51.1	17	9	US-09-930-423-1485	Sequence 1485, Ap	C 505	9.2	51.1	24	9	US-09-940-185-1566	Sequence 1566, App
433	9.2	51.1	17	10	US-09-978-187B-544	Sequence 544, App	C 506	9.2	51.1	24	9	US-09-940-185-1566	Sequence 1566, App
434	9.2	51.1	17	10	US-09-866-108-649	Sequence 649, App	C 507	9.2	51.1	24	9	US-09-940-185-1566	Sequence 1566, App
435	9.2	51.1	17	10	US-09-866-108-654	Sequence 654, App	C 508	9.2	51.1	24	9	US-09-940-185-1566	Sequence 1566, App
436	9.2	51.1	17	10	US-09-866-108-6395	Sequence 6395, App	C 509	9.2	51.1	24	9	US-09-940-185-1566	Sequence 1566, App
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438	9.2	51.1	18	9	US-09-835-370-17	Sequence 17, Appl	C 511	9.2	51.1	24	10	US-09-803-347-1	Sequence 1, Appl1
439	9.2	51.1	18	9	US-09-835-370-17	Sequence 17, Appl	C 512	9.2	51.1	24	10	US-09-466-320-22	Sequence 22, Appl
440	9.2	51.1	18	10	US-09-858-616-3	Sequence 3, Appl1	C 513	9.2	51.1	24	10	US-09-803-549-1	Sequence 1, Appl1
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444	9.2	51.1	19	9	US-10-000-512-26	Sequence 26, Appl	C 517	9.2	51.1	24	10	US-09-860-784-76	Sequence 76, Appl
445	9.2	51.1	19	9	US-10-138-316-42	Sequence 42, Appl	C 518	9.2	51.1	24	10	US-09-860-784-76	Sequence 76, Appl
446	9.2	51.1	19	10	US-09-754-849-16	Sequence 16, Appl	C 519	9.2	51.1	24	12	US-10-066-151-47	Sequence 47, Appl
447	9.2	51.1	19	10	US-09-754-849-16	Sequence 16, Appl	C 520	9.2	51.1	25	9	US-10-066-151-489	Sequence 89, Appl
448	9.2	51.1	19	10	US-09-754-849-16	Sequence 16, Appl	C 521	9.2	51.1	25	9	US-09-860-784-76	Sequence 76, Appl
449	9.2	51.1	19	10	US-09-754-849-16	Sequence 16, Appl	C 522	9.2	51.1	25	9	US-09-860-784-76	Sequence 76, Appl
450	9.2	51.1	20	9	US-09-860-784-73	Sequence 73, Appl	C 523	9.2	51.1	25	9	US-09-860-784-76	Sequence 76, Appl
451	9.2	51.1	20	9	US-09-860-784-73	Sequence 73, Appl	C 524	9.2	51.1	25	9	US-09-860-784-76	Sequence 76, Appl
452	9.2	51.1	20	9	US-09-860-784-73	Sequence 73, Appl	C 525	9.2	51.1	25	9	US-09-860-784-76	Sequence 76, Appl
453	9.2	51.1	20	9	US-09-860-784-73	Sequence 73, Appl	C 526	9.2	51.1	25	9	US-09-860-784-76	Sequence 76, Appl
454	9.2	51.1	20	9	US-09-860-784-73	Sequence 73, Appl	C 527	9.2	51.1	25	9	US-09-860-784-76	Sequence 76, Appl
455	9.2	51.1	20	9	US-09-860-784-73	Sequence 73, Appl	C 528	9.2	51.1	25	9	US-09-860-784-76	Sequence 76, Appl
456	9.2	51.1	20	9	US-09-860-784-73	Sequence 73, Appl	C 529	9.2	51.1	25	9	US-09-860-784-76	Sequence 76, Appl
457	9.2	51.1	20	9	US-09-860-784-73	Sequence 73, Appl	C 530	9.2	51.1	25	9	US-09-860-784-76	Sequence 76, Appl

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C 532	9.2	51.1	25	9	US-10-215-112-11993	Sequence 11993, A	C 605	9	50.0	20	10	US-09-833-648-23	Sequence 23, Appl
C 533	9.2	51.1	25	9	US-10-264-361-14	Sequence 14, Appl	C 606	9	50.0	20	10	US-09-965-662-10	Sequence 10, Appl
C 534	9.2	51.1	25	9	US-09-940-185-4043	Sequence 1043, Ap	C 607	9	50.0	21	9	US-09-978-299A-584	Sequence 584, App
C 535	9.2	51.1	25	10	US-09-866-108-3578	Sequence 3578, Ap	C 608	9	50.0	21	9	US-09-978-697-584	Sequence 584, App
C 536	9.2	51.1	25	10	US-09-866-108-3591	Sequence 3591, Ap	C 609	9	50.0	21	9	US-09-978-192A-584	Sequence 584, App
C 537	9.2	51.1	25	10	US-09-866-108-11287	Sequence 11287, A	C 610	9	50.0	21	9	US-09-999-832A-584	Sequence 584, App
C 538	9.2	51.1	25	10	US-09-866-108-11299	Sequence 11299, A	C 611	9	50.0	21	9	US-09-978-189-584	Sequence 584, App
C 539	9.2	51.1	25	10	US-09-452-599-93	Sequence 93, Appl	C 612	9	50.0	21	9	US-10-132-655-25	Sequence 25, Appl
C 540	9.2	51.1	25	10	US-09-815-330A-8	Sequence 8, Appl	C 613	9	50.0	21	9	US-09-978-608A-584	Sequence 584, App
C 541	9.2	51.1	25	10	US-09-956-998A-6	Sequence 6, Appl	C 614	9	50.0	21	9	US-09-978-191A-584	Sequence 584, App
C 542	9.2	51.1	25	10	US-09-956-998A-13	Sequence 13, Appl	C 615	9	50.0	21	9	US-09-978-403A-584	Sequence 584, App
C 543	9	50.0	9	10	US-09-990-186-2245	Sequence 2245, Ap	C 616	9	50.0	21	9	US-09-978-568A-584	Sequence 584, App
C 544	9	50.0	9	10	US-09-989-789-2245	Sequence 2245, Ap	C 617	9	50.0	21	9	US-09-978-568A-584	Sequence 584, App
C 545	9	50.0	11	10	US-09-813-031-10	Sequence 10, Appl	C 618	9	50.0	21	9	US-10-017-081A-584	Sequence 584, App
C 546	9	50.0	11	10	US-09-813-031-18	Sequence 18, Appl	C 619	9	50.0	21	9	US-09-949-427-402	Sequence 402, App
C 547	9	50.0	11	10	US-09-813-990A-10	Sequence 10, Appl	C 620	9	50.0	21	9	US-09-978-82A-584	Sequence 584, App
C 548	9	50.0	11	10	US-09-813-990A-18	Sequence 18, Appl	C 621	9	50.0	21	9	US-09-981-918A-584	Sequence 584, App
C 549	9	50.0	15	9	US-09-879-813-67	Sequence 67, Appl	C 622	9	50.0	21	9	US-09-999-833A-584	Sequence 584, App
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C 551	9	50.0	15	10	US-09-005-243-91	Sequence 91, Appl	C 624	9	50.0	21	9	US-09-918-584A-584	Sequence 584, App
C 552	9	50.0	15	10	US-09-005-243-92	Sequence 92, Appl	C 625	9	50.0	21	9	US-09-978-423A-584	Sequence 584, App
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C 554	9	50.0	15	10	US-09-224-683-92	Sequence 92, Appl	C 627	9	50.0	21	9	US-09-978-193A-584	Sequence 584, App
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C 556	9	50.0	16	9	US-09-880-113A-219	Sequence 219, App	C 629	9	50.0	21	9	US-10-016-172A-584	Sequence 584, App
C 557	9	50.0	16	9	US-09-880-113A-225	Sequence 225, App	C 630	9	50.0	21	9	US-09-999-833A-584	Sequence 584, App
C 558	9	50.0	16	9	US-09-880-113A-231	Sequence 231, App	C 631	9	50.0	21	9	US-09-978-757A-584	Sequence 584, App
C 559	9	50.0	16	9	US-09-880-113A-237	Sequence 237, App	C 632	9	50.0	21	9	US-09-978-187B-584	Sequence 584, App
C 560	9	50.0	16	9	US-09-880-113A-249	Sequence 249, App	C 633	9	50.0	21	10	US-09-765-001-151	Sequence 151, App
C 561	9	50.0	16	9	US-09-880-113A-273	Sequence 273, App	C 634	9	50.0	21	10	US-09-923-246-16	Sequence 16, Appl
C 562	9	50.0	17	9	US-09-825-805-317	Sequence 317, App	C 635	9	50.0	21	10	US-09-889-238-89	Sequence 89, Appl
C 563	9	50.0	17	9	US-09-825-805-360	Sequence 360, App	C 636	9	50.0	22	10	US-09-880-253A-37	Sequence 37, Appl
C 564	9	50.0	17	9	US-09-818-875-2886	Sequence 2886, Ap	C 637	9	50.0	22	10	US-09-862-027-67	Sequence 67, Appl
C 565	9	50.0	17	9	US-09-818-875-2887	Sequence 2887, Ap	C 638	9	50.0	23	9	US-10-101-461-11	Sequence 11, Appl
C 566	9	50.0	17	10	US-09-766-435-9	Sequence 9, Appl	C 639	9	50.0	23	9	US-10-138-316-53	Sequence 53, Appl
C 567	9	50.0	17	10	US-09-866-108-653	Sequence 653, App	C 640	9	50.0	23	9	US-10-247-287-6	Sequence 6, Appl
C 568	9	50.0	17	10	US-09-866-108-2449	Sequence 2449, Ap	C 641	9	50.0	23	10	US-09-416-3844A-23	Sequence 23, Appl
C 569	9	50.0	17	10	US-09-866-108-9969	Sequence 9969, Ap	C 642	9	50.0	24	9	US-09-978-299A-486	Sequence 486, App
C 570	9	50.0	18	9	US-09-910-483-64	Sequence 47, Appl	C 643	9	50.0	24	9	US-09-978-697-486	Sequence 486, App
C 571	9	50.0	18	9	US-10-096-986-67	Sequence 67, Appl	C 644	9	50.0	24	9	US-10-112-797-2	Sequence 2, Appl
C 572	9	50.0	18	10	US-09-766-113-10	Sequence 10, Appl	C 645	9	50.0	24	9	US-09-978-193A-486	Sequence 486, App
C 573	9	50.0	18	10	US-09-766-113-12	Sequence 12, Appl	C 646	9	50.0	24	9	US-09-978-813A-486	Sequence 486, App
C 574	9	50.0	19	9	US-10-117-983-5	Sequence 5, Appl	C 647	9	50.0	24	9	US-09-999-833A-486	Sequence 486, App
C 575	9	50.0	19	9	US-09-880-113A-253	Sequence 253, App	C 648	9	50.0	24	9	US-09-978-189-486	Sequence 486, App
C 576	9	50.0	19	10	US-09-920-552-90	Sequence 90, Appl	C 649	9	50.0	24	9	US-09-852-416-8	Sequence 8, Appl
C 577	9	50.0	19	10	US-09-832-648-24	Sequence 24, Appl	C 650	9	50.0	24	9	US-09-978-608A-486	Sequence 486, App
C 578	9	50.0	20	9	US-10-060-301-35	Sequence 35, Appl	C 651	9	50.0	24	9	US-09-978-403A-486	Sequence 486, App
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C 584	9	50.0	20	9	US-09-880-113A-243	Sequence 243, App	C 657	9	50.0	24	9	US-09-981-918A-486	Sequence 486, App
C 585	9	50.0	20	9	US-09-880-113A-261	Sequence 261, App	C 658	9	50.0	24	9	US-09-999-833A-486	Sequence 486, App
C 586	9	50.0	20	9	US-09-948-002-55	Sequence 55, Appl	C 659	9	50.0	24	9	US-10-167-748-486	Sequence 486, App
C 587	9	50.0	20	9	US-09-948-002-69	Sequence 69, Appl	C 660	9	50.0	24	9	US-09-918-588A-486	Sequence 486, App
C 588	9	50.0	20	9	US-10-222-334-13	Sequence 13, Appl	C 661	9	50.0	24	9	US-09-978-423A-486	Sequence 486, App
C 589	9	50.0	20	9	US-10-118-100-29	Sequence 29, Appl	C 662	9	50.0	24	9	US-10-013-921A-486	Sequence 486, App
C 590	9	50.0	20	9	US-10-304-136-6	Sequence 6, Appl	C 663	9	50.0	24	9	US-09-978-193A-486	Sequence 486, App
C 591	9	50.0	20	9	US-10-300-616-8	Sequence 8, Appl	C 664	9	50.0	24	9	US-10-013-929A-486	Sequence 486, App
C 592	9	50.0	20	9	US-09-898-556A-15	Sequence 15, Appl	C 665	9	50.0	24	9	US-10-016-177A-486	Sequence 486, App
C 593	9	50.0	20	9	US-09-915-814-65	Sequence 65, Appl	C 666	9	50.0	24	9	US-09-999-833A-486	Sequence 486, App
C 594	9	50.0	20	10	US-09-734-846-46	Sequence 46, Appl	C 667	9	50.0	24	9	US-09-952-522B-10	Sequence 10, Appl
C 595	9	50.0	20	10	US-09-752-983-124	Sequence 124, Appl	C 668	9	50.0	24	9	US-09-978-757A-486	Sequence 486, App
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C 597	9	50.0	20	10	US-09-734-847A-48	Sequence 48, Appl	C 670	9	50.0	24	9	US-09-940-185-263	Sequence 263, App
C 598	9	50.0	20	10	US-09-734-847A-61	Sequence 61, Appl	C 671	9	50.0	24	9	US-09-978-187B-486	Sequence 486, App
C 599	9	50.0	20	10	US-09-734-847A-62	Sequence 62, Appl	C 672	9	50.0	24	10	US-09-784-443-105	Sequence 105, Appl
C 600	9	50.0	20	10	US-09-734-847A-63	Sequence 63, Appl	C 673	9	50.0	24	10	US-09-949-145-24	Sequence 24, Appl
C 601	9	50.0	20	10	US-09-734-847A-64	Sequence 64, Appl	C 674	9	50.0	25	7	US-09-859-854-8	Sequence 8, Appl
C 602	9	50.0	20	10	US-09-734-847A-65	Sequence 65, Appl	C 675	9	50.0	25	10	US-08-722-570-16	Sequence 16, Appl
C 603	9	50.0	20	10	US-09-855-722-26	Sequence 26, Appl	C 676	9	50.0	25	9	US-10-040-497-11	Sequence 11, Appl

677	9	50.0	25	9	US-10-151-668-4	Sequence 4, Appl1	750	8.8	48.9	17	9	US-09-930-423-383	Sequence 383, App
678	9	50.0	25	9	US-09-750-410-25	Sequence 25, Appl1	751	8.8	48.9	17	9	US-09-930-423-385	Sequence 385, App
679	9	50.0	25	9	US-10-215-112-2619	Sequence 2619, Ap	752	8.8	48.9	17	9	US-09-930-423-1350	Sequence 1350, Ap
680	9	50.0	25	9	US-10-215-112-5553	Sequence 5553, Ap	753	8.8	48.9	17	9	US-09-930-423-1458	Sequence 1458, Ap
681	9	50.0	25	9	US-10-215-112-6419	Sequence 6419, Ap	754	8.8	48.9	17	9	US-09-930-423-1459	Sequence 1459, Ap
682	9	50.0	25	9	US-10-215-112-7210	Sequence 7210, Ap	755	8.8	48.9	17	9	US-09-930-423-1478	Sequence 1478, Ap
683	9	50.0	25	9	US-10-215-112-7332	Sequence 7332, Ap	756	8.8	48.9	17	10	US-09-832-382-4	Sequence 4, Appl1
684	9	50.0	25	9	US-10-215-112-8793	Sequence 8793, Ap	757	8.8	48.9	17	10	US-09-866-108-647	Sequence 647, App
685	9	50.0	25	9	US-10-215-112-8919	Sequence 8919, Ap	758	8.8	48.9	17	10	US-09-866-108-648	Sequence 648, App
686	9	50.0	25	9	US-10-215-112-9159	Sequence 9159, Ap	759	8.8	48.9	17	10	US-09-866-108-658	Sequence 2585, Ap
688	9	50.0	25	9	US-10-215-112-9905	Sequence 9905, Ap	760	8.8	48.9	17	10	US-09-866-108-6393	Sequence 6393, Ap
689	9	50.0	25	9	US-10-215-112-10017	Sequence 10017, A	761	8.8	48.9	17	10	US-09-866-108-6394	Sequence 6394, Ap
690	9	50.0	25	9	US-10-215-112-11145	Sequence 11145, A	762	8.8	48.9	17	10	US-09-866-108-10346	Sequence 10346, Ap
691	9	50.0	25	9	US-09-940-185-4092	Sequence 4092, Ap	763	8.8	48.9	17	10	US-09-866-108-10347	Sequence 10347, A
692	9	50.0	25	9	US-09-940-185-4244	Sequence 4244, Ap	764	8.8	48.9	17	10	US-09-866-108-10339	Sequence 10349, A
693	9	50.0	25	9	US-10-161-025-2	Sequence 2, Appl1	765	8.8	48.9	17	10	US-09-866-108-10350	Sequence 10350, A
694	9	50.0	25	10	US-09-866-108-3590	Sequence 3590, Ap	766	8.8	48.9	17	10	US-09-866-108-10351	Sequence 10351, A
695	9	50.0	25	10	US-09-866-108-5378	Sequence 5378, Ap	767	8.8	48.9	17	10	US-09-866-108-10351	Sequence 47, Appl
696	9	50.0	25	10	US-09-866-108-5379	Sequence 5379, Ap	768	8.8	48.9	17	10	US-09-866-108-10351	Sequence 201, App
697	9	50.0	25	10	US-09-866-108-5380	Sequence 5380, Ap	769	8.8	48.9	17	10	US-09-866-108-10351	Sequence 201, App
698	9	50.0	25	10	US-09-866-108-5381	Sequence 5381, Ap	770	8.8	48.9	18	9	US-09-978-295A-201	Sequence 201, App
699	9	50.0	25	10	US-09-866-108-5382	Sequence 5382, Ap	771	8.8	48.9	18	9	US-09-978-697-201	Sequence 201, App
700	9	50.0	25	10	US-09-866-108-5383	Sequence 5383, Ap	772	8.8	48.9	18	9	US-09-978-192A-201	Sequence 201, App
701	9	50.0	25	10	US-09-866-108-5384	Sequence 5384, Ap	773	8.8	48.9	18	9	US-09-999-832A-201	Sequence 201, App
702	9	50.0	25	10	US-09-866-108-5385	Sequence 5385, Ap	774	8.8	48.9	18	9	US-09-978-189-201	Sequence 201, App
703	9	50.0	25	10	US-09-866-108-5386	Sequence 5386, Ap	775	8.8	48.9	18	9	US-09-904-968A-74	Sequence 74, Appl
704	9	50.0	25	10	US-09-866-108-14861	Sequence 14861, A	776	8.8	48.9	18	9	US-09-978-608A-201	Sequence 201, App
705	9	50.0	25	10	US-09-866-108-14862	Sequence 14862, A	777	8.8	48.9	18	9	US-09-978-191A-201	Sequence 201, App
706	9	50.0	25	10	US-09-866-108-14863	Sequence 14863, A	778	8.8	48.9	18	9	US-09-978-403A-201	Sequence 201, App
707	9	50.0	25	10	US-09-866-108-14864	Sequence 14864, A	779	8.8	48.9	18	9	US-09-978-403A-201	Sequence 201, App
708	9	50.0	25	10	US-09-866-108-14865	Sequence 14865, A	780	8.8	48.9	18	9	US-09-978-554A-201	Sequence 201, App
709	9	50.0	25	10	US-09-866-108-14866	Sequence 14866, A	781	8.8	48.9	18	9	US-09-978-554A-201	Sequence 201, App
710	9	50.0	25	10	US-09-866-108-14867	Sequence 14867, A	782	8.8	48.9	18	9	US-10-017-001A-201	Sequence 201, App
711	9	50.0	25	10	US-09-866-108-14868	Sequence 14868, A	783	8.8	48.9	18	9	US-09-948-427-66	Sequence 66, Appl
712	9	50.0	25	10	US-09-866-108-14869	Sequence 14869, A	784	8.8	48.9	18	9	US-09-978-824-201	Sequence 201, App
713	8.8	48.9	15	9	US-09-880-313A-271	Sequence 271, App	785	8.8	48.9	18	9	US-09-981-915A-201	Sequence 201, App
714	8.8	48.9	15	9	US-09-979-593-65	Sequence 65, Appl	786	8.8	48.9	18	9	US-09-999-833A-201	Sequence 201, App
715	8.8	48.9	15	10	US-10-223-074-51	Sequence 51, Appl	787	8.8	48.9	18	9	US-10-167-749-201	Sequence 201, App
716	8.8	48.9	15	10	US-09-504-231A-651	Sequence 651, App	788	8.8	48.9	18	9	US-09-918-585A-201	Sequence 201, App
717	8.8	48.9	15	10	US-09-274-553D-651	Sequence 651, App	789	8.8	48.9	18	9	US-09-978-433A-201	Sequence 201, App
718	8.8	48.9	16	9	US-09-853-526-140	Sequence 140, App	790	8.8	48.9	18	9	US-10-013-921A-201	Sequence 201, App
719	8.8	48.9	16	9	US-10-287-919-1306	Sequence 1306, Ap	791	8.8	48.9	18	9	US-09-978-193A-201	Sequence 201, App
720	8.8	48.9	16	9	US-10-287-919-1307	Sequence 1307, Ap	792	8.8	48.9	18	9	US-10-013-929A-201	Sequence 201, App
721	8.8	48.9	16	9	US-10-287-919-1314	Sequence 1314, Ap	793	8.8	48.9	18	9	US-10-016-117A-201	Sequence 201, App
722	8.8	48.9	17	10	US-09-901-484A-140	Sequence 140, App	794	8.8	48.9	18	9	US-09-999-830A-201	Sequence 201, App
723	8.8	48.9	17	9	US-09-864-785-666	Sequence 666, App	795	8.8	48.9	18	9	US-09-978-757A-201	Sequence 201, App
724	8.8	48.9	17	9	US-09-825-803-431	Sequence 431, App	796	8.8	48.9	18	10	US-09-832-382-2	Sequence 2, Appl1
725	8.8	48.9	17	9	US-09-825-803-566	Sequence 566, App	797	8.8	48.9	18	10	US-09-832-382-2	Sequence 2, Appl1
726	8.8	48.9	17	9	US-09-825-803-569	Sequence 569, App	798	8.8	48.9	18	10	US-09-832-382-2	Sequence 2, Appl1
727	8.8	48.9	17	9	US-09-825-803-739	Sequence 739, App	799	8.8	48.9	18	10	US-09-832-382-2	Sequence 2, Appl1
728	8.8	48.9	17	9	US-10-060-830-80	Sequence 80, Appl	800	8.8	48.9	19	9	US-09-853-526-178	Sequence 178, App
729	8.8	48.9	17	9	US-10-060-830-81	Sequence 81, Appl	801	8.8	48.9	19	9	US-09-974-974-13	Sequence 13, Appl
730	8.8	48.9	17	9	US-10-060-830-82	Sequence 82, Appl	802	8.8	48.9	19	10	US-09-880-313A-61	Sequence 61, Appl
731	8.8	48.9	17	9	US-10-060-830-83	Sequence 83, Appl	803	8.8	48.9	19	10	US-09-947-258-3	Sequence 3, Appl1
732	8.8	48.9	17	9	US-10-060-830-84	Sequence 84, Appl	804	8.8	48.9	19	10	US-09-925-458-56	Sequence 56, Appl
733	8.8	48.9	17	9	US-10-060-830-85	Sequence 85, Appl	805	8.8	48.9	19	10	US-09-901-484A-178	Sequence 178, App
734	8.8	48.9	17	9	US-09-818-875-1535	Sequence 1535, Ap	806	8.8	48.9	20	9	US-09-263-959-1172	Sequence 1172, Ap
735	8.8	48.9	17	9	US-09-818-875-1536	Sequence 1536, Ap	807	8.8	48.9	20	9	US-09-905-291A-327	Sequence 327, App
736	8.8	48.9	17	9	US-09-877-478-477	Sequence 477, App	808	8.8	48.9	20	9	US-09-961-700A-13	Sequence 13, Appl
737	8.8	48.9	17	9	US-09-877-478-1203	Sequence 1203, Ap	809	8.8	48.9	20	9	US-09-902-853-127	Sequence 327, App
738	8.8	48.9	17	9	US-09-877-478-1204	Sequence 1204, Ap	810	8.8	48.9	20	9	US-09-907-824-327	Sequence 327, App
739	8.8	48.9	17	9	US-09-877-478-1771	Sequence 1771, Ap	811	8.8	48.9	20	9	US-09-907-824-327	Sequence 327, App
740	8.8	48.9	17	9	US-09-848-754A-2062	Sequence 2062, Ap	812	8.8	48.9	20	9	US-09-904-809-133	Sequence 327, App
741	8.8	48.9	17	9	US-09-848-754A-1216	Sequence 1216, Ap	813	8.8	48.9	20	9	US-09-904-809-133	Sequence 327, App
742	8.8	48.9	17	9	US-09-848-754A-1217	Sequence 1217, Ap	814	8.8	48.9	20	9	US-09-961-077-1260	Sequence 327, App
743	8.8	48.9	17	9	US-09-848-754A-3313	Sequence 3313, Ap	815	8.8	48.9	20	9	US-09-966-742-127	Sequence 1260, Ap
744	8.8	48.9	17	9	US-09-848-754A-3314	Sequence 3314, Ap	816	8.8	48.9	20	9	US-10-219-248-26	Sequence 327, App
745	8.8	48.9	17	9	US-09-930-423-8	Sequence 8, Appl1	817	8.8	48.9	20	9	US-09-906-638-1327	Sequence 327, App
746	8.8	48.9	17	9	US-09-930-423-302	Sequence 302, App	818	8.8	48.9	20	9	US-09-907-613-327	Sequence 327, App
747	8.8	48.9	17	9	US-09-930-423-303	Sequence 303, App	819	8.8	48.9	20	9	US-09-907-942-327	Sequence 327, App
748	8.8	48.9	17	9	US-09-930-423-356	Sequence 356, App	820	8.8	48.9	20	9	US-10-219-247-26	Sequence 26, Appl
749	8.8	48.9	17	9	US-09-930-423-357	Sequence 357, App	821	8.8	48.9	20	9	US-09-904-820-327	Sequence 327, App
					US-09-930-423-383	Sequence 383, App	822	8.8	48.9	20	9	US-09-909-204-327	Sequence 327, App

C 823	8.8	48.9	20	9	US-09-904-786-327	Sequence 327, App	C 886	8.8	48.9	21	10	US-09-765-081-58	Sequence 58, Appl
C 824	8.8	48.9	20	9	US-09-906-646-327	Sequence 327, App	C 897	8.8	48.9	21	10	US-09-798-058-13	Sequence 13, Appl
C 825	8.8	48.9	20	9	US-09-906-700-327	Sequence 327, App	C 898	8.8	48.9	21	10	US-09-850-115-14	Sequence 14, Appl
C 826	8.8	48.9	20	9	US-10-056-917-6	Sequence 6, Appl	C 899	8.8	48.9	21	10	US-09-880-732-10	Sequence 10, Appl
C 827	8.8	48.9	20	9	US-09-902-903-327	Sequence 327, App	C 900	8.8	48.9	21	10	US-09-880-732-12	Sequence 12, Appl
C 828	8.8	48.9	20	9	US-09-903-749A-327	Sequence 327, App	C 901	8.8	48.9	21	10	US-09-995-442-19	Sequence 19, Appl
C 829	8.8	48.9	20	9	US-09-903-786-327	Sequence 327, App	C 902	8.8	48.9	21	10	US-09-995-442-19	Sequence 19, Appl
C 830	8.8	48.9	20	9	US-09-902-736-327	Sequence 327, App	C 903	8.8	48.9	22	9	US-10-052-092-43	Sequence 43, Appl
C 831	8.8	48.9	20	9	US-09-904-119-327	Sequence 327, App	C 904	8.8	48.9	22	9	US-10-226-579-7	Sequence 7, Appl
C 832	8.8	48.9	20	9	US-09-904-956-327	Sequence 327, App	C 905	8.8	48.9	22	9	US-10-263-330-15	Sequence 15, Appl
C 833	8.8	48.9	20	9	US-09-907-794-327	Sequence 327, App	C 906	8.8	48.9	22	10	US-09-754-949-10	Sequence 10, Appl
C 834	8.8	48.9	20	9	US-09-902-692-327	Sequence 327, App	C 907	8.8	48.9	22	10	US-09-837-669A-30	Sequence 30, Appl
C 835	8.8	48.9	20	9	US-09-903-520-327	Sequence 327, App	C 908	8.8	48.9	22	10	US-09-837-669A-30	Sequence 30, Appl
C 836	8.8	48.9	20	9	US-09-903-943-327	Sequence 327, App	C 909	8.8	48.9	22	10	US-09-918-889-20	Sequence 20, Appl
C 837	8.8	48.9	20	9	US-09-904-462-327	Sequence 327, App	C 910	8.8	48.9	22	10	US-09-919-042-20	Sequence 20, Appl
C 838	8.8	48.9	20	9	US-09-905-056-327	Sequence 327, App	C 911	8.8	48.9	22	10	US-09-915-693-12	Sequence 12, Appl
C 839	8.8	48.9	20	9	US-09-907-925-327	Sequence 327, App	C 912	8.8	48.9	22	10	US-09-841-321A-30	Sequence 30, Appl
C 840	8.8	48.9	20	9	US-09-865-993-21	Sequence 21, Appl	C 913	8.8	48.9	22	10	US-09-841-321A-30	Sequence 30, Appl
C 841	8.8	48.9	20	9	US-09-865-993-86	Sequence 86, Appl	C 914	8.8	48.9	22	10	US-10-027-348-3	Sequence 3, Appl
C 842	8.8	48.9	20	9	US-09-904-553-327	Sequence 327, App	C 915	8.8	48.9	22	12	US-10-027-348-3	Sequence 3, Appl
C 843	8.8	48.9	20	9	US-09-905-381-327	Sequence 327, App	C 916	8.8	48.9	22	12	US-10-026-341A-2	Sequence 2, Appl
C 844	8.8	48.9	20	9	US-09-909-064-327	Sequence 327, App	C 917	8.8	48.9	22	12	US-10-076-900-13	Sequence 13, Appl
C 845	8.8	48.9	20	9	US-09-905-088-327	Sequence 327, App	C 918	8.8	48.9	22	12	US-10-075-425-21	Sequence 21, Appl
C 846	8.8	48.9	20	9	US-09-907-575-327	Sequence 327, App	C 919	8.8	48.9	23	9	US-10-087-451-4	Sequence 4, Appl
C 847	8.8	48.9	20	9	US-09-902-759-327	Sequence 327, App	C 920	8.8	48.9	23	9	US-09-969-763-49	Sequence 49, Appl
C 848	8.8	48.9	20	9	US-09-905-075-327	Sequence 327, App	C 921	8.8	48.9	23	9	US-09-969-763-50	Sequence 50, Appl
C 849	8.8	48.9	20	9	US-09-906-158-132	Sequence 132, App	C 922	8.8	48.9	23	9	US-10-002-974-81	Sequence 81, Appl
C 850	8.8	48.9	20	9	US-10-300-834-9	Sequence 9, Appl	C 923	8.8	48.9	23	9	US-10-082-358-10	Sequence 10, Appl
C 851	8.8	48.9	20	9	US-09-902-634-327	Sequence 327, App	C 924	8.8	48.9	23	9	US-10-085-906-527	Sequence 527, App
C 852	8.8	48.9	20	9	US-09-902-713-327	Sequence 327, App	C 925	8.8	48.9	23	9	US-10-085-906-527	Sequence 527, App
C 853	8.8	48.9	20	9	US-09-907-979-327	Sequence 327, App	C 926	8.8	48.9	23	9	US-10-105-200A-11	Sequence 11, Appl
C 854	8.8	48.9	20	9	US-09-920-677-15	Sequence 15, Appl	C 927	8.8	48.9	23	9	US-10-105-504A-11	Sequence 11, Appl
C 855	8.8	48.9	20	9	US-10-329-735-22	Sequence 22, Appl	C 928	8.8	48.9	23	9	US-10-105-504A-11	Sequence 11, Appl
C 856	8.8	48.9	20	9	US-09-953-611-27	Sequence 27, Appl	C 929	8.8	48.9	23	9	US-09-911-904-106	Sequence 106, App
C 857	8.8	48.9	20	9	US-09-902-615-327	Sequence 327, App	C 930	8.8	48.9	23	10	US-09-871-615-3	Sequence 3, Appl
C 858	8.8	48.9	20	9	US-09-925-139-11	Sequence 11, Appl	C 931	8.8	48.9	23	12	US-10-095-492-34	Sequence 34, Appl
C 859	8.8	48.9	20	9	US-09-852-910-271	Sequence 271, App	C 932	8.8	48.9	24	9	US-09-905-291A-242	Sequence 242, App
C 860	8.8	48.9	20	9	US-09-903-925-327	Sequence 327, App	C 933	8.8	48.9	24	9	US-10-010-050A-17	Sequence 17, Appl
C 861	8.8	48.9	20	9	US-09-906-760A-327	Sequence 327, App	C 934	8.8	48.9	24	9	US-09-902-853-242	Sequence 242, App
C 862	8.8	48.9	20	9	US-10-016-149-54	Sequence 54, Appl	C 935	8.8	48.9	24	9	US-09-907-824-242	Sequence 242, App
C 863	8.8	48.9	20	10	US-09-858-036-3	Sequence 3, Appl	C 936	8.8	48.9	24	9	US-09-907-824-242	Sequence 242, App
C 864	8.8	48.9	20	10	US-09-733-294A-70	Sequence 70, Appl	C 937	8.8	48.9	24	9	US-09-904-011-242	Sequence 242, App
C 865	8.8	48.9	20	10	US-09-733-294A-71	Sequence 71, Appl	C 938	8.8	48.9	24	9	US-10-040-566-22	Sequence 22, Appl
C 866	8.8	48.9	20	10	US-09-853-386-81	Sequence 81, Appl	C 939	8.8	48.9	24	9	US-09-906-742-242	Sequence 242, App
C 867	8.8	48.9	20	10	US-09-734-847A-61	Sequence 61, Appl	C 940	8.8	48.9	24	9	US-09-906-838-242	Sequence 242, App
C 868	8.8	48.9	20	10	US-09-855-722-26	Sequence 26, Appl	C 941	8.8	48.9	24	9	US-09-907-613-242	Sequence 242, App
C 869	8.8	48.9	20	10	US-09-854-683-298	Sequence 298, App	C 942	8.8	48.9	24	9	US-09-907-613-242	Sequence 242, App
C 870	8.8	48.9	20	10	US-09-948-619-3	Sequence 3, Appl	C 943	8.8	48.9	24	9	US-09-904-820-242	Sequence 242, App
C 871	8.8	48.9	20	10	US-09-800-631-44	Sequence 44, Appl	C 944	8.8	48.9	24	9	US-09-904-859-242	Sequence 242, App
C 872	8.8	48.9	20	10	US-09-752-639-14	Sequence 14, Appl	C 945	8.8	48.9	24	9	US-09-909-204-242	Sequence 242, App
C 873	8.8	48.9	20	10	US-09-752-639-27	Sequence 27, Appl	C 946	8.8	48.9	24	9	US-09-852-416-7	Sequence 7, Appl
C 874	8.8	48.9	20	10	US-09-984-198-14	Sequence 14, Appl	C 947	8.8	48.9	24	9	US-09-904-762-242	Sequence 242, App
C 875	8.8	48.9	20	10	US-09-984-198-27	Sequence 27, Appl	C 948	8.8	48.9	24	9	US-09-906-646-242	Sequence 242, App
C 876	8.8	48.9	20	10	US-09-880-732-13	Sequence 13, Appl	C 949	8.8	48.9	24	9	US-09-906-700-242	Sequence 242, App
C 877	8.8	48.9	20	10	US-09-909-330-327	Sequence 327, App	C 950	8.8	48.9	24	9	US-09-258-133-282	Sequence 29, Appl
C 878	8.8	48.9	20	10	US-09-909-088B-327	Sequence 327, App	C 951	8.8	48.9	24	9	US-09-847-102A-21	Sequence 21, Appl
C 879	8.8	48.9	21	8	US-08-765-244-21	Sequence 21, Appl	C 952	8.8	48.9	24	9	US-09-902-903-242	Sequence 242, App
C 880	8.8	48.9	21	9	US-09-991-470-15	Sequence 15, Appl	C 953	8.8	48.9	24	9	US-09-903-792A-242	Sequence 242, App
C 881	8.8	48.9	21	9	US-09-877-705A-81	Sequence 81, Appl	C 954	8.8	48.9	24	9	US-09-903-786A-46	Sequence 46, Appl
C 882	8.8	48.9	21	9	US-09-877-705A-82	Sequence 82, Appl	C 955	8.8	48.9	24	9	US-10-028-366A-46	Sequence 46, Appl
C 883	8.8	48.9	21	9	US-09-877-738A-81	Sequence 81, Appl	C 956	8.8	48.9	24	9	US-09-902-726-242	Sequence 242, App
C 884	8.8	48.9	21	9	US-09-877-738A-82	Sequence 82, Appl	C 957	8.8	48.9	24	9	US-09-904-119-242	Sequence 242, App
C 885	8.8	48.9	21	9	US-09-888-326-115	Sequence 115, App	C 958	8.8	48.9	24	9	US-09-904-956-242	Sequence 242, App
C 886	8.8	48.9	21	9	US-09-888-326-115	Sequence 115, App	C 959	8.8	48.9	24	9	US-09-907-724-242	Sequence 242, App
C 887	8.8	48.9	21	9	US-09-932-300-42	Sequence 42, App	C 960	8.8	48.9	24	9	US-09-902-652-242	Sequence 242, App
C 888	8.8	48.9	21	9	US-09-880-313A-257	Sequence 257, App	C 961	8.8	48.9	24	9	US-09-903-550-242	Sequence 242, App
C 889	8.8	48.9	21	9	US-10-112-653-796	Sequence 796, App	C 962	8.8	48.9	24	9	US-09-903-943-242	Sequence 242, App
C 890	8.8	48.9	21	9	US-10-112-653-797	Sequence 797, App	C 963	8.8	48.9	24	9	US-09-904-462-242	Sequence 242, App
C 891	8.8	48.9	21	9	US-10-017-995-825	Sequence 825, App	C 964	8.8	48.9	24	9	US-09-905-056-442	Sequence 242, App
C 892	8.8	48.9	21	9	US-10-017-995-826	Sequence 826, App	C 965	8.8	48.9	24	9	US-09-907-925-442	Sequence 242, App
C 893	8.8	48.9	21	9	US-10-090-011-7	Sequence 7, Appl	C 966	8.8	48.9	24	9	US-09-904-553-442	Sequence 242, App
C 894	8.8	48.9	21	9	US-09-776-479-825	Sequence 825, App	C 967	8.8	48.9	24	9	US-09-905-381-242	Sequence 242, App
C 895	8.8	48.9	21	9	US-09-776-479-826	Sequence 826, App	C 968	8.8	48.9	24	9	US-09-909-064-242	Sequence 242, App


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C 969 8.8 48.9 24 9 US-09-905-088-242 Sequence 242, App
C 970 8.8 48.9 24 9 US-09-907-575-242 Sequence 242, App
C 971 8.8 48.9 24 9 US-09-902-759-242 Sequence 242, App
C 972 8.8 48.9 24 9 US-09-905-075-242 Sequence 242, App
C 973 8.8 48.9 24 9 US-09-902-634-242 Sequence 242, App
C 974 8.8 48.9 24 9 US-09-902-713-242 Sequence 242, App
C 975 8.8 48.9 24 9 US-09-902-979-242 Sequence 242, App
C 976 8.8 48.9 24 9 US-09-902-615-242 Sequence 242, App
C 977 8.8 48.9 24 9 US-10-046-433-36 Sequence 36, Appl
C 978 8.8 48.9 24 9 US-09-903-923-242 Sequence 242, App
C 979 8.8 48.9 24 9 US-09-906-760A-242 Sequence 34, Appl
C 980 8.8 48.9 24 9 US-09-940-185-1504 Sequence 1504, Ap
C 981 8.8 48.9 24 9 US-09-940-185-1514 Sequence 1514, Ap
C 982 8.8 48.9 24 9 US-09-940-185-1585 Sequence 1585, Ap
C 983 8.8 48.9 24 9 US-09-940-185-1907 Sequence 1907, Ap
C 984 8.8 48.9 24 9 US-09-940-185-2408 Sequence 2408, Ap
C 985 8.8 48.9 24 9 US-09-940-185-2635 Sequence 2635, Ap
C 986 8.8 48.9 24 9 US-09-940-185-2835 Sequence 2835, Ap
C 987 8.8 48.9 24 9 US-09-940-185-2892 Sequence 2892, Ap
C 988 8.8 48.9 24 10 US-09-122-383-17 Sequence 17, Appl
C 989 8.8 48.9 24 10 US-09-785-632A-81 Sequence 81, Appl
C 990 8.8 48.9 24 10 US-09-859-854-7 Sequence 7, Appl
C 991 8.8 48.9 24 10 US-09-909-330-242 Sequence 242, App
C 992 8.8 48.9 24 10 US-09-859-382-6 Sequence 6, Appl
C 993 8.8 48.9 24 10 US-09-909-088B-242 Sequence 242, App
C 994 8.8 48.9 25 9 US-09-745-317-4 Sequence 4, Appl
C 995 8.8 48.9 25 9 US-09-879-461-36 Sequence 36, Appl
C 996 8.8 48.9 25 9 US-09-964-261-119 Sequence 119, Appl
C 997 8.8 48.9 25 9 US-10-228-070-11 Sequence 11, Appl
C 998 8.8 48.9 25 9 US-10-060-830-356 Sequence 356, App
C 999 8.8 48.9 25 9 US-10-060-830-357 Sequence 357, App
C1000 8.8 48.9 25 9 US-10-060-830-357 Sequence 357, App
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ALIGNMENTS

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RESULT 1
US-10-080-959A-5
; Sequence 5, Application US/10080959A
; Publication No. US20030054369A1
; GENERAL INFORMATION:
; APPLICANT: Cruz-Perez, Patricia
; TITLE OF INVENTION: Method for Detection of Stachybotrys chartarum in Pure Culture an
; FILE REFERENCE: 0001-00001
; CURRENT FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: US 60/280,712
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION:
US-10-080-959A-5
Query Match 100.0%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
US-09-911-176B-28/c
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QY 1 CTGCGCCCGATCCAGG 18
DB 1 CTGCGCCCGATCCAGG 18
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; Sequence 28, Application US/09911176B
; Patent No. US20020156243A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: ANTIBODIES THAT BIND AN
; FILE REFERENCE: 97-30D1
; CURRENT APPLICATION NUMBER: US/09/911,176B
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: 09/118,408
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: 60/053,154
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC15035
US-09-911-176B-28
Query Match 67.8%; Score 12.2; DB 9; Length 24;
Best Local Similarity 82.4%; Pred. No. 8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 CTGCGCCCGATCCAGG 17
DB 20 CCGAGCCCGATCCAGG 4
```

```
RESULT 3
US-10-180-762-28/c
; Sequence 28, Application US/10180762
; Publication No. US20030022838A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Laesser, Gerald W.
; TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND IMMUNE FUNCTION
; FILE REFERENCE: 99-12C3
; CURRENT APPLICATION NUMBER: US/10/180,762
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 09/253,604
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/444,794
; PRIOR FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: 09/506,855
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC15035
US-10-180-762-28
```

```
Query Match 67.8%; Score 12.2; DB 9; Length 24;
Best Local Similarity 82.4%; Pred. No. 8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 CTGCGCCCGATCCAGG 17
DB 20 CCGAGCCCGATCCAGG 4
```

```
RESULT 4
US-10-241-258-28/c
; Sequence 28, Application US/10241258
; Publication No. US20030078206A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Shepard, Paul O.
/ APPLICANT: Laeber, Gerald W.
/ APPLICANT: Bishop, Paul D.
/ TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND
/ TITLE OF INVENTION: IMMUNE FUNCTION
/ FILE REFERENCE: 99-12
/ CURRENT APPLICATION NUMBER: US/10/241,258
/ CURRENT FILING DATE: 2002-09-10
/ NUMBER OF SEQ ID NOS: 50
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 28
/ LENGTH: 24
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide ZC15035
US-10-241-258-28
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```
Query Match          67.8%; Score 12.2; DB 9; Length 24;
Best Local Similarity 82.4%; Pred. No. 8e+03; 3; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 CTGCGCCCGATCCAGG 17
         |||||
Db      20 CCGAGCCCGATCCATG  4
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```
RESULT 5
US-09-997-664-54/c
/ Sequence 54, Application US/09997664
/ Patent No. US20020151003A1
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```
/ GENERAL INFORMATION:
/ APPLICANT: Ben-Bassat, Arle
/ APPLICANT: Catermole, Monica
/ APPLICANT: Gatenby, Anthony A.
/ APPLICANT: Gibson, Katherine J.
/ APPLICANT: Ramos-Gonzalez, Isabel
/ APPLICANT: Ramos, Juan
/ APPLICANT: Sariassani, Sima
/ TITLE OF INVENTION: Method for the Production of p-Hydroxybenzoate in Species of
/ TITLE OF INVENTION: Pseudomonas and Agrobacterium
/ FILE REFERENCE: BC1018 US CIP
/ CURRENT APPLICATION NUMBER: US/09/997,664
/ CURRENT FILING DATE: 2001-11-28
/ PRIOR APPLICATION NUMBER: 09/585,174
/ PRIOR FILING DATE: 2000-06-01
/ NUMBER OF SEQ ID NOS: 112
/ SOFTWARE: Microsoft Office 97
/ SEQ ID NO 54
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: primer
/ OTHER INFORMATION: primer used for sequencing pcu
US-09-997-664-54
```

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Query Match          64.4%; Score 11.6; DB 10; Length 19;
Best Local Similarity 77.8%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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```
Qy      1 CTGCGCCCGATCCAGG 18
         |||||
Db      18 CAGCACCCGTATCAAGGC  1
```

```
RESULT 6
US-09-423-800-34/c
/ Sequence 34, Application US/09423800
/ Patent No. US20020165363A1
/ GENERAL INFORMATION:
/ APPLICANT: SATO, KOH
```

```
/ APPLICANT: TSUNENARI, TOSHIKI
/ APPLICANT: ISHII, KIMIE
/ TITLE OF INVENTION: CACHEXIA REMEDY
/ FILE REFERENCE: 04853-0036
/ CURRENT APPLICATION NUMBER: US/09/423,800
/ CURRENT FILING DATE: 1999-11-12
/ PRIOR APPLICATION NUMBER: PCT/JP98/02116
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: JP 125505/1997
/ PRIOR FILING DATE: 1997-05-15
/ PRIOR APPLICATION NUMBER: JP 194445/1997
/ PRIOR FILING DATE: 1997-07-18
/ NUMBER OF SEQ ID NOS: 87
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 34
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-423-800-34
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```
Query Match          63.3%; Score 11.4; DB 9; Length 19;
Best Local Similarity 92.3%; Pred. No. 2e+04; 1; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      5 GCCCGATCCAGG 17
         |||||
Db      13 GCCCGATCCAGG  1
```

```
RESULT 7
US-10-182-018-34/c
/ Sequence 34, Application US/10182018
/ Publication No. US20030049211A1
/ GENERAL INFORMATION:
/ APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
/ TITLE OF INVENTION: THERAPEUTIC AND PREVENTIVE AGENTS FOR DENTAL DISEASES
/ FILE REFERENCE: PH-1092-PCT
/ CURRENT APPLICATION NUMBER: US/10/182,018
/ CURRENT FILING DATE: 2002-07-24
/ PRIOR APPLICATION NUMBER: JP 2000-83034
/ PRIOR FILING DATE: 2000-01-25
/ NUMBER OF SEQ ID NOS: 75
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 34
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic DNA
US-10-182-018-34
```

```
Query Match          63.3%; Score 11.4; DB 9; Length 19;
Best Local Similarity 92.3%; Pred. No. 2e+04; 1; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      5 GCCCGATCCAGG 17
         |||||
Db      13 GCCCGATCCAGG  1
```

```
RESULT 8
US-10-085-906-496/c
/ Sequence 496, Application US/10085906
/ Publication No. US20030054371A1
/ GENERAL INFORMATION:
/ APPLICANT: YING, Vincent
/ APPLICANT: Wu, Paul
/ APPLICANT: Gray, Gary S.
/ TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
/ TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
/ FILE REFERENCE: GNN-5343CP2
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CURRENT APPLICATION NUMBER: US/10/085,906
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 60/126,215
PRIOR FILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: US 09/534,061
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: PCT/US00/07938
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 545
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 496
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-906-496

Query Match 63.3%; Score 11.4; DB 9; Length 21;
Best Local Similarity 92.3%; Pred. No. 2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGCGCCCGATC 13
Db 19 CTGCGCCCGATC 7

RESULT 9
US-09-990-385-20/c
Sequence 20, Application US/09990385
Publication No. US20020192771A1
GENERAL INFORMATION:
APPLICANT: Koji YANAI et al.
TITLE OF INVENTION: BETA-FRUCTOFURANOSIDASE AND ITS GENE, METHOD OF
ISOLATING BETA-FRUCTOFURANOSIDASE GENE, SYSTEM FOR PRODUCT
BETA-FRUCTOFURANOSIDASE, AND BETA-FRUCTOFURANOSIDASE VARI

NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSER: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/990,385
FILING DATE: 10-Sep-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/142,623
FILING DATE: September 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 2001-1611
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: Nucleic acid
STRANDEDNESS: No. US20020192771A1 relevant
MOLECULE TYPE: Synthetic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-990-385-20

Query Match 63.3%; Score 11.4; DB 9; Length 22;
Best Local Similarity 92.3%; Pred. No. 2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCCCGATCCAG 17
Db 16 GCCCGATCCAG 4

RESULT 10
US-09-961-077-531
Sequence 531, Application US/09961077
Publication No. US20030014775A1
GENERAL INFORMATION:
APPLICANT: Zwick, Michael G.
Edington, Brent E.
McSwiggen, James A.
Merlo, Patricia Ann Owens
Guo, Lining
Skokut, Thomas A.
Young, Scott A.
Folkerts, Otto
Merlo, Donald J.

TITLE OF INVENTION: COMPOSITION AND METHODS FOR
MODULATION OF GENE EXPRESSION
IN PLANTS
NUMBER OF SEQUENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/961,077
FILING DATE: 21-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/679,645
FILING DATE: July 12, 1996
APPLICATION NUMBER: 60/001,135
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 531:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 531:
US-09-961-077-531

Query Match 62.2%; Score 11.2; DB 9; Length 16;
Best Local Similarity 68.8%; Pred. No. 2.6e+04;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCGCCCGATCCAG 16
Db 1 CTGCGCCCGATCCAG 16

PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 651
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-651

Query Match 62.2%; Score 11.2; DB 10; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.6e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATCCAG 16
Db 17 CTGAGTCCGGGTCAG 2

RESULT 16
US-09-866-108-652/C
Sequence 652, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yizhong
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 652
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-652

Query Match 62.2%; Score 11.2; DB 10; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.6e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATCCAG 16
Db 16 CTGAGTCCGGGTCAG 1

RESULT 17
US-09-961-077-621
Sequence 621, Application US/09961077
Publication No. US20030014775A1
GENERAL INFORMATION:
APPLICANT: Zwick, Michael G.
Edington, Brent E.
McSwiggan, James A.
Merlo, Patricia Ann Owens
Guo, Lining
Skokut, Thomas A.
Young, Scott A.
Folkerts, Otto
Merlo, Donald J.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR
MODULATION OF GENE EXPRESSION
IN PLANTS
NUMBER OF SEQUENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/961,077
FILING DATE: 21-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

```

/ APPLICATION NUMBER: 08/679,645
/ FILING DATE: July 12, 1996
/ APPLICATION NUMBER: 60/001,135
/ FILING DATE: July 13, 1995
/ APPLICATION NUMBER: 08/300,726
/ FILING DATE: September 2, 1994
/ ATTORNEY/AGENT INFORMATION:
/   NAME: Warburg, Richard J.
/   REGISTRATION NUMBER: 32,327
/   REFERENCE/DOCKET NUMBER: 219/247
/ TELECOMMUNICATION INFORMATION:
/   TELEPHONE: (213) 489-1600
/   TELEFAX: (213) 955-0440
/
/ INFORMATION FOR SEQ ID NO: 621:
/   SEQUENCE CHARACTERISTICS:
/     LENGTH: 18 base pairs
/     TYPE: nucleic acid
/     STRANDEDNESS: single
/     TOPOLOGY: linear
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 621:
US-09-961-077-621

Query Match      62.2%; Score 11.2; DB 9; Length 18;
Best Local Similarity 68.8%; Pred. No. 2.5e+04;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Cy 1 CTCGCCCGGATCCAG 16
    |||||
Db 3 CUGCGGCCUACUCCAG 18

RESULT 18
US-09-734-188-37/c
/ Sequence 37, Application US/09734188
/ Patent No. US2002010645A1
/ GENERAL INFORMATION:
/   APPLICANT: Richardson Ph.D., Mary Ann
/   APPLICANT: Goldman, Assistant Counsel, Robin A.
/   APPLICANT: New York State Office of Mental Health
/   APPLICANT: Nathan S. Kline Institute for Psychiatric Research
/   TITLE OF INVENTION: PAH
/   FILE REFERENCE: Kline Insc.
/   CURRENT APPLICATION NUMBER: US/09/734,188
/   CURRENT FILING DATE: 2000-12-12
/   PRIOR APPLICATION NUMBER: 09/253,025
/   PRIOR FILING DATE: 2001-05-03
/   NUMBER OF SEQ ID NOS: 62
/   SOFTWARE: PatentIn Ver. 2.0
/   SEQ ID NO: 37
/   LENGTH: 21
/   TYPE: DNA
/   ORGANISM: Homo sapiens
/
US-09-734-188-37

Query Match      62.2%; Score 11.2; DB 10; Length 21;
Best Local Similarity 81.2%; Pred. No. 2.5e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 2 TGC GCCCGGATCCAG 17
    |||||
Db 17 TGGGCTCGGATCCAG 2

RESULT 19
US-10-118-100-2/c
/ Sequence 2, Application US/10118100
/ Publication No. US2003007613A1
/ GENERAL INFORMATION:
/   APPLICANT: Bioinvent International AB
/   APPLICANT: Soderblad, Ulf
/   APPLICANT: Borrebaeck, Carl
/   TITLE OF INVENTION: A Method For In Vitro Molecular
```

```

/ TITLE OF INVENTION: Evolution of Protein Function
/ FILE REFERENCE: Newburn 341711
/ CURRENT APPLICATION NUMBER: US/10/118,100
/ CURRENT FILING DATE: 2002-04-08
/ PRIOR APPLICATION NUMBER: US/09/341,711
/ PRIOR FILING DATE: 1999-09-21
/ PRIOR APPLICATION NUMBER: PCT/GB98/00219
/ PRIOR FILING DATE: 1998-01-26
/ PRIOR APPLICATION NUMBER: GB9701425.2
/ PRIOR FILING DATE: 1997-01-24
/ NUMBER OF SEQ ID NOS: 54
/ SOFTWARE: FastSeq for Windows Version 3.0
/   SEQ ID NO: 2
/   LENGTH: 22
/   TYPE: DNA
/   ORGANISM: Artificial Sequence
/   FEATURE:
/     OTHER INFORMATION: Primer
/
US-10-118-100-2

Query Match      62.2%; Score 11.2; DB 9; Length 22;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 2 TGC GCCCGGATCCAG 17
    |||||
Db 18 TCGGCCAGGCTCCAG 3

RESULT 20
US-09-813-289-3/c
/ Sequence 3, Application US/09813289
/ Patent No. US20020061571A1
/ GENERAL INFORMATION:
/   APPLICANT: Mahadevan, M.S.
/   APPLICANT: Tiscornia, G.
/   TITLE OF INVENTION: No. US20020061571A1 isoform of myotonic dysreophy associated pr
/   FILE REFERENCE: 800.027US1
/   CURRENT APPLICATION NUMBER: US/09/813,289
/   CURRENT FILING DATE: 2001-03-20
/   PRIOR APPLICATION NUMBER: US 60/190,590
/   PRIOR FILING DATE: 2000-03-20
/   NUMBER OF SEQ ID NOS: 22
/   SOFTWARE: FastSeq for Windows Version 4.0
/   SEQ ID NO: 3
/   LENGTH: 22
/   TYPE: DNA
/   ORGANISM: Homo sapiens
/
US-09-813-289-3

Query Match      62.2%; Score 11.2; DB 10; Length 22;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 1 CTCGCCCGGATCCAG 16
    |||||
Db 17 CTCGCCAGCTCCAG 2

RESULT 21
US-10-118-100-36/c
/ Sequence 36, Application US/10118100
/ Publication No. US2003007613A1
/ GENERAL INFORMATION:
/   APPLICANT: Bioinvent International AB
/   APPLICANT: Soderblad, Ulf
/   APPLICANT: Borrebaeck, Carl
/   TITLE OF INVENTION: A Method For In Vitro Molecular
/   FILE REFERENCE: Newburn 341711
/   CURRENT APPLICATION NUMBER: US/10/118,100
/   CURRENT FILING DATE: 2002-04-08
```

```

; PRIOR APPLICATION NUMBER: US/09/341,711
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: PCT/GB98/00219
; PRIOR FILING DATE: 1998-01-26
; PRIOR APPLICATION NUMBER: GB9701425.2
; PRIOR FILING DATE: 1997-01-24
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; US-10-118-100-36

Query Match      62.2%; Score 11.2; DB 9; Length 23;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TCGGCGCGGATCCAG 17
      1 ||||| |||||
      19 TCGCGCGGCTCCAG 4.

RESULT 22
US-10-199-550-17/c
; Sequence 17, Application US/10199550
; Publication No. US2003009615A1
; GENERAL INFORMATION:
; APPLICANT: TIKOO, Suresh K.
; TITLE OF INVENTION: PORCINE ADENOVIRUS E1 AND E4 REGIONS
; FILE REFERENCE: 29310203220
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 09/963,038
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Porcine Adenovirus Type 3
; US-10-199-550-17

Query Match      62.2%; Score 11.2; DB 9; Length 24;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CTGCGCGCGGATCCAG 16
      1 ||||| |||||
      16 CAGCGCGCGGATCCG 1

RESULT 23
US-09-866-108-3580/c
; Sequence 3580, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
```

```

; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3580
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-3580
```

```

Query Match      62.2%; Score 11.2; DB 10; Length 25;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CTGCGCGCGGATCCAG 16
      1 ||||| |||||
      25 CTGAGTCCGGGTCAG 10

RESULT 24
US-09-866-108-3581/c
; Sequence 3581, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
```

```
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 60/266,860
/ PRIOR FILING DATE: 2001-02-05
/ NUMBER OF SEQ ID NOS: 15752
/ SOFTWARE: Aecomica Sequence Listing Engine
/ SEQ ID NO: 3581
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-866-108-3581
```

```
Query Match      62.2%; Score 11.2; DB 10; Length 25;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 CTGCGCCCGGATCCAG 16
      ||| ||| ||| ||| |||
Db      24 CTGAGTCCGGGTCAG 9
```

```
RESULT 25
US-09-866-108-3582/c
/ Sequence 3582, Application US/09866108
/ Patent No. US20020048800A1
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharon G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AECOMICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
```

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/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 60/266,860
/ PRIOR FILING DATE: 2001-02-05
/ NUMBER OF SEQ ID NOS: 15752
/ SOFTWARE: Aecomica Sequence Listing Engine
/ SEQ ID NO: 3582
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-866-108-3582
```

```
Query Match      62.2%; Score 11.2; DB 10; Length 25;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 CTGCGCCCGGATCCAG 16
      ||| ||| ||| ||| |||
Db      23 CTGAGTCCGGGTCAG 8
```

```
RESULT 26
US-09-866-108-3583/c
/ Sequence 3583, Application US/09866108
/ Patent No. US20020048800A1
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharon G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AECOMICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 60/266,860
/ PRIOR FILING DATE: 2001-02-05
/ NUMBER OF SEQ ID NOS: 15752
/ SOFTWARE: Aecomica Sequence Listing Engine
/ SEQ ID NO: 3583
```


LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-3583

Query Match 62.2%; Score 11.2; DB 10; Length 25;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATCCAG 16
DB 22 CTGAGTCCGGGTCCAG 7

RESULT 27
US-09-866-108-3584/C
Sequence 3584, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOmica-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: AeoMica Sequence Listing Engine
SEQ ID NO 3584
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-3584

Query Match 62.2%; Score 11.2; DB 10; Length 25;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATCCAG 16

DB 21 CTGAGTCCGGGTCCAG 6

RESULT 28
US-09-866-108-3585/C
Sequence 3585, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOmica-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: AeoMica Sequence Listing Engine
SEQ ID NO 3585
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-3585

Query Match 62.2%; Score 11.2; DB 10; Length 25;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATCCAG 16
DB 20 CTGAGTCCGGGTCCAG 5

RESULT 29
US-09-866-108-3586/C
Sequence 3586, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong

APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO: 3586
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-3586

Query Match 62.2%; Score 11.2; DB 10; Length 25;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGGCGCCGGATCCAG 16
DB 19 CTGAGTCCGGATCCAG 4

RESULT 30
US-09-866-108-3587/c
Sequence 3587, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO: 3587
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-3587

Query Match 62.2%; Score 11.2; DB 10; Length 25;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGGCGCCGGATCCAG 16
DB 18 CTGAGTCCGGATCCAG 3

RESULT 31
US-09-866-108-3588/c
Sequence 3588, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667

;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
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;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
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;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 60/266,860
;; PRIOR FILING DATE: 2001-02-05
;; NUMBER OF SEQ ID NOS: 15752
;; SOFTWARE: Aecomica Sequence Listing Engine
;; SEQ ID NO: 3588
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-866-108-3588

Query Match 62.2%; Score 11.2; DB 10; Length 25;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCGCCCGGATCCAG 16
DB 17 CTGAGTCCGGGTCAG 2

RESULT 32
US-09-866-108-3589/c
;; Sequence 3589, Application US/09866108
;; Patent No. US20020048800A1
;; GENERAL INFORMATION:
;; APPLICANT: GU, Yizhong
;; APPLICANT: JI, Yonggang
;; APPLICANT: PENN, Sharon G.
;; APPLICANT: HANZEL, David K.
;; APPLICANT: RANK, David R.
;; APPLICANT: CHEN, Wensheng
;; APPLICANT: SHANNON, Mark
;; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;; FILE REFERENCE: AECOMICA-7
;; CURRENT APPLICATION NUMBER: US/09/866,108
;; CURRENT FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: GB 24263,6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
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;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 60/266,860
;; PRIOR FILING DATE: 2001-02-05
;; NUMBER OF SEQ ID NOS: 15752
;; SOFTWARE: Aecomica Sequence Listing Engine
;; SEQ ID NO: 3589
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-866-108-3589

Query Match 62.2%; Score 11.2; DB 10; Length 25;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCGCCCGGATCCAG 16
DB 16 CTGAGTCCGGGTCAG 1

RESULT 33
US-10-080-959a-5/c
;; Sequence 5, Application US/10080959A
;; Publication No. US20030054369A1
;; GENERAL INFORMATION:
;; APPLICANT: Cruz-Perez, Patricia
;; APPLICANT: Butner, Mark P.
;; TITLE OF INVENTION: Method for Detection of Stachybotrys chartarum in Pure Culture an
;; FILE REFERENCE: 0001-00001
;; CURRENT APPLICATION NUMBER: US/10/080,959A
;; CURRENT FILING DATE: 2002-05-16
;; PRIOR APPLICATION NUMBER: US 60/280,712
;; PRIOR FILING DATE: 2001-03-29
;; NUMBER OF SEQ ID NOS: 5
;; SEQ ID NO: 5
;; LENGTH: 18
;; TYPE: DNA
;; ORGANISM: Stachybotrys chartarum
;; FEATURE:
;; NAME/KEY:
;; LOCATION:
;; OTHER INFORMATION:
US-10-080-959a-5

Query Match 60.0%; Score 10.8; DB 9; Length 18;
Best Local Similarity 85.7%; Pred. No. 3.9e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCCCGATCCAGGC 18
DB 18 GCCTGATCCGGGC 5

RESULT 34
US-10-251-482-17
;; Sequence 17, Application US/10251482
;; Publication No. US20030099631A1
;; GENERAL INFORMATION:
;; APPLICANT: Koji, Yoshimura
;; APPLICANT: Yuichi, Hikichi
;; APPLICANT: Atsushi, Nishimura
;; TITLE OF INVENTION: NOVEL PROTEINS, THEIR PRODUCTION AND USE
;; FILE REFERENCE: 48712/342
;; CURRENT APPLICATION NUMBER: US/10/251,482
;; CURRENT FILING DATE: 2002-09-19

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; PRIOR APPLICATION NUMBER: US/09/171,545
; PRIOR FILING DATE: 1999-07-26
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: primer
US-10-251-482-17

Query Match      60.0%; Score 10.8; DB 9; Length 19;
Best Local Similarity 85.7%; Pred. No. 3.9e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 GCGCCGATCCAGC 18
DB      2 GCAGGATCCAGC 15

RESULT 35
US-10-057-550-82/c
; Sequence 82, Application US/10057550
; Publication No. US20030032607A1
; GENERAL INFORMATION:
; APPLICANT: Monla, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/057,550
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/506,073
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 09/143,214
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: PCT/US98/13961
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: US 08/888,982
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US 08/756,806
; PRIOR FILING DATE: 1996-11-26
; PRIOR APPLICATION NUMBER: PCT/US95/07111
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/250,856
; PRIOR FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-057-550-82

Query Match      60.0%; Score 10.8; DB 9; Length 20;
Best Local Similarity 85.7%; Pred. No. 3.8e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GCGCCGATCCAG 16
DB      14 GCGCCGATCCGG 1

RESULT 36
US-10-122-434-7
; Sequence 7, Application US/10122434
; Publication No. US20030078402A1
; GENERAL INFORMATION:
; APPLICANT: Leon G.J. FRENKEN
; APPLICANT: Cornelis P.E. VAN DER LOGT
; TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODY FRAGMENTS
; FILE REFERENCE: 60113/266062 - 13076(C)
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; CURRENT APPLICATION NUMBER: US/10/122,434
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 09/487,253
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: MS word
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PRIMER
US-10-122-434-7

Query Match      60.0%; Score 10.8; DB 9; Length 20;
Best Local Similarity 85.7%; Pred. No. 3.8e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 GCGCCGATCCAG 17
DB      7 CGCCAGCTCCAG 20

RESULT 37
US-09-733-151-8/c
; Sequence 8, Application US/09733151
; Patent No. US20010029620A1
; GENERAL INFORMATION:
; APPLICANT: De Boch, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/09/733,151
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: primer 254
US-09-733-151-8

Query Match      60.0%; Score 10.8; DB 10; Length 21;
Best Local Similarity 85.7%; Pred. No. 3.8e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 GCGCCGATCCAGC 18
DB      18 GCGCTGACCCAGC 5

RESULT 38
US-09-940-185-964/c
; Sequence 964, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
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/ SEQ ID NO 964
/ LENGTH: 24
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-964

Query Match
Best Local Similarity 60.0%; Score 10.8; DB 9; Length 24;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGCCGATCCAG 16
DB 21 GCGCTCGATCCAG 8

RESULT 39
US-10-076-157-21/c
/ Sequence 21, Application US/10076157
/ Publication No. US20030027309A1
/ GENERAL INFORMATION:
/ APPLICANT: Pompejus, Markus
/ APPLICANT: Suelberger, Harald
/ APPLICANT: Joefken, Hans Wolfgang
/ APPLICANT: Doval, Jose Luis Revuelta
/ APPLICANT: Jimenez, Alberto;
/ APPLICANT: Garcia, Maria Angeles Santos
/ TITLE OF INVENTION: Genes of purine biosynthesis from Ashbya Gossypii and the use the
/ TITLE OF INVENTION: in
/ FILE REFERENCE: 48684DIY
/ CURRENT APPLICATION NUMBER: US/10/076,157
/ CURRENT FILING DATE: 2002-02-15
/ PRIOR APPLICATION NUMBER: US 09/212,247
/ PRIOR FILING DATE: 1998-12-16
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: WordPerfect v. 6.1
/ SEQ ID NO 21
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: PCR primer
US-10-076-157-21

Query Match
Best Local Similarity 60.0%; Score 10.8; DB 9; Length 25;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCGCCGATCCAGC 18
DB 15 GCCAGATCCAGC 2

RESULT 40
US-09-864-785-1566
/ Sequence 1566, Application US/09864785
/ Patent No. US20020177568A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Draper, Ken
/ APPLICANT: McSwiggen, Jim
/ TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
/ FILE REFERENCE: 400/022 (MBH90-812-D)
/ CURRENT APPLICATION NUMBER: US/09/864,785
/ CURRENT FILING DATE: 2001-05-23
/ NUMBER OF SEQ ID NOS: 3929
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1566
/ LENGTH: 17
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/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-1566

Query Match
Best Local Similarity 58.9%; Score 10.6; DB 9; Length 17;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 TCGCCGATCCAGC 18
DB 1 UGCCCCAGGCTCCAGC 17
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Search completed: June 7, 2003, 11:39:16
Job time : 76.7273 secs

C 101	10.4	57.8	23	2	US-08-469-609A-36	Sequence 36, Appl
C 102	10.4	57.8	23	3	US-09-143-190-36	Sequence 36, Appl
C 103	10.4	57.8	23	3	US-09-143-190-36	Sequence 36, Appl
C 104	10.4	57.8	23	4	US-09-502-344-36	Sequence 36, Appl
C 105	10.4	57.8	23	4	US-08-178-606-12	Sequence 12, Appl
C 106	10.4	57.8	24	1	US-08-199-507B-56	Sequence 56, Appl
C 107	10.4	57.8	24	1	US-08-199-507B-56	Sequence 56, Appl
C 108	10.4	57.8	24	1	US-08-243-870-3	Sequence 3, Appl
C 109	10.4	57.8	24	1	US-08-243-870-3	Sequence 3, Appl
C 110	10.4	57.8	24	1	US-08-442-572-59	Sequence 59, Appl
C 111	10.4	57.8	24	1	US-08-442-572-59	Sequence 59, Appl
C 112	10.4	57.8	24	1	US-08-399-412A-3	Sequence 3, Appl
C 113	10.4	57.8	24	1	US-08-399-412A-3	Sequence 3, Appl
C 114	10.4	57.8	24	1	US-08-477-530-3	Sequence 3, Appl
C 115	10.4	57.8	24	1	US-08-477-530-3	Sequence 3, Appl
C 116	10.4	57.8	24	1	US-08-477-530-3	Sequence 3, Appl
C 117	10.4	57.8	24	1	US-08-477-530-3	Sequence 3, Appl
C 118	10.4	57.8	24	1	US-08-409-439A-3	Sequence 3, Appl
C 119	10.4	57.8	24	1	US-08-409-439A-3	Sequence 3, Appl
C 120	10.4	57.8	24	1	US-08-441-591-3	Sequence 3, Appl
C 121	10.4	57.8	24	1	US-08-384-708A-3	Sequence 3, Appl
C 122	10.4	57.8	24	1	US-08-384-708A-3	Sequence 3, Appl
C 123	10.4	57.8	24	1	US-08-384-708A-3	Sequence 3, Appl
C 124	10.4	57.8	24	1	US-08-303-362A-3	Sequence 3, Appl
C 125	10.4	57.8	24	1	US-08-303-362A-3	Sequence 3, Appl
C 126	10.4	57.8	24	1	US-08-477-830-3	Sequence 3, Appl
C 127	10.4	57.8	24	1	US-08-477-830-3	Sequence 3, Appl
C 128	10.4	57.8	24	1	US-08-441-828-56	Sequence 56, Appl
C 129	10.4	57.8	24	1	US-08-441-828-56	Sequence 56, Appl
C 130	10.4	57.8	24	1	US-08-361-795-59	Sequence 59, Appl
C 131	10.4	57.8	24	1	US-08-361-795-59	Sequence 59, Appl
C 132	10.4	57.8	24	1	US-08-447-169A-3	Sequence 3, Appl
C 133	10.4	57.8	24	1	US-08-447-169A-3	Sequence 3, Appl
C 134	10.4	57.8	24	1	US-08-233-012C-3	Sequence 3, Appl
C 135	10.4	57.8	24	1	US-08-233-012C-3	Sequence 3, Appl
C 136	10.4	57.8	24	2	US-08-477-527A-207	Sequence 207, App
C 137	10.4	57.8	24	2	US-08-477-527A-207	Sequence 207, App
C 138	10.4	57.8	24	3	US-08-481-710-207	Sequence 207, App
C 139	10.4	57.8	24	3	US-08-481-710-207	Sequence 207, App
C 140	10.4	57.8	24	3	US-08-687-421-3	Sequence 3, Appl
C 141	10.4	57.8	24	4	US-08-687-421-3	Sequence 3, Appl
C 142	10.4	57.8	24	4	US-08-687-421-3	Sequence 3, Appl
C 143	10.4	57.8	24	5	PCT-US95-05600-20	Sequence 20, Appl
C 144	10.4	57.8	24	5	PCT-US95-05600-20	Sequence 20, Appl
C 145	10.4	57.8	24	5	PCT-US95-05600-142	Sequence 142, App
C 146	10.4	57.8	24	5	PCT-US95-05600-142	Sequence 142, App
C 147	10.4	57.8	24	5	PCT-US96-09537-207	Sequence 207, App
C 148	10.4	57.8	24	5	PCT-US96-09537-207	Sequence 207, App
C 149	10.4	57.8	25	2	US-08-633-879C-20	Sequence 20, Appl
C 150	10.4	57.8	25	2	US-08-633-879C-20	Sequence 20, Appl
C 151	10.4	57.8	25	3	US-08-384-106A-12	Sequence 12, Appl
C 152	10.4	57.8	25	3	US-09-197-649-24	Sequence 24, Appl
C 153	10.4	57.8	25	5	PCT-US96-01643-12	Sequence 12, Appl
C 154	10.2	56.7	16	4	US-09-142-310-1	Sequence 1, Appl
C 155	10.2	56.7	17	4	US-09-216-909-4	Sequence 4, Appl
C 156	10.2	56.7	17	4	US-09-702-843-4	Sequence 4, Appl
C 157	10.2	56.7	17	4	US-09-702-843-4	Sequence 4, Appl
C 158	10.2	56.7	17	4	US-08-679-645-13	Sequence 13, App
C 159	10.2	56.7	17	4	US-09-593-012-106	Sequence 106, App
C 160	10.2	56.7	17	4	US-09-261-115-3	Sequence 3, Appl
C 161	10.2	56.7	19	1	US-08-559-303B-10	Sequence 10, Appl
C 162	10.2	56.7	19	3	US-08-894-483-1	Sequence 1, Appl
C 163	10.2	56.7	19	4	US-09-252-806-1	Sequence 2, Appl
C 164	10.2	56.7	19	4	US-09-342-579-2	Sequence 2, Appl
C 165	10.2	56.7	19	4	US-09-175-828-18	Sequence 18, Appl
C 166	10.2	56.7	19	4	US-09-504-358-28	Sequence 28, Appl
C 167	10.2	56.7	19	4	US-09-617-854A-2	Sequence 2, Appl
C 168	10.2	56.7	19	4	US-09-954-314-28	Sequence 28, Appl
C 169	10.2	56.7	20	1	US-08-170-688-3	Sequence 3, Appl
C 170	10.2	56.7	20	1	US-08-263-072A-3	Sequence 3, Appl
C 171	10.2	56.7	20	1	US-08-665-565B-1	Sequence 1, Appl
C 172	10.2	56.7	20	1	US-08-665-565B-3	Sequence 3, Appl
C 173	10.2	56.7	20	2	US-08-757-653-151	Sequence 151, App
C 174	10.2	56.7	20	2	US-09-108-051-13	Sequence 13, Appl
C 175	10.2	56.7	20	3	US-09-034-724-1	Sequence 1, Appl
C 176	10.2	56.7	20	3	US-09-034-724-3	Sequence 3, Appl
C 177	10.2	56.7	20	3	US-08-782-798-3	Sequence 3, Appl
C 178	10.2	56.7	20	3	US-08-191-099-9	Sequence 9, Appl
C 179	10.2	56.7	20	4	US-09-193-377B-62	Sequence 62, Appl
C 180	10.2	56.7	20	4	US-09-487-445-96	Sequence 96, Appl
C 181	10.2	56.7	20	4	US-09-593-711A-122	Sequence 122, Appl
C 182	10.2	56.7	20	4	US-09-440-833-13	Sequence 3, Appl
C 183	10.2	56.7	20	4	US-08-943-571-3	Sequence 3, Appl
C 184	10.2	56.7	20	4	US-08-520-946-151	Sequence 151, App
C 185	10.2	56.7	20	4	US-09-549-953-5	Sequence 5, Appl
C 186	10.2	56.7	20	4	US-09-920-663-13	Sequence 13, Appl
C 187	10.2	56.7	20	4	US-09-920-663-14	Sequence 14, Appl
C 188	10.2	56.7	20	4	US-09-920-663-15	Sequence 15, Appl
C 189	10.2	56.7	20	4	US-09-437-905-1	Sequence 1, Appl
C 190	10.2	56.7	20	4	US-09-437-905-1	Sequence 1, Appl
C 191	10.2	56.7	20	4	US-08-469-260A-142	Sequence 142, App
C 192	10.2	56.7	21	1	US-08-138-641-5	Sequence 5, Appl
C 193	10.2	56.7	21	1	US-08-138-641-5	Sequence 5, Appl
C 194	10.2	56.7	21	1	US-08-462-305-9	Sequence 9, Appl
C 195	10.2	56.7	21	1	US-08-613-417A-9	Sequence 9, Appl
C 196	10.2	56.7	21	2	US-08-594-452-9	Sequence 9, Appl
C 197	10.2	56.7	21	3	US-08-578-686C-8	Sequence 8, Appl
C 198	10.2	56.7	21	3	US-09-094-405-9	Sequence 9, Appl
C 199	10.2	56.7	21	3	US-09-258-408-9	Sequence 9, Appl
C 200	10.2	56.7	21	3	US-09-146-112-8	Sequence 8, Appl
C 201	10.2	56.7	21	3	US-09-146-112-8	Sequence 8, Appl
C 202	10.2	56.7	21	4	US-09-311-260-29	Sequence 29, Appl
C 203	10.2	56.7	21	4	US-09-311-260-31	Sequence 31, Appl
C 204	10.2	56.7	21	4	US-08-943-731-245	Sequence 245, App
C 205	10.2	56.7	21	4	US-08-895-981-9	Sequence 9, Appl
C 206	10.2	56.7	21	4	US-08-337-120A-9	Sequence 9, Appl
C 207	10.2	56.7	22	2	US-08-457-273B-20	Sequence 20, Appl
C 208	10.2	56.7	22	2	US-09-237-115-1	Sequence 1, Appl
C 209	10.2	56.7	23	3	US-08-594-452-57	Sequence 57, Appl
C 210	10.2	56.7	23	3	US-09-073-445-1	Sequence 1, Appl
C 211	10.2	56.7	23	3	US-09-258-408-57	Sequence 57, Appl
C 212	10.2	56.7	24	1	US-08-102-751-6	Sequence 6, Appl
C 213	10.2	56.7	24	1	US-08-102-751-6	Sequence 6, Appl
C 214	10.2	56.7	24	2	US-08-467-607-9	Sequence 9, Appl
C 215	10.2	56.7	24	2	US-08-469-362-9	Sequence 9, Appl
C 216	10.2	56.7	24	2	US-08-850-392-9	Sequence 9, Appl
C 217	10.2	56.7	24	2	US-08-564-110C-15	Sequence 15, Appl
C 218	10.2	56.7	24	4	US-09-336-447A-97	Sequence 97, Appl
C 219	10.2	56.7	25	3	US-09-053-831-3	Sequence 3, Appl
C 220	10.2	56.7	25	3	US-08-671-975A-14	Sequence 14, Appl
C 221	10.2	56.7	25	3	US-08-840-316-88	Sequence 88, Appl
C 222	10.2	56.7	25	4	US-08-809-523-88	Sequence 88, Appl
C 223	10.2	56.7	25	4	US-09-018-578A-125	Sequence 125, App
C 224	10.2	56.7	25	4	US-08-471-971-88	Sequence 88, Appl
C 225	10.2	56.7	25	4	US-09-592-891A-10	Sequence 10, Appl
C 226	10.2	56.7	25	4	US-09-402-776-88	Sequence 88, Appl
C 227	10.2	56.7	25	5	PCT-US93-08849A-88	Sequence 88, Appl
C 228	10.2	56.7	25	5	PCT-US93-08849A-88	Sequence 88, Appl
C 229	10.2	56.7	25	5	PCT-US93-08849A-88	Sequence 88, Appl
C 230	10.2	56.7	25	5	PCT-US93-08849A-88	Sequence 88, Appl
C 231	10.2	56.7	25	5	PCT-US93-08849A-88	Sequence 88, Appl
C 232	10.2	56.7	25	5	PCT-US93-08849A-88	Sequence 88, Appl
C 233	10.2	56.7	25	5	PCT-US93-08849A-88	Sequence 88, Appl
C 234	10.2	56.7	25	5	PCT-US93-08849A-88	Sequence 88, Appl
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C 240	10.2	56.7	25	5	PCT-US93-08849A-88	Sequence 88, Appl
C 241	10.2	56.7	25	5	PCT-US93-08849A-88	Sequence 88, Appl
C 242	10.2	56.7	25	5	PCT-US93-08849A-88	Sequence 88, Appl
C 243	10.2	56.7	25	5	PCT-US93-08849A-88	Sequence 88, Appl
C 244	10.2	56.7	25	5	PCT-US93-08849A-88	Sequence 88, Appl
C 245	10.2	56.7	25	5	PCT-US93-08849A-88	Sequence 88, Appl
C 246	10.2	56.7	25	5	PCT-US93-08849A-88	Sequence 88, Appl

C 247	10	55.6	20	4	US-09-445-472-18	Sequence 18, Appl	C 320	9.8	54.4	21	1	US-08-044-506B-2	Sequence 2, Appl
C 248	10	55.6	21	4	US-09-535-008-6	Sequence 6, Appl	C 321	9.8	54.4	21	2	US-08-696-944-13	Sequence 13, Appl
C 249	10	55.6	22	2	US-08-244-122-4	Sequence 4, Appl	C 322	9.8	54.4	21	4	US-08-776-927-7	Sequence 7, Appl
C 250	10	55.6	22	2	US-08-244-122-6	Sequence 6, Appl	C 323	9.8	54.4	21	4	US-09-453-562A-7	Sequence 8, Appl
C 251	10	55.6	22	2	US-09-117-927-12	Sequence 12, Appl	C 324	9.8	54.4	22	2	US-08-766-982-8	Sequence 8, Appl
C 252	10	55.6	22	4	US-09-117-927-14	Sequence 14, Appl	C 325	9.8	54.4	22	4	US-08-766-982-8	Sequence 8, Appl
C 253	10	55.6	22	4	US-09-560-639-32	Sequence 32, Appl	C 326	9.8	54.4	22	4	US-08-766-982-8	Sequence 8, Appl
C 254	10	55.6	22	4	US-09-308-090-3	Sequence 3, Appl	C 327	9.8	54.4	22	4	US-08-766-982-8	Sequence 8, Appl
C 255	10	55.6	24	2	US-08-547-979-2	Sequence 2, Appl	C 328	9.8	54.4	22	4	US-08-766-982-8	Sequence 8, Appl
C 256	10	55.6	24	2	US-08-708-958-4	Sequence 4, Appl	C 329	9.8	54.4	22	4	US-08-766-982-8	Sequence 8, Appl
C 257	10	55.6	25	1	US-08-605-541B-5	Sequence 5, Appl	C 330	9.8	54.4	22	4	US-09-142-623-20	Sequence 20, Appl
C 258	10	55.6	25	3	US-08-737-607-31	Sequence 31, Appl	C 331	9.8	54.4	22	4	US-09-343-634-6	Sequence 6, Appl
C 259	10	55.6	25	4	US-09-305-681-32	Sequence 32, Appl	C 332	9.8	54.4	23	2	US-08-850-293-1	Sequence 1, Appl
C 260	9.8	54.4	15	1	US-08-311-760A-13	Sequence 13, Appl	C 333	9.8	54.4	23	3	US-08-746-397-3	Sequence 3, Appl
C 261	9.8	54.4	15	1	US-08-311-760A-14	Sequence 14, Appl	C 334	9.8	54.4	23	4	US-09-415-784-76	Sequence 76, Appl
C 262	9.8	54.4	15	1	US-08-311-760A-44	Sequence 44, Appl	C 335	9.8	54.4	23	4	US-09-415-785A-76	Sequence 76, Appl
C 263	9.8	54.4	15	1	US-08-311-760A-64	Sequence 64, Appl	C 336	9.8	54.4	23	4	US-08-944-465-76	Sequence 76, Appl
C 264	9.8	54.4	15	1	US-08-311-760A-168	Sequence 168, App	C 337	9.8	54.4	23	4	US-09-415-900-76	Sequence 76, Appl
C 265	9.8	54.4	15	1	US-08-393-219-9	Sequence 9, Appl	C 338	9.8	54.4	23	4	US-09-415-900-76	Sequence 76, Appl
C 266	9.8	54.4	15	2	US-08-774-310-13	Sequence 13, Appl	C 339	9.8	54.4	24	1	US-08-090-523-17	Sequence 17, Appl
C 267	9.8	54.4	15	2	US-08-774-310-14	Sequence 14, Appl	C 340	9.8	54.4	24	1	US-08-398-627-17	Sequence 17, Appl
C 268	9.8	54.4	15	2	US-08-774-310-44	Sequence 44, Appl	C 341	9.8	54.4	24	1	US-08-406-858-17	Sequence 17, Appl
C 269	9.8	54.4	15	2	US-08-774-310-64	Sequence 64, Appl	C 342	9.8	54.4	24	3	US-08-981-462-48	Sequence 48, Appl
C 270	9.8	54.4	15	2	US-08-774-310-168	Sequence 168, App	C 343	9.8	54.4	24	4	US-09-385-028-2	Sequence 2, Appl
C 271	9.8	54.4	16	1	US-08-778-702-16	Sequence 16, Appl	C 344	9.8	54.4	24	4	US-09-385-028-25	Sequence 25, Appl
C 272	9.8	54.4	16	4	US-09-338-907-139	Sequence 139, App	C 345	9.8	54.4	24	4	US-08-809-802-14	Sequence 14, Appl
C 273	9.8	54.4	16	4	US-09-218-207-139	Sequence 139, App	C 346	9.8	54.4	24	5	PCT-US91-04036-17	Sequence 17, Appl
C 274	9.8	54.4	17	1	US-07-767-135-12	Sequence 12, Appl	C 347	9.8	54.4	24	5	PCT-US94-05275-17	Sequence 17, Appl
C 275	9.8	54.4	17	1	US-07-841-652-16	Sequence 16, Appl	C 348	9.8	54.4	25	1	US-08-317-432A-45	Sequence 45, Appl
C 276	9.8	54.4	17	4	US-08-584-040-7437	Sequence 7437, Ap	C 349	9.8	54.4	25	3	US-09-081-180-26	Sequence 26, Appl
C 277	9.8	54.4	18	1	US-07-977-284A-44	Sequence 44, Appl	C 350	9.8	54.4	25	3	US-09-081-180-26	Sequence 26, Appl
C 278	9.8	54.4	18	1	US-08-175-155-12	Sequence 12, Appl	C 351	9.8	54.4	25	3	US-09-040-786-26	Sequence 26, Appl
C 279	9.8	54.4	18	1	US-08-366-577-5	Sequence 5, Appl	C 352	9.8	54.4	25	3	US-09-040-786-26	Sequence 26, Appl
C 280	9.8	54.4	18	1	US-08-477-509B-46	Sequence 46, Appl	C 353	9.8	54.4	25	3	US-09-415-784-78	Sequence 78, Appl
C 281	9.8	54.4	18	2	US-08-707-237A-18	Sequence 18, Appl	C 354	9.8	54.4	25	4	US-09-402-515A-78	Sequence 78, Appl
C 282	9.8	54.4	18	2	US-08-533-306A-13	Sequence 13, Appl	C 355	9.8	54.4	25	4	US-09-415-785A-78	Sequence 78, Appl
C 283	9.8	54.4	18	2	US-08-543-020-2	Sequence 2, Appl	C 356	9.8	54.4	25	4	US-08-944-465-78	Sequence 78, Appl
C 284	9.8	54.4	18	2	US-08-742-923A-13	Sequence 13, Appl	C 357	9.8	54.4	25	4	US-09-415-988-78	Sequence 78, Appl
C 285	9.8	54.4	18	2	US-08-468-551-3	Sequence 3, Appl	C 358	9.8	54.4	25	4	US-09-415-988-78	Sequence 78, Appl
C 286	9.8	54.4	18	2	US-08-256-426B-44	Sequence 44, Appl	C 359	9.8	53.3	16	2	US-08-527-060-11	Sequence 11, Appl
C 287	9.8	54.4	18	2	US-08-735-692-4	Sequence 4, Appl	C 360	9.8	53.3	17	2	US-08-626-023-1	Sequence 1, Appl
C 288	9.8	54.4	18	3	US-08-542-051-26	Sequence 26, Appl	C 361	9.8	53.3	17	2	US-08-626-023-3	Sequence 3, Appl
C 289	9.8	54.4	18	3	US-08-482-085B-46	Sequence 46, Appl	C 362	9.8	53.3	17	3	US-08-985-162-104	Sequence 104, Appl
C 290	9.8	54.4	18	3	US-08-482-304-44	Sequence 44, Appl	C 363	9.8	53.3	17	3	US-08-679-645-80	Sequence 80, Appl
C 291	9.8	54.4	18	3	US-08-483-474-44	Sequence 44, Appl	C 364	9.8	53.3	17	4	US-08-679-645-82	Sequence 82, Appl
C 292	9.8	54.4	18	3	US-09-213-719-11	Sequence 11, Appl	C 365	9.8	53.3	18	2	US-09-212-771-8	Sequence 8, Appl
C 293	9.8	54.4	18	3	US-09-487-444-40	Sequence 40, Appl	C 366	9.8	53.3	18	3	US-09-008-481A-19	Sequence 19, Appl
C 294	9.8	54.4	18	4	US-09-423-439-6	Sequence 6, Appl	C 367	9.8	53.3	18	4	US-08-718-388A-14	Sequence 14, Appl
C 295	9.8	54.4	18	4	US-08-679-645-1179	Sequence 1179, Ap	C 368	9.8	53.3	18	4	US-09-309-592-19	Sequence 19, Appl
C 296	9.8	54.4	18	4	US-09-444-791A-46	Sequence 46, Appl	C 369	9.8	53.3	18	4	US-08-584-040-6210	Sequence 6210, Ap
C 297	9.8	54.4	18	5	PCT-US96-00005-5	Sequence 5, Appl	C 370	9.8	53.3	20	2	US-08-466-337A-12	Sequence 12, Appl
C 298	9.8	54.4	19	3	US-08-846-020A-40	Sequence 40, Appl	C 371	9.8	53.3	20	2	US-08-465-359-12	Sequence 12, Appl
C 299	9.8	54.4	19	3	US-09-125-324-2	Sequence 2, Appl	C 372	9.8	53.3	20	3	US-08-465-887A-12	Sequence 12, Appl
C 300	9.8	54.4	19	4	US-09-617-871-40	Sequence 40, Appl	C 373	9.8	53.3	20	3	US-09-280-789-172	Sequence 172, App
C 301	9.8	54.4	20	2	US-08-733-816-1	Sequence 1, Appl	C 374	9.8	53.3	20	4	US-09-277-020-63	Sequence 63, Appl
C 302	9.8	54.4	20	2	US-08-837-201C-15	Sequence 45, Appl	C 375	9.8	53.3	20	4	US-09-277-020-64	Sequence 64, Appl
C 303	9.8	54.4	20	3	US-08-995-960-17	Sequence 17, Appl	C 376	9.8	53.3	20	4	US-09-732-199A-21	Sequence 21, Appl
C 304	9.8	54.4	20	3	US-08-981-462-3	Sequence 8, Appl	C 377	9.8	53.3	20	4	US-09-487-253A-9	Sequence 9, Appl
C 305	9.8	54.4	20	3	US-08-981-462-8	Sequence 8, Appl	C 378	9.8	53.3	20	4	US-09-487-253A-9	Sequence 9, Appl
C 306	9.8	54.4	20	3	US-08-892-540-1	Sequence 21, Appl	C 379	9.8	53.3	20	4	US-09-853-768-65	Sequence 65, Appl
C 307	9.8	54.4	20	3	US-08-953-171-21	Sequence 21, Appl	C 380	9.8	53.3	20	4	US-09-780-173A-24	Sequence 24, Appl
C 308	9.8	54.4	20	3	US-08-953-171-23	Sequence 23, Appl	C 381	9.8	53.3	21	4	US-09-362-616A-39	Sequence 39, Appl
C 309	9.8	54.4	20	3	US-09-428-584-14	Sequence 14, Appl	C 382	9.8	53.3	21	4	US-09-499-362-2	Sequence 2, Appl
C 310	9.8	54.4	20	3	US-09-428-584-15	Sequence 15, Appl	C 383	9.8	53.3	22	4	US-08-943-731-554	Sequence 554, App
C 311	9.8	54.4	20	4	US-09-557-246-3	Sequence 3, Appl	C 384	9.8	53.3	23	1	US-08-181-556-5	Sequence 5, Appl
C 312	9.8	54.4	20	4	US-09-364-415-45	Sequence 45, Appl	C 385	9.8	53.3	23	1	US-08-181-556-11	Sequence 11, Appl
C 313	9.8	54.4	20	4	US-09-270-542-15	Sequence 15, App	C 386	9.8	53.3	24	1	US-08-559-806-12	Sequence 12, Appl
C 314	9.8	54.4	20	4	US-09-556-031-17	Sequence 17, Appl	C 387	9.8	53.3	24	2	US-08-928-992-2	Sequence 2, Appl
C 315	9.8	54.4	20	4	US-09-506-073-78	Sequence 78, Appl	C 388	9.8	53.3	24	3	US-08-871-267B-33	Sequence 33, Appl
C 316	9.8	54.4	20	4	US-09-657-452A-142	Sequence 142, App	C 389	9.8	53.3	24	3	US-09-010-641-29	Sequence 29, Appl
C 317	9.8	54.4	20	4	US-09-657-452A-143	Sequence 143, Appl	C 390	9.8	53.3	24	4	US-09-356-281-39	Sequence 39, Appl
C 318	9.8	54.4	20	4	US-09-920-663-12	Sequence 12, Appl	C 391	9.8	53.3	24	4	US-09-618-419-33	Sequence 33, Appl
C 319	9.8	54.4	20	4	US-09-657-453A-30	Sequence 30, Appl	C 392	9.8	53.3	24	4	US-09-339-972-2	Sequence 2, Appl

C 393	9.6	53.3	24	4	US-09-171-710-14	Sequence 14, Appl	466	9.4	52.2	20	4	US-08-851-896-49	Sequence 49, Appl
C 394	9.6	53.3	24	4	US-09-117-847E-6	Sequence 6, Appl	467	9.4	52.2	20	4	US-09-167-109-51	Sequence 51, Appl
C 395	9.6	53.3	24	4	US-09-117-847E-12	Sequence 12, Appl	468	9.4	52.2	20	4	US-09-851-896-71	Sequence 71, Appl
C 396	9.6	53.3	24	6	5457089-28	Patent No. 5457089	C 469	9.4	52.2	20	4	US-09-506-073-78	Sequence 78, Appl
C 397	9.6	53.3	25	1	US-08-140-349-11	Sequence 11, Appl	C 470	9.4	52.2	20	4	US-09-657-452A-144	Sequence 144, Appl
C 398	9.6	53.3	25	1	US-08-145-236-11	Sequence 11, Appl	C 471	9.4	52.2	20	4	US-09-517-467B-85	Sequence 85, Appl
C 399	9.6	53.3	25	1	US-08-683-877-5	Sequence 5, Appl	C 472	9.4	52.2	20	5	PCT-US94-09881-75	Sequence 75, Appl
C 400	9.6	53.3	25	4	US-08-679-645-1250	Sequence 1250, Ap	C 473	9.4	52.2	21	1	US-07-661-378A-8	Sequence 8, Appl
C 401	9.6	53.3	25	5	PCT-US93-07051-11	Sequence 11, Appl	C 474	9.4	52.2	21	1	US-08-454-097-40	Sequence 40, Appl
C 402	9.6	53.3	25	6	5428147-6	Patent No. 5428147	C 475	9.4	52.2	21	2	US-08-637-899-14	Sequence 14, Appl
C 403	9.4	52.2	12	1	US-08-086-410-4	Sequence 4, Appl	C 476	9.4	52.2	21	2	US-08-522-84-10	Sequence 2, Appl
C 404	9.4	52.2	12	1	US-07-939-501A-17	Sequence 17, Appl	C 477	9.4	52.2	21	3	US-08-185-359-42	Sequence 40, Appl
C 405	9.4	52.2	14	3	US-08-923-558-5	Sequence 5, Appl	C 478	9.4	52.2	21	3	US-07-974-409C-355	Sequence 355, Appl
C 406	9.4	52.2	14	4	US-09-486-553-5	Sequence 5, Appl	C 479	9.4	52.2	22	1	US-08-367-927-24	Sequence 4, Appl
C 407	9.4	52.2	15	4	US-09-535-262-7	Sequence 7, Appl	C 480	9.4	52.2	22	2	US-08-543-020-4	Sequence 4, Appl
C 408	9.4	52.2	16	1	US-08-229-279-1	Sequence 1, Appl	C 481	9.4	52.2	22	2	US-08-10-484-4	Sequence 4, Appl
C 409	9.4	52.2	16	1	US-08-701-269-1	Sequence 1, Appl	C 482	9.4	52.2	22	2	US-08-735-692-6	Sequence 6, Appl
C 410	9.4	52.2	16	1	US-08-299-849B-38	Sequence 38, Appl	C 483	9.4	52.2	22	3	US-08-542-051-28	Sequence 28, Appl
C 411	9.4	52.2	17	1	US-08-373-124A-418	Sequence 418, Appl	C 484	9.4	52.2	22	3	US-09-178-089-13	Sequence 13, Appl
C 412	9.4	52.2	17	1	US-08-147-596E-3	Sequence 3, Appl	C 485	9.4	52.2	22	3	US-08-589-028-49	Sequence 49, Appl
C 413	9.4	52.2	17	1	US-08-484-334-3	Sequence 3, Appl	C 486	9.4	52.2	22	3	US-08-784-582-49	Sequence 49, Appl
C 414	9.4	52.2	17	1	US-08-435-628-418	Sequence 418, Appl	C 487	9.4	52.2	22	4	US-08-785-271-49	Sequence 49, Appl
C 415	9.4	52.2	17	2	US-08-292-620A-1654	Sequence 1654, Ap	C 488	9.4	52.2	23	1	US-07-920-519-7	Sequence 7, Appl
C 416	9.4	52.2	17	2	US-08-292-620A-1957	Sequence 1957, Ap	C 489	9.4	52.2	23	1	US-07-621-093C-20	Sequence 20, Appl
C 417	9.4	52.2	17	3	US-09-013-092-3	Sequence 3, Appl	C 490	9.4	52.2	23	1	US-08-314-586-7	Sequence 7, Appl
C 418	9.4	52.2	17	3	US-08-375-151-4	Sequence 4, Appl	C 491	9.4	52.2	23	1	US-08-371-121-18	Sequence 18, Appl
C 419	9.4	52.2	17	3	US-09-071-845-1654	Sequence 1654, Ap	C 492	9.4	52.2	23	1	US-08-047-413-1	Sequence 1, Appl
C 420	9.4	52.2	17	3	US-09-071-845-1957	Sequence 1957, Ap	C 493	9.4	52.2	23	1	US-08-738-944-34	Sequence 34, Appl
C 421	9.4	52.2	17	3	US-09-280-999-3	Sequence 3, Appl	C 494	9.4	52.2	23	2	US-08-821-914-6	Sequence 6, Appl
C 422	9.4	52.2	17	4	US-09-425-072-4	Sequence 4, Appl	C 495	9.4	52.2	23	2	US-08-399-889-20	Sequence 20, Appl
C 423	9.4	52.2	18	1	US-08-019-870-13	Sequence 13, Appl	C 496	9.4	52.2	23	2	US-08-332-562A-95	Sequence 95, Appl
C 424	9.4	52.2	18	1	US-08-633-760-57	Sequence 57, Appl	C 497	9.4	52.2	23	2	US-07-927-391-19	Sequence 19, Appl
C 425	9.4	52.2	18	1	US-08-633-760-58	Sequence 58, Appl	C 498	9.4	52.2	23	3	US-09-167-364-20	Sequence 20, Appl
C 426	9.4	52.2	18	3	US-08-757-024-4	Sequence 4, Appl	C 499	9.4	52.2	23	3	US-08-579-452-28	Sequence 28, Appl
C 427	9.4	52.2	18	3	US-08-472-527-11	Sequence 11, Appl	C 500	9.4	52.2	23	3	US-08-858-876A-5	Sequence 5, Appl
C 428	9.4	52.2	18	3	US-09-280-409-11	Sequence 11, Appl	C 501	9.4	52.2	23	3	US-08-379-452-28	Sequence 28, Appl
C 429	9.4	52.2	18	4	US-09-290-577-36	Sequence 36, Appl	C 502	9.4	52.2	23	3	US-08-229-050-1	Sequence 1, Appl
C 430	9.4	52.2	18	4	US-09-316-083-4	Sequence 4, Appl	C 503	9.4	52.2	23	3	US-08-589-028-47	Sequence 47, Appl
C 431	9.4	52.2	18	4	US-09-290-452-36	Sequence 36, Appl	C 504	9.4	52.2	23	3	US-08-801-563-1	Sequence 1, Appl
C 432	9.4	52.2	18	4	US-09-290-338-36	Sequence 36, Appl	C 505	9.4	52.2	23	3	US-08-784-582-47	Sequence 47, Appl
C 433	9.4	52.2	19	1	US-07-964-589-4	Sequence 4, Appl	C 506	9.4	52.2	23	3	US-09-409-680-28	Sequence 28, Appl
C 434	9.4	52.2	19	1	US-08-196-016A-34	Sequence 34, Appl	C 507	9.4	52.2	23	4	US-08-785-271-47	Sequence 47, Appl
C 435	9.4	52.2	19	2	US-08-481-658B-4	Sequence 4, Appl	C 508	9.4	52.2	23	4	US-09-263-352-25	Sequence 25, Appl
C 436	9.4	52.2	19	2	US-08-477-504A-4	Sequence 4, Appl	C 509	9.4	52.2	23	4	US-09-472-880-5	Sequence 5, Appl
C 437	9.4	52.2	19	2	US-08-486-756A-4	Sequence 4, Appl	C 510	9.4	52.2	23	4	US-09-439-897-22	Sequence 22, Appl
C 438	9.4	52.2	19	2	US-08-485-862B-4	Sequence 4, Appl	C 511	9.4	52.2	23	4	US-09-415-784-76	Sequence 76, Appl
C 439	9.4	52.2	19	3	US-08-335-469-4	Sequence 4, Appl	C 512	9.4	52.2	23	4	US-09-415-785A-76	Sequence 76, Appl
C 440	9.4	52.2	19	3	US-08-787-739-4	Sequence 4, Appl	C 513	9.4	52.2	23	4	US-08-944-465-76	Sequence 76, Appl
C 441	9.4	52.2	19	3	US-08-467-077A-4	Sequence 4, Appl	C 514	9.4	52.2	23	4	US-09-415-868-76	Sequence 76, Appl
C 442	9.4	52.2	19	3	US-08-485-863A-4	Sequence 4, Appl	C 515	9.4	52.2	23	4	US-09-415-900-76	Sequence 76, Appl
C 443	9.4	52.2	19	4	US-08-485-049D-4	Sequence 4, Appl	C 516	9.4	52.2	24	1	US-08-684-612-5	Sequence 5, Appl
C 444	9.4	52.2	19	4	US-09-110-517-31	Sequence 31, Appl	C 517	9.4	52.2	24	2	US-08-437-607A-34	Sequence 34, Appl
C 445	9.4	52.2	19	4	US-09-117-349-12	Sequence 12, Appl	C 518	9.4	52.2	24	2	US-08-564-96C-27	Sequence 27, Appl
C 446	9.4	52.2	19	4	US-09-178-115-4	Sequence 4, Appl	C 519	9.4	52.2	24	3	US-08-981-462-33	Sequence 33, Appl
C 447	9.4	52.2	19	4	US-09-177-776-4	Sequence 4, Appl	C 520	9.4	52.2	24	3	US-08-981-462-43	Sequence 43, Appl
C 448	9.4	52.2	19	4	US-09-178-606-13	Sequence 13, Appl	C 521	9.4	52.2	24	3	PCT-US95-15428-27	Sequence 27, Appl
C 449	9.4	52.2	19	5	PCT-US93-02024-4	Sequence 4, Appl	C 522	9.4	52.2	25	2	US-08-244-122-15	Sequence 15, Appl
C 450	9.4	52.2	20	1	US-07-780-973-7	Sequence 7, Appl	C 523	9.4	52.2	25	2	US-08-461-030C-7	Sequence 7, Appl
C 451	9.4	52.2	20	1	US-07-906-393-3	Sequence 3, Appl	C 524	9.4	52.2	25	2	US-08-467-265-12	Sequence 12, Appl
C 452	9.4	52.2	20	1	US-08-178-606-13	Sequence 13, Appl	C 525	9.4	52.2	25	3	US-08-384-106A-10	Sequence 10, Appl
C 453	9.4	52.2	20	1	US-08-178-606-13	Sequence 13, Appl	C 526	9.4	52.2	25	3	US-09-291-562-8	Sequence 8, Appl
C 454	9.4	52.2	20	1	US-08-325-071-37	Sequence 37, Appl	C 527	9.4	52.2	25	4	US-09-398-193-101	Sequence 101, Appl
C 455	9.4	52.2	20	1	US-08-246-862-3	Sequence 3, Appl	C 528	9.4	52.2	25	4	US-08-467-265-12	Sequence 12, Appl
C 456	9.4	52.2	20	2	US-08-609-443B-49	Sequence 49, Appl	C 529	9.4	52.2	25	4	US-09-407-891-12	Sequence 12, Appl
C 457	9.4	52.2	20	2	US-08-474-450A-21	Sequence 21, Appl	C 530	9.4	52.2	25	5	PCT-US95-07135-7	Sequence 7, Appl
C 458	9.4	52.2	20	3	US-08-338-579A-75	Sequence 75, Appl	C 531	9.4	52.2	25	5	PCT-US96-01643-10	Sequence 10, Appl
C 459	9.4	52.2	20	3	US-09-288-461-56	Sequence 56, Appl	C 532	9.2	51.1	14	1	US-08-406-089A-1	Sequence 1, Appl
C 460	9.4	52.2	20	3	US-08-983-466-52	Sequence 52, Appl	C 533	9.2	51.1	14	1	US-08-406-089A-1	Sequence 1, Appl
C 461	9.4	52.2	20	4	US-08-461-004A-37	Sequence 37, Appl	C 534	9.2	51.1	15	2	US-08-418-085-49	Sequence 49, Appl
C 462	9.4	52.2	20	4	US-09-110-517-35	Sequence 35, Appl	C 535	9.2	51.1	15	4	US-09-099-011A-49	Sequence 23, Appl
C 463	9.4	52.2	20	4	US-09-487-368A-203	Sequence 203, Appl	C 536	9.2	51.1	15	4	US-09-056-995-22	Sequence 22, Appl
C 464	9.4	52.2	20	4	US-08-943-136-10	Sequence 10, Appl	C 537	9.2	51.1	15	4	US-09-056-995-23	Sequence 23, Appl
C 465	9.4	52.2	20	4	US-08-973-518-10	Sequence 10, Appl	C 538	9.2	51.1	15	4	US-09-753-562-14	Sequence 14, Appl

539	9.2	51.1	16	1	US-08-281-106-6	Sequence 6, Appli	c 612	9.2	51.1	20	4	US-08-829-637A-118	Sequence 118, App
540	9.2	51.1	16	1	US-08-314-309A-9	Sequence 9, Appli	613	9.2	51.1	20	4	US-09-702-246-66	Sequence 66, Appli
541	9.2	51.1	16	1	US-08-626-023-2	Sequence 2, Appli	614	9.2	51.1	20	4	US-09-798-096-21	Sequence 21, Appli
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543	9.2	51.1	16	2	US-09-142-320-2	Sequence 2, Appli	616	9.2	51.1	20	4	US-09-689-291A-12	Sequence 12, Appli
544	9.2	51.1	16	4	US-08-820-931-10	Sequence 10, Appli	617	9.2	51.1	20	4	US-09-702-327-21	Sequence 21, Appli
545	9.2	51.1	17	4	US-08-820-931-15	Sequence 15, Appli	618	9.2	51.1	20	4	US-09-920-663-16	Sequence 16, Appli
546	9.2	51.1	17	4	US-08-584-040-5329	Sequence 5329, Ap	619	9.2	51.1	20	4	US-09-661-753-33	Sequence 33, Appli
547	9.2	51.1	17	4	US-08-679-645-1251	Sequence 1251, Ap	620	9.2	51.1	20	4	US-09-907-843-50	Sequence 50, Appli
548	9.2	51.1	17	4	US-08-679-645-1251	Sequence 1251, Ap	621	9.2	51.1	20	4	US-09-517-678-136	Sequence 136, App
549	9.2	51.1	17	4	US-08-379-081B-222	Sequence 222, App	622	9.2	51.1	20	4	US-09-517-678-221	Sequence 221, App
550	9.2	51.1	18	1	US-08-379-078-222	Sequence 222, App	623	9.2	51.1	20	5	PCT-US94-07770-81	Sequence 81, Appli
551	9.2	51.1	18	1	US-08-361-479-32	Sequence 32, Appli	624	9.2	51.1	20	5	PCT-US95-11114-10	Sequence 10, Appli
552	9.2	51.1	18	1	US-08-361-479-33	Sequence 33, Appli	625	9.2	51.1	21	1	US-07-969-931-22	Sequence 22, Appli
553	9.2	51.1	18	1	US-08-462-305-16	Sequence 16, Appli	626	9.2	51.1	21	1	US-07-855-417A-22	Sequence 22, Appli
554	9.2	51.1	18	1	US-08-473-576-32	Sequence 32, Appli	627	9.2	51.1	21	1	US-07-865-960A-39	Sequence 39, Appli
555	9.2	51.1	18	1	US-08-473-576-33	Sequence 33, Appli	628	9.2	51.1	21	1	US-08-106-802-39	Sequence 39, Appli
556	9.2	51.1	18	2	US-08-843-718-32	Sequence 32, Appli	629	9.2	51.1	21	2	US-08-703-136-39	Sequence 39, Appli
557	9.2	51.1	18	2	US-08-843-718-33	Sequence 33, Appli	630	9.2	51.1	21	3	US-09-014-065-16	Sequence 16, Appli
558	9.2	51.1	18	2	US-08-843-718-33	Sequence 33, Appli	631	9.2	51.1	21	3	US-08-732-240-13	Sequence 13, Appli
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561	9.2	51.1	18	3	US-08-594-452-16	Sequence 16, Appli	634	9.2	51.1	21	4	US-09-485-636-19	Sequence 19, Appli
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564	9.2	51.1	18	3	US-09-094-405-18	Sequence 18, Appli	637	9.2	51.1	22	2	US-08-910-484-5	Sequence 5, Appli
565	9.2	51.1	18	3	US-09-258-408-16	Sequence 16, Appli	638	9.2	51.1	22	2	US-08-766-982-8	Sequence 8, Appli
566	9.2	51.1	18	3	US-09-196-132-16	Sequence 16, Appli	639	9.2	51.1	22	2	US-08-888-497-13	Sequence 13, Appli
567	9.2	51.1	18	3	US-09-144-112-15	Sequence 15, Appli	640	9.2	51.1	22	4	US-09-226-219-8	Sequence 8, Appli
568	9.2	51.1	18	4	US-09-270-751-37	Sequence 37, Appli	641	9.2	51.1	22	4	US-09-560-639-32	Sequence 32, Appli
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573	9.2	51.1	18	4	US-09-387-341-211	Sequence 211, App	646	9.2	51.1	23	1	US-07-665-960A-14	Sequence 14, Appli
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575	9.2	51.1	19	3	US-08-594-452-73	Sequence 73, Appli	648	9.2	51.1	23	1	US-08-458-477A-3	Sequence 3, Appli
576	9.2	51.1	19	3	US-09-258-408-73	Sequence 73, Appli	649	9.2	51.1	23	2	US-09-033-153-3	Sequence 3, Appli
577	9.2	51.1	19	3	US-09-135-021-40	Sequence 40, Appli	650	9.2	51.1	23	2	US-08-703-136-14	Sequence 14, Appli
578	9.2	51.1	19	3	US-09-135-021-42	Sequence 42, Appli	651	9.2	51.1	23	3	US-08-594-452-2	Sequence 2, Appli
579	9.2	51.1	19	3	US-09-135-021-42	Sequence 42, Appli	652	9.2	51.1	23	3	US-08-276-968A-28	Sequence 28, Appli
580	9.2	51.1	19	4	US-09-135-020A-42	Sequence 42, Appli	653	9.2	51.1	23	3	US-08-276-968A-28	Sequence 28, Appli
581	9.2	51.1	19	4	US-09-444-871-42	Sequence 42, Appli	654	9.2	51.1	23	3	US-09-258-408-74	Sequence 74, Appli
582	9.2	51.1	19	4	US-09-612-964-12	Sequence 12, Appli	655	9.2	51.1	23	4	US-09-325-430B-3	Sequence 3, Appli
583	9.2	51.1	19	4	US-09-597-735-42	Sequence 42, Appli	656	9.2	51.1	24	1	US-08-102-757-6	Sequence 6, Appli
584	9.2	51.1	19	4	US-09-597-735-42	Sequence 42, Appli	657	9.2	51.1	24	1	US-08-064-271-1	Sequence 1, Appli
585	9.2	51.1	19	4	US-09-597-733-42	Sequence 42, Appli	658	9.2	51.1	24	1	US-08-180-209B-47	Sequence 47, Appli
586	9.2	51.1	20	1	US-08-299-187-10	Sequence 10, Appli	659	9.2	51.1	24	2	US-08-547-979-2	Sequence 2, Appli
587	9.2	51.1	20	2	US-08-609-443B-37	Sequence 37, Appli	660	9.2	51.1	24	2	US-08-702-682-2	Sequence 2, Appli
588	9.2	51.1	20	2	US-08-609-443B-50	Sequence 50, Appli	661	9.2	51.1	24	3	US-08-594-452-75	Sequence 75, Appli
589	9.2	51.1	20	2	US-08-478-178A-118	Sequence 118, App	662	9.2	51.1	24	3	US-08-594-452-76	Sequence 76, Appli
590	9.2	51.1	20	2	US-08-488-177-118	Sequence 118, App	663	9.2	51.1	24	3	US-08-712-610-1	Sequence 1, Appli
591	9.2	51.1	20	2	US-08-481-072A-118	Sequence 118, App	664	9.2	51.1	24	3	US-08-930-569A-1	Sequence 1, Appli
592	9.2	51.1	20	2	US-08-664-336-118	Sequence 118, App	665	9.2	51.1	24	3	US-09-258-408-75	Sequence 75, Appli
593	9.2	51.1	20	2	US-08-910-443-2	Sequence 2, Appli	666	9.2	51.1	24	3	US-09-258-408-76	Sequence 76, Appli
594	9.2	51.1	20	2	US-08-910-443-10	Sequence 10, Appli	667	9.2	51.1	24	4	US-08-474-853-47	Sequence 47, Appli
595	9.2	51.1	20	2	US-08-481-066A-118	Sequence 118, App	668	9.2	51.1	24	4	US-09-309-423-1	Sequence 4, Appli
596	9.2	51.1	20	3	US-08-578-615A-81	Sequence 81, Appli	669	9.2	51.1	24	4	US-09-053-831-9	Sequence 9, Appli
597	9.2	51.1	20	3	US-09-366-257-8	Sequence 8, Appli	670	9.2	51.1	24	4	US-09-053-831-9	Sequence 9, Appli
598	9.2	51.1	20	3	US-09-287-796-112	Sequence 112, App	671	9.2	51.1	24	4	US-09-599-781-1	Sequence 1, Appli
599	9.2	51.1	20	3	US-09-288-461-21	Sequence 21, Appli	672	9.2	51.1	24	4	US-09-166-205B-47	Sequence 47, Appli
600	9.2	51.1	20	3	US-09-435-296-58	Sequence 58, Appli	673	9.2	51.1	24	4	US-09-600-031-9	Sequence 9, Appli
601	9.2	51.1	20	4	US-09-290-640-70	Sequence 70, Appli	674	9.2	51.1	24	5	PCT-US94-02629-47	Sequence 47, Appli
602	9.2	51.1	20	4	US-09-226-012-50	Sequence 50, Appli	675	9.2	51.1	25	1	US-08-137-594-51	Sequence 51, Appli
603	9.2	51.1	20	4	US-09-277-020-62	Sequence 62, Appli	676	9.2	51.1	25	1	US-08-050-073-59	Sequence 59, Appli
604	9.2	51.1	20	4	US-09-277-020-65	Sequence 65, Appli	677	9.2	51.1	25	1	US-08-336-132-47	Sequence 27, Appli
605	9.2	51.1	20	4	US-09-130-616-112	Sequence 112, App	678	9.2	51.1	25	1	US-08-421-356-18	Sequence 18, Appli
606	9.2	51.1	20	4	US-09-171-878-22	Sequence 22, App	679	9.2	51.1	25	1	US-08-811-492-128	Sequence 128, App
607	9.2	51.1	20	4	US-09-593-711A-103	Sequence 103, App	680	9.2	51.1	25	2	US-08-807-332B-17	Sequence 17, Appli
608	9.2	51.1	20	4	US-09-484-617-120	Sequence 120, App	681	9.2	51.1	25	2	US-08-743-637B-93	Sequence 93, Appli
609	9.2	51.1	20	4	US-08-851-896-37	Sequence 37, Appli	682	9.2	51.1	25	3	US-08-526-840B-93	Sequence 93, Appli
610	9.2	51.1	20	4	US-08-851-896-50	Sequence 50, Appli	683	9.2	51.1	25	3	US-08-750-145A-15	Sequence 15, Appli
611	9.2	51.1	20	4	US-08-851-896-50	Sequence 50, Appli	684	9.2	51.1	25	3	US-08-975-698A-19	Sequence 19, Appli

C 685	9 2	51.1	25	4	US-08-338-876-17	Sequence 17, Appl	C 758	9	50.0	20	4	US-09-364-416-34	Sequence 34, Appl
C 686	9 2	51.1	25	4	US-08-914-029-12	Sequence 12, Appl	C 759	9	50.0	20	4	US-09-657-042A-45	Sequence 45, Appl
C 687	9 2	51.1	25	4	US-09-417-090-19	Sequence 19, Appl	C 760	9	50.0	20	4	US-09-716-161A-86	Sequence 86, Appl
C 688	9 2	51.1	25	4	US-09-102-528-1	Sequence 1, Appl	C 761	9	50.0	20	4	US-09-629-642A-98	Sequence 98, Appl
C 689	9 2	51.1	25	4	US-08-683-409-12	Sequence 12, Appl	C 762	9	50.0	20	4	US-09-396-642A-98	Sequence 9, Appl
C 690	9 2	51.1	25	4	US-09-446-402A-6	Sequence 6, Appl	C 763	9	50.0	20	4	US-09-472-367-3	Sequence 3, Appl
C 691	9 2	51.1	25	4	US-09-446-402A-13	Sequence 13, Appl	C 764	9	50.0	20	4	US-09-659-791A-57	Sequence 57, Appl
C 692	9 2	51.1	25	4	US-09-592-891A-10	Sequence 10, Appl	C 765	9	50.0	20	4	US-09-661-751-55	Sequence 55, Appl
C 693	9 2	51.1	25	4	US-08-579-645-1250	Sequence 1250, Ap	C 766	9	50.0	20	4	US-09-780-175-66	Sequence 66, Appl
C 694	9 2	51.1	25	4	US-09-727-578-19	Sequence 19, Appl	C 767	9	50.0	20	4	US-09-658-672A-45	Sequence 25, Appl
C 695	9 2	51.1	25	4	US-09-212-247C-21	Sequence 21, Appl	C 768	9	50.0	20	4	US-09-517-467B-240	Sequence 74, Appl
C 696	9 2	51.1	25	4	US-09-457-066-31	Sequence 31, Appl	C 769	9	50.0	20	4	US-09-844-525A-74	Sequence 74, Appl
C 697	9 2	51.1	25	4	US-09-046-783-18	Sequence 18, Appl	C 770	9	50.0	20	6	5210025-17	Patent No. 5210025
C 698	9	50.0	15	4	US-08-482-918-91	Sequence 91, Appl	C 771	9	50.0	21	1	US-08-105-483-224	Sequence 224, Appl
C 699	9	50.0	15	4	US-08-482-918-92	Sequence 92, Appl	C 772	9	50.0	21	1	US-08-434-201-3	Sequence 3, Appl
C 700	9	50.0	15	4	US-09-224-681-91	Sequence 91, Appl	C 773	9	50.0	21	1	US-08-709-203-224	Sequence 224, Appl
C 701	9	50.0	15	4	US-09-224-681-92	Sequence 92, Appl	C 774	9	50.0	21	1	US-08-433-583-3	Sequence 3, Appl
C 702	9	50.0	15	4	US-08-336-728A-91	Sequence 91, Appl	C 775	9	50.0	21	1	US-08-358-171-13	Sequence 13, Appl
C 703	9	50.0	15	4	US-08-336-728A-92	Sequence 92, Appl	C 776	9	50.0	21	1	US-08-458-101-224	Sequence 224, Appl
C 704	9	50.0	17	1	US-08-064-400B-6	Sequence 6, Appl	C 777	9	50.0	21	1	US-08-434-423-3	Sequence 3, Appl
C 705	9	50.0	17	1	US-08-064-400B-7	Sequence 7, Appl	C 778	9	50.0	21	1	US-08-399-988B-20	Sequence 20, Appl
C 706	9	50.0	17	1	US-08-458-067-39	Sequence 39, Appl	C 779	9	50.0	21	1	US-08-493-754A-20	Sequence 20, Appl
C 707	9	50.0	17	3	US-08-981-256A-14	Sequence 14, Appl	C 780	9	50.0	21	2	US-08-437-667-3	Sequence 3, Appl
C 708	9	50.0	17	4	US-08-584-040-1463	Sequence 1463, Ap	C 781	9	50.0	21	2	US-08-798-738-11	Sequence 11, Appl
C 709	9	50.0	17	4	US-08-584-040-7436	Sequence 7436, Ap	C 782	9	50.0	21	2	US-09-090-947-13	Sequence 13, Appl
C 710	9	50.0	17	5	PCT-US94-05617-7	Sequence 7, Appl	C 783	9	50.0	21	3	US-08-906-955-3	Sequence 3, Appl
C 711	9	50.0	17	5	PCT-US94-05617-8	Sequence 8, Appl	C 784	9	50.0	21	4	US-08-943-731-506	Sequence 506, Appl
C 712	9	50.0	17	5	PCT-US96-07795-39	Sequence 39, Appl	C 785	9	50.0	21	4	US-09-245-041-89	Sequence 89, Appl
C 713	9	50.0	17	5	PCT-US96-07795-39	Sequence 39, Appl	C 786	9	50.0	21	4	US-09-522-21-16	Sequence 16, Appl
C 714	9	50.0	18	1	US-08-256-720-2	Sequence 2, Appl	C 787	9	50.0	21	4	US-09-468-826-5	Sequence 5, Appl
C 715	9	50.0	18	1	US-08-175-155-13	Sequence 13, Appl	C 788	9	50.0	21	5	PCT-US96-06060-3	Sequence 3, Appl
C 716	9	50.0	18	1	US-08-477-509B-47	Sequence 47, Appl	C 789	9	50.0	22	1	US-08-285-440-30	Sequence 30, Appl
C 717	9	50.0	18	2	US-08-707-237A-19	Sequence 19, Appl	C 790	9	50.0	22	1	US-08-630-344-30	Sequence 30, Appl
C 718	9	50.0	18	2	US-08-633-289-2	Sequence 2, Appl	C 791	9	50.0	22	2	US-08-569-150A-5	Sequence 5, Appl
C 719	9	50.0	18	3	US-08-482-085B-47	Sequence 47, Appl	C 792	9	50.0	22	2	US-08-951-718-12	Sequence 12, Appl
C 720	9	50.0	18	3	US-09-150-805-3	Sequence 3, Appl	C 793	9	50.0	22	3	US-08-480-640A-129	Sequence 129, Appl
C 721	9	50.0	18	3	US-09-150-805-13	Sequence 13, Appl	C 794	9	50.0	22	3	US-08-491-954-63	Sequence 63, Appl
C 722	9	50.0	18	4	US-09-034-205-57	Sequence 57, Appl	C 795	9	50.0	22	3	US-09-010-641-5	Sequence 5, Appl
C 723	9	50.0	18	4	US-08-986-069A-3	Sequence 3, Appl	C 796	9	50.0	22	3	US-08-295-802-129	Sequence 129, Appl
C 724	9	50.0	18	4	US-08-996-069A-13	Sequence 13, Appl	C 797	9	50.0	22	4	US-09-356-281-5	Sequence 5, Appl
C 725	9	50.0	18	4	US-09-677-218B-57	Sequence 57, Appl	C 798	9	50.0	22	4	US-08-686-968C-78	Sequence 78, Appl
C 726	9	50.0	18	4	US-09-444-791A-47	Sequence 47, Appl	C 799	9	50.0	22	4	US-09-041-886-66	Sequence 66, Appl
C 727	9	50.0	18	4	US-09-677-192-57	Sequence 57, Appl	C 800	9	50.0	22	4	US-08-488-237A-129	Sequence 129, Appl
C 728	9	50.0	18	4	US-09-593-012-200	Sequence 200, App	C 801	9	50.0	22	4	US-08-943-731-435	Sequence 435, Appl
C 729	9	50.0	18	6	5166318-19	Patent No. 5166318	C 802	9	50.0	22	4	US-09-099-749-5	Sequence 5, Appl
C 730	9	50.0	19	3	US-08-846-020A-40	Sequence 40, Appl	C 803	9	50.0	22	4	US-09-090-535-15	Sequence 15, Appl
C 731	9	50.0	19	4	US-09-438-016-26	Sequence 26, Appl	C 804	9	50.0	22	4	US-08-375-992A-129	Sequence 129, Appl
C 732	9	50.0	19	4	US-09-617-871-40	Sequence 40, Appl	C 805	9	50.0	23	1	US-08-776-088-22	Sequence 22, Appl
C 733	9	50.0	20	1	US-07-952-817-2	Sequence 2, Appl	C 806	9	50.0	23	1	US-08-776-088-22	Sequence 2, Appl
C 734	9	50.0	20	1	US-07-906-393-2	Sequence 2, Appl	C 807	9	50.0	23	3	US-08-943-336A-6	Sequence 6, Appl
C 735	9	50.0	20	1	US-08-122-520C-6	Sequence 6, Appl	C 808	9	50.0	23	3	US-09-135-021-51	Sequence 51, Appl
C 736	9	50.0	20	1	US-08-246-862-2	Sequence 2, Appl	C 809	9	50.0	23	4	US-09-215-098-3	Sequence 3, Appl
C 737	9	50.0	20	2	US-08-145-658D-10	Sequence 10, Appl	C 810	9	50.0	23	4	US-08-913-778-1	Sequence 1, Appl
C 741	9	50.0	20	3	US-09-249-730-15	Sequence 15, Appl	C 815	9	50.0	23	4	US-09-444-871-53	Sequence 53, Appl
C 742	9	50.0	20	3	US-09-428-584-13	Sequence 13, Appl	C 814	9	50.0	23	4	US-09-597-735-53	Sequence 53, Appl
C 743	9	50.0	20	3	US-09-386-607-12	Sequence 12, Appl	C 816	9	50.0	23	4	US-09-444-871-53	Sequence 53, Appl
C 744	9	50.0	20	4	US-09-167-921-46	Sequence 46, Appl	C 817	9	50.0	23	5	US-09-597-732-53	Sequence 53, Appl
C 745	9	50.0	20	4	US-09-280-805-124	Sequence 124, App	C 818	9	50.0	23	6	PCT-US95-09145A-22	Patent No. 5520913
C 746	9	50.0	20	4	US-09-277-020-48	Sequence 48, Appl	C 819	9	50.0	24	1	US-08-566-037A-22	Sequence 22, Appl
C 747	9	50.0	20	4	US-09-277-020-61	Sequence 61, Appl	C 820	9	50.0	24	1	US-08-665-628-10	Sequence 10, Appl
C 748	9	50.0	20	4	US-09-277-020-62	Sequence 62, Appl	C 821	9	50.0	24	2	US-08-302-044-29	Sequence 29, Appl
C 749	9	50.0	20	4	US-09-277-020-63	Sequence 63, Appl	C 822	9	50.0	24	3	US-08-945-726-4	Sequence 4, Appl
C 750	9	50.0	20	4	US-09-277-020-64	Sequence 64, Appl	C 823	9	50.0	24	3	US-09-068-655-2	Sequence 2, Appl
C 751	9	50.0	20	4	US-09-277-020-65	Sequence 65, Appl	C 824	9	50.0	24	4	US-08-751-344B-28	Sequence 28, Appl
C 752	9	50.0	20	4	US-09-323-743-46	Sequence 46, Appl	C 825	9	50.0	24	4	US-09-018-584A-105	Sequence 105, Appl
C 753	9	50.0	20	4	US-09-489-869-20	Sequence 20, Appl	C 826	9	50.0	24	4	US-09-008-892-13	Sequence 13, Appl
C 754	9	50.0	20	4	US-09-593-711A-102	Sequence 102, App	C 827	9	50.0	24	4	US-08-881-450A-21	Sequence 21, Appl
C 755	9	50.0	20	4	US-09-593-711A-202	Sequence 202, Appl	C 828	9	50.0	25	4	US-08-816-772-4	Sequence 4, Appl
C 756	9	50.0	20	4	US-08-803-346-47	Sequence 47, Appl	C 829	9	50.0	25	4	US-07-989-845-9	Sequence 9, Appl
C 757	9	50.0	20	4	US-09-214-278-26	Sequence 26, Appl	C 830	9	50.0	25	1	US-07-989-845-16	Sequence 16, Appl

831	9	50.0	25	1	US-07-964-624D-11	Sequence 11, Appl	C 904	8.8	48.9	18	1	US-08-479-173-5	Sequence 5, Appl1
832	9	50.0	25	1	US-08-155-746-17	Sequence 17, Appl	905	8.8	48.9	18	1	US-08-342-029-2	Sequence 2, Appl1
833	9	50.0	25	1	US-08-261-206A-14	Sequence 14, Appl	C 906	8.8	48.9	18	1	US-08-363-585-95	Sequence 95, Appl
834	9	50.0	25	1	US-08-442-572-60	Sequence 60, Appl	907	8.8	48.9	18	1	US-08-363-240A-1230	Sequence 1230, Ap
835	9	50.0	25	1	US-08-442-062-11	Sequence 11, Appl	908	8.8	48.9	18	1	US-08-340-732-2	Sequence 2, Appl1
836	9	50.0	25	1	US-08-341-148-19	Sequence 19, Appl	C 909	8.8	48.9	18	1	US-08-579-223-21	Sequence 21, Appl
837	9	50.0	25	1	US-08-477-530-27	Sequence 27, Appl	C 910	8.8	48.9	18	1	US-08-464-192-6	Sequence 6, Appl1
838	9	50.0	25	1	US-08-477-530-27	Sequence 27, Appl	C 911	8.8	48.9	18	1	US-08-484-192-22	Sequence 22, Appl
839	9	50.0	25	1	US-08-477-830-27	Sequence 27, Appl	C 912	8.8	48.9	18	1	US-08-753-054-21	Sequence 21, Appl
840	9	50.0	25	1	US-08-410-941-15	Sequence 15, Appl	913	8.8	48.9	18	1	US-08-640-672-5	Sequence 5, Appl1
841	9	50.0	25	1	US-08-361-795-60	Sequence 60, Appl	914	8.8	48.9	18	1	US-08-623-891-19	Sequence 19, Appl
842	9	50.0	25	1	US-08-468-546-15	Sequence 15, Appl	915	8.8	48.9	18	2	US-08-684-98A-5	Sequence 5, Appl1
843	9	50.0	25	1	US-08-623-891-81	Sequence 81, Appl	916	8.8	48.9	18	2	US-08-577-858A-1	Sequence 3, Appl1
844	9	50.0	25	1	US-08-748-697A-11	Sequence 11, Appl	C 917	8.8	48.9	18	2	US-08-237-973-3	Sequence 3, Appl1
845	9	50.0	25	2	US-08-468-547-15	Sequence 15, Appl	918	8.8	48.9	18	3	US-08-755-558-1	Sequence 11, Appl
846	9	50.0	25	2	US-08-588-983-27	Sequence 27, Appl	919	8.8	48.9	18	3	US-09-280-409-11	Sequence 11, Appl
847	9	50.0	25	2	US-08-467-937-15	Sequence 15, Appl	920	8.8	48.9	18	4	US-08-880-313A-4	Sequence 4, Appl1
848	9	50.0	25	2	US-08-588-976-27	Sequence 27, Appl	C 921	8.8	48.9	18	4	US-08-880-313A-5	Sequence 5, Appl1
849	9	50.0	25	2	US-08-859-998-934	Sequence 934, App	922	8.8	48.9	18	4	US-09-078-994-9	Sequence 9, Appl1
850	9	50.0	25	3	US-08-750-145A-16	Sequence 16, Appl	923	8.8	48.9	18	4	US-08-864-641B-2	Sequence 2, Appl1
C 851	9	50.0	25	3	US-08-975-698A-20	Sequence 20, Appl	924	8.8	48.9	18	4	US-08-864-641B-9	Sequence 9, Appl1
C 852	9	50.0	25	3	US-08-737-607-22	Sequence 22, Appl	925	8.8	48.9	18	4	US-09-389-855A-4	Sequence 4, Appl1
C 853	9	50.0	25	3	US-09-074-950-15	Sequence 15, Appl	C 926	8.8	48.9	18	4	US-09-389-855A-5	Sequence 5, Appl1
C 854	9	50.0	25	4	US-09-417-090-20	Sequence 20, Appl	927	8.8	48.9	18	4	US-09-668-822-4	Sequence 4, Appl1
C 855	9	50.0	25	4	US-09-165-616-11	Sequence 11, Appl	C 928	8.8	48.9	18	4	US-09-668-822-5	Sequence 5, Appl1
C 856	9	50.0	25	4	US-09-225-928-934	Sequence 934, App	929	8.8	48.9	18	4	US-09-340-661-19	Sequence 19, Appl
C 857	9	50.0	25	4	US-09-727-578-20	Sequence 20, Appl	930	8.8	48.9	18	4	US-09-634-262-12	Sequence 12, Appl
C 858	9	50.0	25	4	US-09-343-634-2	Sequence 2, Appl1	C 931	8.8	48.9	18	5	PCT-US94-12947A-91	Sequence 91, Appl
C 859	9	50.0	25	4	US-09-051-239A-4	Sequence 4, Appl1	C 932	8.8	48.9	18	5	PCT-US95-14957-2	Sequence 2, Appl1
C 860	9	50.0	25	4	US-09-340-861-81	Sequence 81, Appl	933	8.8	48.9	18	6	US-08-846-020A-36	Patent No. 5,45022
C 861	9	50.0	25	4	US-09-634-262-81	Sequence 81, Appl	934	8.8	48.9	19	3	US-09-338-907-178	Sequence 36, Appl
C 862	9	50.0	25	5	PCT-US93-11298-9	Sequence 9, Appl1	935	8.8	48.9	19	4	US-09-218-207-178	Sequence 178, App
C 863	9	50.0	25	5	PCT-US93-11298-16	Sequence 16, Appl	936	8.8	48.9	19	4	US-09-617-871-36	Sequence 36, Appl
C 864	9	50.0	25	5	PCT-US94-00771-17	Sequence 17, Appl	937	8.8	48.9	19	4	US-09-228-302-23	Sequence 23, Appl
C 865	9	50.0	25	5	PCT-US94-14096-19	Sequence 19, Appl	C 938	8.8	48.9	19	4	US-07-906-393-3	Sequence 3, Appl1
C 866	9	50.0	25	5	PCT-US95-05600-143	Sequence 143, App	939	8.8	48.9	20	1	US-08-136-811-24	Sequence 24, Appl
C 867	8.8	48.9	14	1	US-08-175-471-13	Sequence 13, Appl	940	8.8	48.9	20	1	US-08-445-289B-9	Sequence 9, Appl1
C 868	8.8	48.9	14	2	US-07-963-538B-30	Sequence 30, Appl	941	8.8	48.9	20	1	US-08-835-770A-24	Sequence 24, Appl1
C 869	8.8	48.9	14	2	US-08-718-777-14	Sequence 14, Appl	942	8.8	48.9	20	1	US-08-835-770A-24	Sequence 24, Appl
C 870	8.8	48.9	14	3	US-09-051-341-14	Sequence 14, Appl	943	8.8	48.9	20	1	US-08-628-731-24	Sequence 24, Appl
C 871	8.8	48.9	15	1	US-08-379-496-8	Sequence 8, Appl1	944	8.8	48.9	20	1	US-08-246-662-3	Sequence 3, Appl1
C 872	8.8	48.9	15	1	US-08-276-594A-5	Sequence 5, Appl1	945	8.8	48.9	20	2	US-08-651-692-8	Sequence 8, Appl1
C 873	8.8	48.9	15	1	US-08-276-594A-5	Sequence 5, Appl1	946	8.8	48.9	20	2	US-08-852-173-2	Sequence 23, Appl
C 874	8.8	48.9	15	1	US-08-363-240A-9	Sequence 9, Appl1	947	8.8	48.9	20	2	US-08-852-173-2	Sequence 23, Appl
C 875	8.8	48.9	15	1	US-08-363-240A-765	Sequence 765, App	C 948	8.8	48.9	20	2	US-08-852-173-2	Sequence 23, Appl
C 876	8.8	48.9	15	4	US-08-779-072A-2	Sequence 2, Appl1	C 949	8.8	48.9	20	2	US-08-837-201C-67	Sequence 67, Appl
C 877	8.8	48.9	16	1	US-08-050-073-140	Sequence 140, App	950	8.8	48.9	20	3	US-09-357-072-55	Sequence 65, Appl
C 878	8.8	48.9	16	2	US-08-770-235A-60	Sequence 60, Appl	C 951	8.8	48.9	20	3	US-09-073-465-17	Sequence 17, Appl
C 879	8.8	48.9	16	4	US-09-338-907-140	Sequence 140, App	952	8.8	48.9	20	3	US-08-914-266-2	Sequence 31, Appl
C 880	8.8	48.9	16	4	US-09-218-207-140	Sequence 140, App	953	8.8	48.9	20	3	US-09-418-661-31	Sequence 31, Appl
C 881	8.8	48.9	17	1	US-07-990-297-16	Sequence 16, Appl	954	8.8	48.9	20	3	US-09-287-786-23	Sequence 23, Appl
C 882	8.8	48.9	17	1	US-08-152-313-93	Sequence 93, Appl	955	8.8	48.9	20	3	US-09-428-564-15	Sequence 15, Appl
C 883	8.8	48.9	17	1	US-08-390-850-526	Sequence 526, App	C 956	8.8	48.9	20	3	US-08-640-906-16	Sequence 16, Appl
C 884	8.8	48.9	17	1	US-08-373-124A-418	Sequence 418, App	957	8.8	48.9	20	3	US-09-418-640-10	Sequence 10, Appl
C 885	8.8	48.9	17	1	US-08-373-124A-418	Sequence 418, App	C 958	8.8	48.9	20	3	US-09-429-499-11	Sequence 11, Appl
C 886	8.8	48.9	17	1	US-08-579-223-93	Sequence 93, Appl	959	8.8	48.9	20	3	US-09-106-216-28	Sequence 28, Appl
C 887	8.8	48.9	17	1	US-08-435-634-526	Sequence 526, App	960	8.8	48.9	20	4	US-09-101-886B-82	Sequence 82, Appl
C 888	8.8	48.9	17	1	US-08-435-628-418	Sequence 418, App	C 961	8.8	48.9	20	4	US-08-983-466-15	Sequence 15, Appl
C 889	8.8	48.9	17	4	US-08-435-628-1190	Sequence 1190, Ap	962	8.8	48.9	20	4	US-09-277-020-61	Sequence 61, Appl
C 890	8.8	48.9	17	4	US-08-864-641B-4	Sequence 4, Appl1	963	8.8	48.9	20	4	US-09-130-616-23	Sequence 23, Appl
C 891	8.8	48.9	17	4	US-08-584-040-2502	Sequence 2502, Ap	964	8.8	48.9	20	4	US-09-428-583-17	Sequence 17, Appl
C 892	8.8	48.9	17	5	PCT-US93-11702-16	Sequence 16, Appl	965	8.8	48.9	20	4	US-09-214-278-26	Sequence 26, Appl
C 893	8.8	48.9	17	5	PCT-US94-12947A-93	Sequence 93, Appl	C 966	8.8	48.9	20	4	US-09-364-416-67	Sequence 67, Appl
C 894	8.8	48.9	18	1	US-07-827-690-1	Sequence 1, Appl1	C 967	8.8	48.9	20	4	US-09-488-856A-59	Sequence 59, Appl
C 895	8.8	48.9	18	1	US-07-827-690-2	Sequence 2, Appl1	C 968	8.8	48.9	20	4	US-09-395-936-16	Sequence 16, Appl
C 896	8.8	48.9	18	1	US-08-208-486-35	Sequence 35, Appl	C 969	8.8	48.9	20	4	US-08-750-088A-67	Sequence 67, Appl
C 897	8.8	48.9	18	1	US-08-208-486-35	Sequence 35, Appl	C 970	8.8	48.9	20	4	US-09-488-074-3	Sequence 3, Appl1
C 898	8.8	48.9	18	1	US-08-308-486-44	Sequence 44, Appl	C 971	8.8	48.9	20	4	US-08-679-665-1260	Sequence 1260, Ap
C 899	8.8	48.9	18	1	US-08-152-313-91	Sequence 91, Appl	C 972	8.8	48.9	20	4	US-09-656-286-2	Sequence 26, Appl
C 900	8.8	48.9	18	1	US-08-379-081B-227	Sequence 227, App	C 973	8.8	48.9	20	4	US-09-623-655A-26	Sequence 26, Appl
C 901	8.8	48.9	18	1	US-08-334-613-3	Sequence 3, Appl1	C 974	8.8	48.9	20	4	US-09-844-634-126	Sequence 126, App
C 902	8.8	48.9	18	1	US-08-379-078-227	Sequence 227, App	C 975	8.8	48.9	20	4	US-09-051-962-20	Sequence 20, Appl
C 903	8.8	48.9	18	1	US-08-479-173-4	Sequence 4, Appl1	C 976	8.8	48.9	21	1	US-08-554-642-4	Sequence 4, Appl1

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C 977      8.8  48.9    21  1  US-08-554-135-4  Sequence 4, Appli
C 978      8.8  48.9    21  1  US-08-624-545-50  Sequence 50, Appli
C 979      8.8  48.9    21  1  US-08-353-476-44  Sequence 44, Appli
C 980      8.8  48.9    21  2  US-08-460-751-19  Sequence 19, Appli
C 981      8.8  48.9    21  2  US-08-554-137-4  Sequence 4, Appli
C 982      8.8  48.9    21  4  US-08-849-488-14  Sequence 14, Appli
C 983      8.8  48.9    21  4  US-09-168-406A-7  Sequence 7, Appli
C 984      8.8  48.9    21  4  US-09-109-663-42  Sequence 42, Appli
C 985      8.8  48.9    21  4  US-09-318-191-2  Sequence 2, Appli
C 986      8.8  48.9    21  4  US-09-130-339-5  Sequence 5, Appli
C 987      8.8  48.9    22  1  US-08-125-012-27  Sequence 27, Appli
C 988      8.8  48.9    22  1  US-08-474-021-8  Sequence 8, Appli
C 989      8.8  48.9    22  1  US-08-221-579A-21  Sequence 21, Appli
C 990      8.8  48.9    22  1  US-08-783-818-27  Sequence 27, Appli
C 991      8.8  48.9    22  2  US-08-453-349-27  Sequence 27, Appli
C 992      8.8  48.9    22  2  US-08-474-020A-8  Sequence 8, Appli
C 993      8.8  48.9    22  2  US-08-327-832-12  Sequence 12, Appli
C 994      8.8  48.9    22  2  US-08-828-584-12  Sequence 12, Appli
C 995      8.8  48.9    22  2  US-08-704-701-21  Sequence 21, Appli
C 996      8.8  48.9    22  2  US-08-837-302-9  Sequence 9, Appli
C 997      8.8  48.9    22  2  US-08-979-385B-25  Sequence 25, Appli
C 998      8.8  48.9    22  3  US-08-798-668-9  Sequence 9, Appli
C 999      8.8  48.9    22  3  US-08-906-443-7  Sequence 7, Appli
C1000     8.8  48.9    22  3  US-08-906-443-8  Sequence 8, Appli
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ALIGNMENTS

RESULT 1

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US-09-593-012-188
; Sequence 188, Application US/09593012
; Patent No. 6387652
; GENERAL INFORMATION:
; APPLICANT: HAUGLAND, Richard
; APPLICANT: VESPER, Stephen
; TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
; FILE REFERENCE: HAUGLAND-1A
; CURRENT APPLICATION NUMBER: US/09/593,012
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 09/290,990
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 60/081,773
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 188
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-09-593-012-188
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Query Match      100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CTGGCGCCCGATCCAGGC 18

Db 1 CTGGCGCCCGATCCAGGC 18

RESULT 2

```
US-09-318-191-2
; Sequence 2, Application US/09318191A
; Patent No. 6291190
; GENERAL INFORMATION:
; APPLICANT: Marcel Behr
; APPLICANT: Peter Small
; APPLICANT: Gary Schoonik
; APPLICANT: Michael Wilson
; TITLE OF INVENTION: Molecular differences between species of
; TITLE OF INVENTION: the M. tuberculosis complex
; FILE REFERENCE: SUN-102P
```

```
; CURRENT APPLICATION NUMBER: US/09/318,191A
; CURRENT FILING DATE: 1999-05-25
; EARLIER APPLICATION NUMBER: 60/097,936
; EARLIER FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: M. tuberculosis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: genome sequence, segment 160, position 16989
US-09-318-191-2
```

QY 4 CGCCCGGATCCAG 16

Db 9 CGCCCGGATCCAG 21

RESULT 3

```
US-09-593-012-106/c
; Sequence 106, Application US/09593012
; Patent No. 6387652
; GENERAL INFORMATION:
; APPLICANT: HAUGLAND, Richard
; APPLICANT: VESPER, Stephen
; TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTERIA
; FILE REFERENCE: HAUGLAND-1A
; CURRENT APPLICATION NUMBER: US/09/593,012
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 09/290,990
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 60/081,773
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 106
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Myrothecium verrucaria/roxiidum
US-09-593-012-106
```

```
Query Match      71.1%; Score 12.8; DB 4; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 3 GCGCCCGATCCAGGC 18

Db 17 GCGCCCGATCCAGGC 2

RESULT 4

```
US-08-284-566A-2/c
; Sequence 2, Application US/08284566A
; Patent No. 5681725
; GENERAL INFORMATION:
; APPLICANT: Jensen, Ejner Bech
; TITLE OF INVENTION: A PROCESS FOR PRODUCING HEME PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5681725 No. 5681725disk of No. 5681725th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
```

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,566A
FILING DATE: 09-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 3679,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-284-566A-2

Query Match 68.9%; Score 12.4; DB 1; Length 22;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGCGCCCGGATCC 14
Db 16 CTGCGCCCGGATCC 3

RESULT 5
US-09-118-408-28/c
Sequence 28, Application US/09118408A
Patent No. 6265544
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ADIPOCTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-30
CURRENT APPLICATION NUMBER: US/09/118,408A
CURRENT FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/053,154
EARLIER FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 28
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide ZC15035
US-09-118-408-28

Query Match 67.8%; Score 12.2; DB 4; Length 24;
Best Local Similarity 82.4%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCGCCCGGATCCAGG 17
Db 20 CCGAGCCCGGATCCATG 4

RESULT 6
US-09-506-855-28/c
Sequence 28, Application US/09506855
Patent No. 6448221
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Laeser, Gerald W.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND

TITLE OF INVENTION: IMMUNE FUNCTION
FILE REFERENCE: 99-12
CURRENT APPLICATION NUMBER: US/09/506,855
CURRENT FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 28
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide ZC15035
US-09-506-855-28

Query Match 67.8%; Score 12.2; DB 4; Length 24;
Best Local Similarity 82.4%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCGCCCGGATCCAGG 17
Db 20 CCGAGCCCGGATCCATG 4

RESULT 7
US-08-840-316-88/c
Sequence 88, Application US/08840316
Patent No. 6054567
GENERAL INFORMATION:
APPLICANT: Emerson, Suzanne U., Purcell, Robert H.,
APPLICANT: Tsarev, Sergei, A., and Robinson, Robin A.
TITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis B And Their
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,316
FILING DATE: 11-APR-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Richard W. Bork
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4255
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-840-316-88

Query Match 66.7%; Score 12; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCGATCCAGGC 18
| | | | |
Db 20 CCGATCCAGGC 9

RESULT 8
US-08-809-523-88/c
Sequence 88, Application US/08809523
Patent No. 6207416

GENERAL INFORMATION:
APPLICANT: Tearev, Sergei. A., Emerson,
APPLICANT: Suzanne U., Purcell, Robert H.
TITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis B And Their
TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,523
FILING DATE: 28-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13102
FILING DATE: 03-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US08/316,765
FILING DATE: 03-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/947,263
FILING DATE: 18-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Richard W. Bork
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4032US4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-809-523-88

Query Match 66.7%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCGATCCAGGC 18
| | | | |
Db 20 CCGATCCAGGC 9

RESULT 9
US-08-471-971-88/c
Sequence 88, Application US/08471971
Patent No. 6287759

GENERAL INFORMATION:
APPLICANT: Tearev, Sergei. A., Emerson,
APPLICANT: Suzanne U., Purcell, Robert H.
TITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis B And Their

TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,971
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US08/316,765
FILING DATE: 03-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US07/947,263
FILING DATE: 18-SEP-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Richard W. Bork
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4032US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-471-971-88

Query Match 66.7%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCGATCCAGGC 18
| | | | |
Db 20 CCGATCCAGGC 9

RESULT 10
US-09-402-776-88/c
Sequence 88, Application US/09402776
Patent No. 6458562

GENERAL INFORMATION:
APPLICANT: Emerson, Suzanne U., Purcell, Robert H.,
APPLICANT: Tearev, Sergei. A., and Robinson, Robin A.
TITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis B And Their
TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,776
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/840,316
; FILING DATE: 11-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard W. Bork
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4255
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-402-776-88
```

```

Query Match          66.7%; Score 12; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      7 CCGGATCCAGGC 18
        |||||
        20 CCGGATCCAGGC 9
```

```

RESULT 11
PCT-US93-08849A-88/c
; Sequence 88, Application PC/TUS9308849A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & PINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08849A
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US07/947,263
; FILING DATE: 18-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: William S. Feller
; REGISTRATION NUMBER: 26,728
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
PCT-US93-08849A-88
```

```

Query Match          66.7%; Score 12; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      7 CCGGATCCAGGC 18
        |||||
        20 CCGGATCCAGGC 9
```

```

RESULT 12
PCT-US93-08849-88/c
; Sequence 88, Application PC/TUS9308849
; GENERAL INFORMATION:
; APPLICANT: Tsarev, Sergei A., Emerson,
; APPLICANT: Suzanne U., Purcell, Robert H.
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & PINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08849
; FILING DATE: 17-SEP-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/947,263
; FILING DATE: 18-SEP-1992
; NAME:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bork, Richard, W.
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
PCT-US93-08849-88
```

```

Query Match          66.7%; Score 12; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      7 CCGGATCCAGGC 18
        |||||
        20 CCGGATCCAGGC 9
```

```

RESULT 13
US-08-474-140-3/c
; Sequence 3, Application US/08474140
; Patent No. 5721127
; GENERAL INFORMATION:
; APPLICANT: DEMEER, PHILIPPE
; APPLICANT: AMORY, ANTOINE
; TITLE OF INVENTION: PULULANASE, MICROORGANISMS WHICH
; TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION OF THIS
; TITLE OF INVENTION: PULULANASE AND THE USES THEREOF
```


NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K Street, N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,140
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: William F. Gaddano, Esq.
REGISTRATION NUMBER: 37,136
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid (other);
US-08-474-140-3
Query Match 65.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 CTGCGCCCGGATCCA 15
Db 16 CTGCGCCGAGAGCA 2
RESULT 14
US-08-477-630-3/c
Sequence 3, Application US/08477630
Patent No. 5721128
GENERAL INFORMATION:
APPLICANT: DEMER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULULANASE, MICROORGANISMS WHICH
PRODUCE IT, PROCESSES FOR THE PREPARATION OF THIS
TITLE OF INVENTION: PULULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K Street, N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,630
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: William F. Gaddano, Esq.

REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-42
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid (other);
US-08-477-630-3
Query Match 65.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 CTGCGCCCGGATCCA 15
Db 16 CTGCGCCGAGAGCA 2
RESULT 15
US-08-472-293-3/c
Sequence 3, Application US/08472293
Patent No. 5731174
GENERAL INFORMATION:
APPLICANT: DEMER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULULANASE, MICROORGANISMS WHICH
PRODUCE IT, PROCESSES FOR THE PREPARATION OF THIS
TITLE OF INVENTION: PULULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K Street, N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,293
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: William F. Gaddano, Esq.
REGISTRATION NUMBER: 37,136
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid (other);
US-08-472-293-3
Query Match 65.6%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCGCCCGGATCCA 15
 DB 16 CTGCGCCGAGAGCCA 2

RESULT 16

US-08-474-545-3/C
 ; Sequence 3, Application US/08474545
 ; Patent No. 5736375
 ; GENERAL INFORMATION:
 ; APPLICANT: DEMEER, PHILIPPE
 ; APPLICANT: AMORY, ANTOINE
 ; TITLE OF INVENTION: PULULANASE, MICROORGANISMS WHICH
 ; TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION OF THIS
 ; TITLE OF INVENTION: PULULANASE AND THE USES THEREOF
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
 ; STREET: 2000 K Street, N.W., Suite 200
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/474,545
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Wilhem F. Gadiano, Esq.
 ; REGISTRATION NUMBER: 37,136
 ; REFERENCE/DOCKET NUMBER: 4121-43
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 429-0625
 ; TELEFAX: (202) 293-1850
 ; TELEX: 650 383-5605
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 18 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: nucleic acid (other);
 ; DESCRIPTION: synthetic DNA
 ; US-08-474-545-3

Query Match 65.6%; Score 11.8; DB 1; Length 18;
 Best Local Similarity 86.7%; Pred. No. 4.7e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCGCCCGGATCCA 15
 DB 16 CTGCGCCGAGAGCCA 2

RESULT 17
 US-08-478-341-3/C
 ; Sequence 3, Application US/08478341
 ; Patent No. 5817498
 ; GENERAL INFORMATION:
 ; APPLICANT: DEMEER, PHILIPPE
 ; APPLICANT: AMORY, ANTOINE
 ; TITLE OF INVENTION: PULULANASE, MICROORGANISMS WHICH
 ; TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION OF THIS
 ; TITLE OF INVENTION: PULULANASE AND THE USES THEREOF
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.

STREET: 2000 K Street, N.W., Suite 200
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/478,341
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Wilhem F. Gadiano, Esq.
 ; REGISTRATION NUMBER: 37,136
 ; REFERENCE/DOCKET NUMBER: 4121-45
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 429-0625
 ; TELEFAX: (202) 293-1850
 ; TELEX: 650 383-5605
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 18 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: nucleic acid (other);
 ; DESCRIPTION: synthetic DNA
 ; US-08-478-341-3

Query Match 65.6%; Score 11.8; DB 1; Length 18;
 Best Local Similarity 86.7%; Pred. No. 4.7e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCGCCCGGATCCA 15
 DB 16 CTGCGCCGAGAGCCA 2

RESULT 18
 US-08-996-733-3/C
 ; Sequence 3, Application US/08996733
 ; Patent No. 6074854
 ; GENERAL INFORMATION:
 ; APPLICANT: DEMEER, PHILIPPE
 ; APPLICANT: AMORY, ANTOINE
 ; TITLE OF INVENTION: PULULANASE, MICROORGANISMS WHICH
 ; TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION OF THIS
 ; TITLE OF INVENTION: PULULANASE AND THE USES THEREOF
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genecor International, Inc.
 ; STREET: 925 Page Mill Road
 ; CITY: Palo Alto,
 ; STATE: CA
 ; COUNTRY: U.S.A.
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/996,733
 ; FILING DATE: 23-DEC-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/472,293
 ; FILING DATE: 07-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/174,893
 ; FILING DATE: 28-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: BE 09301278
FILING DATE: 19-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BE 09300744
FILING DATE: 15-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BE 09201156
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Debra J. Gaiaster, Esq.
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC446C1-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 846-7620
TELEFAX: (650) 845-6504
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid (other);
DESCRIPTION: synthetic DNA
US-08-996-733-3

Query Match 65.6%; Score 11.8; DB 3; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGCGCCCGGATCCA 15
Db 16 CTGCGCCGAGAGCCA 2.

RESULT 19
US-08-275-526C-17/c
Sequence 17, Application US/08275526C
Patent No. 6180382
GENERAL INFORMATION:
APPLICANT: DE BUYL, ERIC
APPLICANT: LAHAYE, ANDR E
APPLICANT: LEDOUX, PIERRE
APPLICANT: AMORY, ANTOINE
APPLICANT: DETROZ, REN
APPLICANT: ANDRE, CHRISTOPHE
TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
TITLE OF INVENTION: EXPRESSION VECTORS FOR SUCH XYLANASE AND
TITLE OF INVENTION: OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
TITLE OF INVENTION: USE THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/275.526C
FILING DATE: 15-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gagliano, Wilhlem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-49
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-0625
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid (synthetic oligonucleotide)
US-08-275-526C-17

Query Match 65.6%; Score 11.8; DB 4; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGCGCCCGGATCCA 15
Db 16 CTGCGCCGAGAGCCA 2

RESULT 20
US-09-076-677-17/c
Sequence 17, Application US/09076677
Patent No. 6423523
GENERAL INFORMATION:
APPLICANT: DE BUYL, ERIC
APPLICANT: LAHAYE, ANDR E
APPLICANT: LEDOUX, PIERRE
APPLICANT: AMORY, ANTOINE
APPLICANT: DETROZ, REN E
APPLICANT: ANDRE, CHRISTOPHE
TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
TITLE OF INVENTION: EXPRESSION VECTORS FOR SUCH XYLANASE AND
TITLE OF INVENTION: OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
TITLE OF INVENTION: USE THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076.677
FILING DATE: 12-May-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/275.526
FILING DATE: 15-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gagliano, Wilhlem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-0625
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid (synthetic oligonucleotide)
SEQUENCE DESCRIPTION: SEQ ID NO: 17;

US-09-076-677-17

Query Match 65.6%; Score 11.8; DB 4; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCGCGCGGATCCA 15
DB 16 CTGCGCCAGAGCCA 2

RESULT 21

US-09-073-055-17/c
Sequence 17, Application US/09073055
Patent No. 6426211

GENERAL INFORMATION:

APPLICANT: DE BUYL, ERIC
LAHAYE, ANDR E
LEDOUX, PIERRE
AMORY, ANTOINE
DETROZ, REN
ANDRE, CHRISTOPHE
VETTER, ROMAN

TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
EXPRESSION VECTORS FOR SUCH XYLANASE AND
OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
USE THEREOF

NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:

ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.

ZIP: 20006
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/073,055
FILING DATE: 05-May-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/275,526
FILING DATE: 15-JUL-1994
ATTORNEY/AGENT INFORMATION:

NAME: Gagliano, Wilhelm F.

REGISTRATION NUMBER: 37,136

REFERENCE/DOCKET NUMBER: 4121-49

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 429-0625

TELEFAX: (202) 293-0625

TELEX: 650 383 5605

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: nucleic acid (synthetic oligonucleotide)

SEQUENCE DESCRIPTION: SEQ ID NO: 17:

US-09-073-055-17

Query Match 65.6%; Score 11.8; DB 4; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCGCGCGGATCCA 15
DB 16 CTGCGCCAGAGCCA 2

RESULT 22

US-08-425-299A-13
Sequence 13, Application US/08425299A
Patent No. 5726025

GENERAL INFORMATION:

APPLICANT: Kirschner, Marc W.
APPLICANT: King, Randall W.
TITLE OF INVENTION: Assay and Reagents for Detecting Inhibitors
of Ubiquitin-Dependent Degradation of
TITLE OF INVENTION: Cell Cycle Regulatory Proteins
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA

ZIP: 02109
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII(text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/425,299A

FILING DATE: 20-APR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: HMI-014

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-425-299A-13

Query Match 65.6%; Score 11.8; DB 1; Length 24;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGCGCGATCCAG 17
DB 1 GCGCGCGATCCAG 15

RESULT 23

US-08-480-173A-25/c
Sequence 25, Application US/08480173A
Patent No. 6072049

GENERAL INFORMATION:

APPLICANT: Thoma, Hans A

TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: Popovich & Wiles, P.A.

STREET: 80 S. 8th Street, Suite 1902

CITY: Minneapolis

STATE: MN

COUNTRY: USA

ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,173A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Popovich, Thomas E
REGISTRATION NUMBER: 30,099
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-334-8994
TELEFAX: 612-334-8994
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..4
OTHER INFORMATION: /note= "Nucleotides 1-4 form a
OTHER INFORMATION: single-stranded "sticky end"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 5..24
OTHER INFORMATION: /note= "Adapter sequence results
OTHER INFORMATION: from oligonucleotide duplex formation with nucleotides 5-24 c
OTHER INFORMATION: SEQ ID NO: 26"
US-08-480-173A-25

Query Match 65.6%; Score 11.8; DB 3; Length 24;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 2 TGCGCCCGATCCAG 16
24 TGAGCTCGATCCAG 10

RESULT 24
US-08-480-173A-26
Sequence 26, Application US/08480173A
Patent No. 6072049
GENERAL INFORMATION:
APPLICANT: Thoma, Hans A.
TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Popovich & Wiles, P.A.
STREET: 80 S. 8th Street, Suite 1902
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,173A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Popovich, Thomas E
REGISTRATION NUMBER: 30,099
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-334-8994
TELEFAX: 612-334-8994
INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..4
OTHER INFORMATION: /note= "Nucleotides 1-4 form a
OTHER INFORMATION: single-stranded "sticky end"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 5..24
OTHER INFORMATION: /note= "Adapter sequence results
OTHER INFORMATION: from oligonucleotide duplex formation with nucleotides 5-24
OTHER INFORMATION: SEQ ID NO: 25"
US-08-480-173A-26

Query Match 65.6%; Score 11.8; DB 3; Length 24;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 2 TGCGCCCGATCCAG 16
5 TGAGCTCGATCCAG 19

RESULT 25
US-08-484-408A-25/c
Sequence 25, Application US/08484408A
Patent No. 6117653
GENERAL INFORMATION:
APPLICANT: Thoma, Hans A.
TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Popovich & Wiles, P.A.
STREET: 80 S. 8th Street, Suite 1902
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,408A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Popovich, Thomas E
REGISTRATION NUMBER: 30,099
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-334-8994
TELEFAX: 612-334-8994
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..4
OTHER INFORMATION: /note= "Nucleotides 1-4 form a
OTHER INFORMATION: single-stranded "sticky end"
FEATURE:
NAME/KEY: misc_feature

LOCATION: 5..24 /note="Adapter sequence results
OTHER INFORMATION: from oligonucleotide duplex formation with nucleotides 5-24 c
OTHER INFORMATION: SEQ ID NO: 26"
US-08-484-408A-25

Query Match 65.6%; Score 11.8; DB 3; Length 24;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGCCCGGATCCAG 16
DB 24 TGAGCTCGATCCAG 10

RESULT 26
US-08-484-408A-26
Sequence 26, Application US/08484408A
Patent No. 6117653
GENERAL INFORMATION:
APPLICANT: Thoma, Hans A
TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Popovich & Wiles, P.A.
STREET: 80 S. 8th Street, Suite 1902
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,408A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Popovich, Thomas E
REGISTRATION/DOCKET NUMBER: 30,099
REFERENCE/DOCKET NUMBER: MED1003USD4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-334-8991
TELEFAX: 612-334-8994
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..4
OTHER INFORMATION: /note="Nucleotides 1-4 form a
OTHER INFORMATION: single-stranded "sticky end"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 5..24
OTHER INFORMATION: /note="Adapter sequence results
OTHER INFORMATION: from oligonucleotide duplex formation with nucleotides 5-24 c
OTHER INFORMATION: SEQ ID NO: 25"
US-08-484-408A-26

Query Match 65.6%; Score 11.8; DB 3; Length 24;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGCCCGGATCCAG 16
DB 5 TGAGCTCGATCCAG 19

RESULT 27
US-08-318-837-43/c
Sequence 43, Application US/08318837
Patent No. 5981277
GENERAL INFORMATION:
APPLICANT: FRANKEN, LUCIA; DEVOS, KATHLEEN; VAN DE VOORDE,
APPLICANT: ANDRE; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: NEW POLYPEPTIDES AND PEPTIDES, NUCLEIC ACID
TITLE OF INVENTION: CODING FOR THEM, AND THEIR USE IN THE FIELD OF TUMOR THERAPY O
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN AND MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,837
FILING DATE: 13-OCT-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP 93/01022
FILING DATE: 28-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 92,401,231.3
FILING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION/DOCKET NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410,007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
CELL LINE: THP-1
US-08-318-837-43

Query Match 65.6%; Score 11.8; DB 2; Length 25;
Best Local Similarity 86.7%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGCCCGATCCAGGC 18
DB 17 CGCCCTGCTCCAGGC 3

RESULT 28
US-08-602-036A-23/c
Sequence 23, Application US/08602036A
Patent No. 5789248
GENERAL INFORMATION:
APPLICANT: Oestreich, Fodstad
APPLICANT: Hovig, Rivind
APPLICANT: Engedraaten, Olav
APPLICANT: Maelandemo, Gunhild H.

APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,036A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-039CIP
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-602-036A-23

Query Match 64.4%; Score 11.6; DB 1; Length 21;
Best Local Similarity 77.8%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTGCGCCGCGATCCAGGC 18
Db 18 CTGCTCCAGATCCTGAC 1

RESULT 23
US-08-642-407A-23/c
Sequence 23, Application US/08642407A
Patent No. 5677308
GENERAL INFORMATION:
APPLICANT: Oeystein, Fodestad
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,036A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-039CIP
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA

APPLICATION NUMBER: US/08/642,407A
FILING DATE: 03-May-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-039CPDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-642-407A-23

Query Match 64.4%; Score 11.6; DB 2; Length 21;
Best Local Similarity 77.8%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTGCGCCGCGATCCAGGC 18
Db 18 CTGCTCCAGATCCTGAC 1

RESULT 30
US-08-602-036A-3/c
Sequence 3, Application US/08602036A
Patent No. 5789248
GENERAL INFORMATION:
APPLICANT: Oeystein, Fodestad
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,036A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-039CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA

HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-602-036A-3

Query Match 64.4%; Score 11.6; DB 1; Length 22;
Best Local Similarity 77.8%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATCCAGGC 18
18 CTGCTCCAGATCTGAC 1

RESULT 31
US-08-602-036A-4/C
Sequence 4, Application US/08602036A
Patent No. 5789248

GENERAL INFORMATION:
APPLICANT: Ovestein, Podstad
APPLICANT: Hovig, Elvind
APPLICANT: Engestraten, Olav
APPLICANT: Maeldamo, Gunhild H.
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602, 036A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-039CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-602-036A-4

Query Match 64.4%; Score 11.6; DB 1; Length 22;
Best Local Similarity 77.8%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATCCAGGC 18
18 CTGCTCCAGATCTGAC 1

RESULT 32
US-08-502-374A-3/C
Sequence 3, Application US/08502374A
Patent No. 5872007

GENERAL INFORMATION:

APPLICANT: Podstad, Ovestein
APPLICANT: Hovig, Elvind
APPLICANT: Engestraten, Olav
APPLICANT: Maeldamo, Gunhild H.
TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,374A
FILING DATE: 14-Jul-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-039DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-526-6000
TELEFAX: 617-526-5000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-502-374A-3

Query Match 64.4%; Score 11.6; DB 2; Length 22;
Best Local Similarity 77.8%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATCCAGGC 18
18 CTGCTCCAGATCTGAC 1

RESULT 33
US-08-502-374A-4/C
Sequence 4, Application US/08502374A
Patent No. 5872007

GENERAL INFORMATION:
APPLICANT: Podstad, Ovestein
APPLICANT: Hovig, Elvind
APPLICANT: Engestraten, Olav
APPLICANT: Maeldamo, Gunhild H.
TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502.374A
CLASSIFICATION: 514
FILING DATE: 14-Jul-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-039DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-526-6000
TELEFAX: 617-526-5000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-502-374A-4

Query Match 64.4%; Score 11.6; DB 2; Length 22;
Best Local Similarity 77.8%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATCCAGC 18
18 CTGCTCCAGATCTGAC 1

Db 18 CTGCTCCAGATCTGAC 1

RESULT 34
US-08-642-407A-3/C
Sequence 3, Application US/08642407A
Patent No. 5877308
GENERAL INFORMATION:
APPLICANT: Oeystein, Fodstad
APPLICANT: Hovig, Elvind
APPLICANT: Engbraaten, Olav
APPLICANT: Maelandemo, Gunhild H.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642.407A
CLASSIFICATION: 514
FILING DATE: 03-May-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-039CPDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-642-407A-3

Query Match 64.4%; Score 11.6; DB 2; Length 22;
Best Local Similarity 77.8%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATCCAGC 18
18 CTGCTCCAGATCTGAC 1

Db 18 CTGCTCCAGATCTGAC 1

RESULT 35
US-08-642-407A-4/C
Sequence 4, Application US/08642407A
Patent No. 5877308
GENERAL INFORMATION:
APPLICANT: Oeystein, Fodstad
APPLICANT: Hovig, Elvind
APPLICANT: Engbraaten, Olav
APPLICANT: Maelandemo, Gunhild H.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642.407A
CLASSIFICATION: 514
FILING DATE: 03-May-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-039CPDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-642-407A-4

Query Match 64.4%; Score 11.6; DB 2; Length 22;
Best Local Similarity 77.8%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTGCGCCCGATCCAGC 18
18 CTGCTCCAGATCTGAC 1

Db 18 CTGCTCCAGATCTGAC 1

RESULT 36
US-09-428-583-17/c
; Sequence 17, Application US/09428583
; Patent No. 6271029
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowest
; TITLE OF INVENTION: ANTISENSE MODULATION OF CYTOSIN-2 EXPRESSION
; FILE REFERENCE: R1S-0096
; CURRENT APPLICATION NUMBER: US/09/428,583
; CURRENT FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-428-583-17
Query Match 63.3%; Score 11.4; DB 4; Length 20;
Best Local Similarity 92.3%; Pred. No. 7.2e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 CCGGATCCAGC 18
DB 16 CCGGATCCAGC 4
RESULT 37
US-08-585-595-35/c
; Sequence 35, Application US/08585595
; Patent No. 5795761
; GENERAL INFORMATION:
; APPLICANT: POWERS, DAVID B.
; APPLICANT: ANDERSON, STEPHEN
; TITLE OF INVENTION: IMPROVED METHODS FOR PRODUCING VITAMIN C
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585,595
; FILING DATE: 16-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/584,019
; FILING DATE: 11-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: AUBERACH, JEFFREY I.
; REGISTRATION NUMBER: 32680
; REFERENCE/DOCKET NUMBER: 6137-0014 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: CORYNEBACTERIUM SP
US-08-585-595-35
Query Match 63.3%; Score 11.4; DB 1; Length 22;
Best Local Similarity 92.3%; Pred. No. 7.1e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTGCGCCCGATC 13
DB 13 CCGGCGCCCGATC 1
RESULT 38
US-09-142-623-20/c
; Sequence 20, Application US/09142623
; Patent No. 6337201
; GENERAL INFORMATION:
; APPLICANT: KOJI YAMAI et al.
; TITLE OF INVENTION: -FRUCTOFURANOSIDASE AND ITS GENE, METHOD OF
; TITLE OF INVENTION: ISOLATING -FRUCTOFURANOSIDASE GENE, SYSTEM FOR PRODUCING
; TITLE OF INVENTION: -FRUCTOFURANOSIDASE, AND -FRUCTOFURANOSIDASE VARIANT
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Menderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/142,623
; FILING DATE: September 10, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee Cheng
; REGISTRATION NUMBER: 40,949
; REFERENCE/DOCKET NUMBER: 98-0989*/LC (WMC)/144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8250
; TELEFAX: 202-721-8250
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: No. 6337201 relevant
; TOPOLOGY: Linear
; MOLECULE TYPE: Synthetic DNA
US-09-142-623-20
Query Match 63.3%; Score 11.4; DB 4; Length 22;
Best Local Similarity 92.3%; Pred. No. 7.1e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 GCCCGATCCAGG 17
DB 16 GCCCGATCCAGG 4
RESULT 39
US-08-244-122-25/c
; Sequence 25, Application US/08244122
; Patent No. 5665777
; GENERAL INFORMATION:
; APPLICANT: Sijmons, Peter J.

APPLICANT: Goddijn, Oscar J.M.
APPLICANT: Van Den Elzen, Petrus J. M.
APPLICANT: Van Der Lee, Frederique M.
TITLE OF INVENTION: Method for Obtaining Plants with
NUMBER OF SEQUENCES: Reduced Susceptibility to Plant-Parasitic Nematodes
CORRESPONDENCE ADDRESS: 31
ADDRESSEE: Ladas & Parry
STREET: 26 West 61st Street
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10023
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM PC/XT/AT or compatibles
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,122
FILING DATE: 19-MAY-1994
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: PCT/EP92/02559
FILING DATE: 02-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL91203041
FILING DATE: 20-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL9200046
FILING DATE: 10-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: MASS, CLIFFORD, J.
REGISTRATION NUMBER: 30086
REFERENCE/DOCKET NUMBER: U-9672-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 708-1800
TELEFAX: (212) 246-8959
TELEX: 233288
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
HYPOTHETICAL: YES
US-08-244-122-25
Query Match 63.3%; Score 11.4; DB 2; Length 24;
Best Local Similarity 92.3%; Pred. No. 7.1e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 5 GCCCGATCCAG 17
Db 14 GTCCGATCCAG 2
RESULT 40
US-08-679-645-531
Sequence 531. Application US/08679645
Patent No. 6350934
GENERAL INFORMATION:
APPLICANT: Zwick, Michael G.
APPLICANT: Edington, Brent E.
APPLICANT: McSwigen, James A.
APPLICANT: Merlo, Patricia Ann Owens
APPLICANT: Guo, Lining
APPLICANT: Skokut, Thomas A.
APPLICANT: Young, Scott A.
APPLICANT: Folkerts, Otto
APPLICANT: Merlo, Donald J.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR

TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
TITLE OF INVENTION: IN PLANTS
NUMBER OF SEQUENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,645
FILING DATE: July 12, 1996
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: 60/001,135
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 531:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-679-645-531
Query Match 62.2%; Score 11.2; DB 4; Length 16;
Best Local Similarity 68.8%; Pred. No. 8.9e+03;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Oy 1 CTGCGCCGATCCAG 16
Db 1 CUGCGGCTCCUACCCAG 16
Search completed: June 7, 2003, 09:45:39
Job time : 47.9636 secs